

```

tct gct acc act gtc gat gct gaa gtc atc gcc gct gcc cct aac ttg 307
Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala Ala Ala Pro Asn Leu
    55                      60                      65

aag atc gtc ggt cgt gcc ggc gtg ggc ttg gac aac gtt gac atc cct 355
Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp Asn Val Asp Ile Pro
    70                      75                      80                      85

gct gcc act gaa gct ggc gtc atg gtt gct aac gca ccg acc tct aat 403
Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn Ala Pro Thr Ser Asn
                      90                      95                      100

att cac tcc gct tgt gag cac gca att tct ttg ctg ctg tct act gct 451
Ile His Ser Ala Cys Glu His Ala Ile Ser Leu Leu Leu Ser Thr Ala
    105                      110                      115

cgc cag atc ctg ctg ctg atg cga cgc tgc gtg agg gcg agt gga agc 499
Arg Gln Ile Leu Leu Leu Met Arg Arg Cys Val Arg Ala Ser Gly Ser
    120                      125                      130

ggg ctt ctt tca acg gtg tgg aaa ttt tgc gaa aaa ctg tgc gta tgc 547
Gly Leu Leu Ser Thr Val Trp Lys Phe Ser Glu Lys Leu Ser Val Ser
    135                      140                      145

tcg gtt ttg gcc aca ttg gtc agt tgt ttg ctc agc gtc ttg ctg cgt 595
Ser Val Leu Ala Thr Leu Val Ser Cys Leu Leu Ser Val Leu Leu Arg
    150                      155                      160                      165

ttg aga cca cca ttg ttg ctt acg atc ctt acg cta acc ctg ctt cgt 643
Leu Arg Pro Pro Leu Leu Leu Thr Ile Leu Thr Leu Thr Leu Leu Arg
    170                      175                      180

gcg ggt
Ala Gly
649

```

<210> 152  
 <211> 183  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

```

<400> 152
Val Ser Gln Asn Gly Arg Pro Val Val Leu Ile Ala Asp Lys Leu Ala
    1                      5                      10                      15

Gln Ser Thr Val Asp Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val
    20                      25                      30

Asp Gly Pro Asn Arg Pro Glu Leu Leu Asp Ala Val Lys Glu Ala Asp
    35                      40                      45

Ala Leu Leu Val Arg Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala
    50                      55                      60

Ala Ala Pro Asn Leu Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp
    65                      70                      75                      80

Asn Val Asp Ile Pro Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn
    85                      90                      95

```

Ala Pro Thr Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ser Leu  
 100 105 110

Leu Leu Ser Thr Ala Arg Gln Ile Leu Leu Leu Met Arg Arg Cys Val  
 115 120 125

Arg Ala Ser Gly Ser Gly Leu Leu Ser Thr Val Trp Lys Phe Ser Glu  
 130 135 140

Lys Leu Ser Val Ser Ser Val Leu Ala Thr Leu Val Ser Cys Leu Leu  
 145 150 155 160

Ser Val Leu Leu Arg Leu Arg Pro Pro Leu Leu Leu Thr Ile Leu Thr  
 165 170 175

Leu Thr Leu Leu Arg Ala Gly  
 180

<210> 153  
 <211> 1011  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(988)  
 <223> RXN00871

<400> 153  
 gggaaaaggc gatcaccagc cggtggctcg acccagcaac ccacggtggc attaacctcg 60

gtttcccaca gaacgattaa ttgaaggaga gcacaggact atg cgt tgg ttc cat 115  
 Met Arg Trp Phe His  
 1 5

aag aag ggc gaa ctg gcc cga gat ggt tgg caa agc gtt gtc gat gcc 163  
 Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln Ser Val Val Asp Ala  
 10 15 20

acc acc cca ggt tgg gaa tat acc ggc atc cgc att gcc gaa ctg ggc 211  
 Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg Ile Ala Glu Leu Gly  
 25 30 35

agt ggt gaa tcg ctt gaa ctg aat gac act ggt gtg gaa cgc atc ttc 259  
 Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly Val Glu Arg Ile Phe  
 40 45 50

att cca ctt cag ggc agc ttc gat gtt gcc cac cat ggt cag gtg acc 307  
 Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His His Gly Gln Val Thr  
 55 60 65

cat ctt cac gga aga aag tca gtc ttt gat gga cca acc gat gtg ctc 355  
 His Leu His Gly Arg Lys Ser Val Phe Asp Gly Pro Thr Asp Val Leu  
 70 75 80 85

tac ctc ccc act gga caa aca gca acg ctc agt ggt cag gga cga gtc 403  
 Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser Gly Gln Gly Arg Val  
 90 95 100

gcc gtg gcg gaa gct ccc act cag gaa ccc aag gag tgg aag tac atc 451



Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys Glu Trp Lys Tyr Ile  
105 110 115

gct cca gca gaa act cct gtg gag ttg cgt gga gct ggc cgc tcg agc 499  
Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly Ala Gly Arg Ser Ser  
120 125 130

cga caa gtc cac aac ttt ggc acc ccg gaa gct ctc gat gct gct cga 547  
Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala Leu Asp Ala Ala Arg  
135 140 145

cta atc gtg tgt gaa gta atc acc cca ggt gaa aac tgg agc tct tac 595  
Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu Asn Trp Ser Ser Tyr  
150 155 160 165

cct cca cac aag cat gat gag cac atc cca gga cac gag tcc aag ctg 643  
Pro Pro His Lys His Asp Glu His Ile Pro Gly His Glu Ser Lys Leu  
170 175 180

gag gaa atc tac tac ttc gaa agc gcc cca tcg cga gtt ggt ggc agg 691  
Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser Arg Val Gly Gly Arg  
185 190 195

gcc gaa gca gca gaa gga gct ttc gga atg ttt tcc acc tac tcc tca 739  
Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe Ser Thr Tyr Ser Ser  
200 205 210

cca gcg ggg gag atc gat atc aac gcc atg gtg tac agc ggc gat atc 787  
Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val Tyr Ser Gly Asp Ile  
215 220 225

gcg cta gtt cct ttc gga tac cac ggc cct gcc gtg gca gca cct ggc 835  
Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala Val Ala Ala Pro Gly  
230 235 240 245

tat gac ttg tac tac ctc aac gtc atg gca gga cct gat ccg gag aga 883  
Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly Pro Asp Pro Glu Arg  
250 255 260

atc tgg ctg att aac gat gac cca gcg cac gcc tgg gtt cga gat aca 931  
Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala Trp Val Arg Asp Thr  
265 270 275

tgg acc ggg caa gca ttt gat gat cgc ttg cca tat gag aac gca aac 979  
Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro Tyr Glu Asn Ala Asn  
280 285 290

aag gag gga taaaatttca tggctgaaac gaa 1011  
Lys Glu Gly  
295

&lt;210&gt; 154

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 154

Met Arg Trp Phe His Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln  
1 5 10 15

Ser Val Val Asp Ala Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg  
                   20                  25                  30  
 Ile Ala Glu Leu Gly Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly  
                   35                  40                  45  
 Val Glu Arg Ile Phe Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His  
                   50                  55                  60  
 His Gly Gln Val Thr His Leu His Gly Arg Lys Ser Val Phe Asp Gly  
                   65                  70                  75                  80  
 Pro Thr Asp Val Leu Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser  
                   85                  90                  95  
 Gly Gln Gly Arg Val Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys  
                   100                  105                  110  
 Glu Trp Lys Tyr Ile Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly  
                   115                  120                  125  
 Ala Gly Arg Ser Ser Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala  
                   130                  135                  140  
 Leu Asp Ala Ala Arg Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu  
                   145                  150                  155                  160  
 Asn Trp Ser Ser Tyr Pro Pro His Lys His Asp Glu His Ile Pro Gly  
                   165                  170                  175  
 His Glu Ser Lys Leu Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser  
                   180                  185                  190  
 Arg Val Gly Gly Arg Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe  
                   195                  200                  205  
 Ser Thr Tyr Ser Ser Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val  
                   210                  215                  220  
 Tyr Ser Gly Asp Ile Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala  
                   225                  230                  235                  240  
 Val Ala Ala Pro Gly Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly  
                   245                  250                  255  
 Pro Asp Pro Glu Arg Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala  
                   260                  265                  270  
 Trp Val Arg Asp Thr Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro  
                   275                  280                  285  
 Tyr Glu Asn Ala Asn Lys Glu Gly  
                   290                  295

&lt;210&gt; 155

&lt;211&gt; 964

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(964)

&lt;223&gt; FRXA00871

&lt;400&gt; 155

```

gggaaaaggc gatcaccagc cgttggtctcg acccagcaac ccacggtggc attaacctcg 60

gtttcccaca gaacgattaa ttgaaggaga gcacaggact atg cgt tgg ttc cat 115
                                         Met Arg Trp Phe His
                                         1                               5

aag aag ggc gaa ctg gcc cga gat ggt tgg caa agc gtt gtc gat gcc 163
Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln Ser Val Val Asp Ala
                        10                               15                               20

acc acc cca ggt tgg gaa tat acc ggc atc cgc att gcc gaa ctg ggc 211
Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg Ile Ala Glu Leu Gly
                        25                               30                               35

agt ggt gaa tcg ctt gaa ctg aat gac act ggt gtg gaa cgc atc ttc 259
Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly Val Glu Arg Ile Phe
                        40                               45                               50

att cca ctt cag ggc agc ttc gat gtt gcc cac cat ggt cag gtg acc 307
Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His His Gly Gln Val Thr
                        55                               60                               65

cat ctt cac gga aga aag tca gtc ttt gat gga cca acc gat gtg ctc 355
His Leu His Gly Arg Lys Ser Val Phe Asp Gly Pro Thr Asp Val Leu
                        70                               75                               80                               85

tac ctc ccc act gga caa aca gca acg ctc agt ggt cag gga cga gtc 403
Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser Gly Gln Gly Arg Val
                        90                               95                               100

gcc gtg gcg gaa gct ccc act cag gaa ccc aag gag tgg aag tac atc 451
Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys Glu Trp Lys Tyr Ile
                        105                               110                               115

gct cca gca gaa act cct gtg gag ttg cgt gga gct ggc cgc tcg agc 499
Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly Ala Gly Arg Ser Ser
                        120                               125                               130

cga caa gtc cac aac ttt ggc acc ccg gaa gct ctc gat gct gct cga 547
Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala Leu Asp Ala Ala Arg
                        135                               140                               145

cta atc gtg tgt gaa gta atc acc cca ggt gaa aac tgg agc tct tac 595
Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu Asn Trp Ser Ser Tyr
                        150                               155                               160                               165

cct cca cac aag cat gat gag cac atc cca gga cac gag tcc aag ctg 643
Pro Pro His Lys His Asp Glu His Ile Pro Gly His Glu Ser Lys Leu
                        170                               175                               180

gag gaa atc tac tac ttc gaa agc gcc cca tcg cga gtt ggt ggc agg 691
Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser Arg Val Gly Gly Arg
                        185                               190                               195

gcc gaa gca gca gaa gga gct ttc gga atg ttt tcc acc tac tcc tca 739
Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe Ser Thr Tyr Ser Ser

```

200	205	210	
cca gcg ggg gag atc gat	atc aac gcc atg gtg tac	agc ggc gat atc	787
Pro Ala Gly Glu Ile Asp	Ile Asn Ala Met Val Tyr	Ser Gly Asp Ile	
215	220	225	
gcg cta gtt cct ttc gga	tac cac ggc cct gcc	gtg gca gca cct ggc	835
Ala Leu Val Pro Phe Gly	Tyr His Gly Pro Ala	Val Ala Ala Pro Gly	
230	235	240 245	
tat gac ttg tac tac ctc	aac gtc atg gca gga	cct gat ccg gag aga	883
Tyr Asp Leu Tyr Tyr Leu	Asn Val Met Ala Gly	Pro Asp Pro Glu Arg	
250	255	260	
atc tgg ctg att aac gat	gac cca gcg cac gcc	tgg gtt cga gat aca	931
Ile Trp Leu Ile Asn Asp	Asp Pro Ala His Ala	Trp Val Arg Asp Thr	
265	270	275	
tgg acc ggg caa gca ttt	gat gat cgc ttg cca		964
Trp Thr Gly Gln Ala Phe	Asp Asp Arg Leu Pro		
280	285		

&lt;210&gt; 156

&lt;211&gt; 288

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 156

Met Arg Trp Phe His Lys	Lys Gly Glu Leu Ala Arg	Asp Gly Trp Gln
1	5	10 15

Ser Val Val Asp Ala Thr	Thr Pro Gly Trp Glu Tyr	Thr Gly Ile Arg
20	25	30

Ile Ala Glu Leu Gly Ser	Gly Glu Ser Leu Glu Leu	Asn Asp Thr Gly
35	40	45

Val Glu Arg Ile Phe Ile	Pro Leu Gln Gly Ser	Phe Asp Val Ala His
50	55	60

His Gly Gln Val Thr His	Leu His Gly Arg Lys	Ser Val Phe Asp Gly
65	70	75 80

Pro Thr Asp Val Leu Tyr	Leu Pro Thr Gly Gln Thr	Ala Thr Leu Ser
85	90	95

Gly Gln Gly Arg Val Ala	Val Ala Glu Ala Pro Thr	Gln Glu Pro Lys
100	105	110

Glu Trp Lys Tyr Ile Ala	Pro Ala Glu Thr Pro Val	Glu Leu Arg Gly
115	120	125

Ala Gly Arg Ser Ser Arg	Gln Val His Asn Phe	Gly Thr Pro Glu Ala
130	135	140

Leu Asp Ala Ala Arg Leu	Ile Val Cys Glu Val Ile	Thr Pro Gly Glu
145	150	155 160

Asn Trp Ser Ser Tyr Pro	Pro His Lys His Asp	Glu His Ile Pro Gly
165	170	175

His Glu Ser Lys Leu Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser  
 180 185 190

Arg Val Gly Gly Arg Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe  
 195 200 205

Ser Thr Tyr Ser Ser Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val  
 210 215 220

Tyr Ser Gly Asp Ile Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala  
 225 230 235 240

Val Ala Ala Pro Gly Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly  
 245 250 255

Pro Asp Pro Glu Arg Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala  
 260 265 270

Trp Val Arg Asp Thr Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro  
 275 280 285

<210> 157  
 <211> 373  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(373)  
 <223> RXN02829

<400> 157  
 tttttcggtt aatctcatat ttaaacacgt tccttttaaat tgggtttata aattgataaa 60

ctgaattcgt cagttaaagt gtatcgaaag gagactggac atg caa aaa aat att 115  
 Met Gln Lys Asn Ile  
 1 5

cta aaa agt ggc atc gaa att tct gaa ctt ggg tta ggt tgc atg agt 163  
 Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly Leu Gly Cys Met Ser  
 10 15 20

tta ggc aca gat tat aaa aaa gcg caa cca att att gaa agt gca att 211  
 Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile Ile Glu Ser Ala Ile  
 25 30 35

gat aat ggt att acg tat ttt gat act gca gat att tac gat caa gga 259  
 Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp Ile Tyr Asp Gln Gly  
 40 45 50

gtt aat gaa gaa att gtt ggt aaa gcc tta aaa aaa tat caa aat cgt 307  
 Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys Lys Tyr Gln Asn Arg  
 55 60 65

gat gac atc gtt atc gga act aaa gtt gga aat cga tta act gac gat 355  
 Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn Arg Leu Thr Asp Asp

70 75 80 85 373  
 gga cat atg acg tgg gat  
 Gly His Met Thr Trp Asp  
 90

<210> 158  
 <211> 91  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 158  
 Met Gln Lys Asn Ile Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly  
 1 5 10 15  
 Leu Gly Cys Met Ser Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile  
 20 25 30  
 Ile Glu Ser Ala Ile Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp  
 35 40 45  
 Ile Tyr Asp Gln Gly Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys  
 50 55 60  
 Lys Tyr Gln Asn Arg Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn  
 65 70 75 80  
 Arg Leu Thr Asp Asp Gly His Met Thr Trp Asp  
 85 90

<210> 159  
 <211> 376  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(376)  
 <223> FRXA02829

<400> 159  
 tttttcgttt aatctcatat ttaaacacgt tccttttaat tggttttata aattgataaa 60  
 ctgaattcgt cagttaaagt gtatcgaaag gagactggac atg caa aaa aat att 115  
 Met Gln Lys Asn Ile  
 1 5  
 cta aaa agt ggc atc gaa att tct gaa ctt ggg tta ggt tgc atg agt 163  
 Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly Leu Gly Cys Met Ser  
 10 15 20  
 tta ggc aca gat tat aaa aaa gcg caa cca att att gaa agt gca att 211  
 Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile Ile Glu Ser Ala Ile  
 25 30 35  
 gat aat ggt att acg tat ttt gat act gca gat att tac gat caa gga 259  
 Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp Ile Tyr Asp Gln Gly  
 40 45 50

ggt aat gaa gaa att gtt ggt aaa gcc tta aaa aaa tat caa aat cgt 307  
Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys Lys Tyr Gln Asn Arg  
55 60 65

gat gac atc gtt atc gga act aaa gtt gga aat cga tta act gac gat 355  
Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn Arg Leu Thr Asp Asp  
70 75 80 85

gga cat atg acg tgg gga tcc 376  
Gly His Met Thr Trp Gly Ser  
90

```
<210> 160
<211> 92
<212> PRT
<213> Corynebacterium glutamicum
```

```

<400> 160
Met Gln Lys Asn Ile Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly
  1             5             10             15
Leu Gly Cys Met Ser Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile
          20             25             30
Ile Glu Ser Ala Ile Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp
          35             40             45
Ile Tyr Asp Gln Gly Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys
          50             55             60
Lys Tyr Gln Asn Arg Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn
          65             70             75             80
Arg Leu Thr Asp Asp Gly His Met Thr Trp Gly Ser
          85             90

```

```
<210> 161
<211> 948
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(925)  
<223> RXN01468
```

```

<400> 161
tgccaaggat ttgaccaccg tgcaggattt gattgacttt attaacacca ataaggctga 60

ttagcgggaa aatttcgccc aaaacaggga caatggtggt atg aca gtg aac att 115
                                         Met Thr Val Asn Ile
                                         1                               5

tca tat ctg acc gac atg gac ggc gtc ctc atc aaa gag ggc gag ata 163
Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile Lys Glu Gly Glu Ile
                        10                               15                               20

att ccg ggt gca gat cgt ttt ctt cag tct ctc acc gat aac aat gtg 211
Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu Thr Asp Asn Asn Val

```

25						30						35						
gag	ttt	atg	gtt	ttg	acc	aac	aac	tcc	att	ttc	acc	ccg	agg	gat	ctt	259		
Glu	Phe	Met	Val	Leu	Thr	Asn	Asn	Ser	Ile	Phe	Thr	Pro	Arg	Asp	Leu			
40						45						50						
tct	gca	cgt	ctt	aag	act	tcc	ggg	ttg	gat	atc	ccg	ccg	gag	cgt	att	307		
Ser	Ala	Arg	Leu	Lys	Thr	Ser	Gly	Leu	Asp	Ile	Pro	Pro	Glu	Arg	Ile			
55						60						65						
tgg	act	tct	gca	acc	gcc	act	gct	cac	ttc	ctg	aaa	tcc	cag	gtc	aag	355		
Trp	Thr	Ser	Ala	Thr	Ala	Thr	Ala	His	Phe	Leu	Lys	Ser	Gln	Val	Lys			
70						75						80			85			
gag	ggc	aca	gcc	tat	gtt	gtt	ggc	gag	tcc	ggg	ctg	acc	act	gcg	ttg	403		
Glu	Gly	Thr	Ala	Tyr	Val	Val	Gly	Glu	Ser	Gly	Leu	Thr	Thr	Ala	Leu			
			90						95						100			
cat	acc	gcg	ggg	ttg	att	ttg	acg	gat	gca	aat	cct	gag	ttt	gtt	gtc	451		
His	Thr	Ala	Gly	Trp	Ile	Leu	Thr	Asp	Ala	Asn	Pro	Glu	Phe	Val	Val			
			105						110						115			
ctg	ggc	gaa	acc	cgc	aca	tat	tcc	ttc	gag	gca	atc	act	act	gcg	ata	499		
Leu	Gly	Glu	Thr	Arg	Thr	Tyr	Ser	Phe	Glu	Ala	Ile	Thr	Thr	Ala	Ile			
			120						125						130			
aat	ctg	att	ttg	ggg	ggc	gct	cgc	ttt	att	tgc	acc	aac	ccg	gat	gtc	547		
Asn	Leu	Ile	Leu	Gly	Gly	Ala	Arg	Phe	Ile	Cys	Thr	Asn	Pro	Asp	Val			
135						140						145						
act	gga	cct	tca	cca	agt	ggc	att	ttg	cct	gct	act	ggc	tct	gtc	gcc	595		
Thr	Gly	Pro	Ser	Pro	Ser	Gly	Ile	Leu	Pro	Ala	Thr	Gly	Ser	Val	Ala			
150						155						160			165			
gca	ctt	att	acc	gca	gct	act	ggc	gct	gag	cct	tat	tac	atc	ggc	aag	643		
Ala	Leu	Ile	Thr	Ala	Ala	Thr	Gly	Ala	Glu	Pro	Tyr	Tyr	Ile	Gly	Lys			
			170						175						180			
cca	aac	cct	gtg	atg	atg	cgc	agt	gcg	ctg	aac	acc	atc	ggg	gcg	cat	691		
Pro	Asn	Pro	Val	Met	Met	Arg	Ser	Ala	Leu	Asn	Thr	Ile	Gly	Ala	His			
			185						190						195			
tcc	gag	cac	act	gtc	atg	atc	ggc	gac	cgc	atg	gac	acc	gac	gtg	aaa	739		
Ser	Glu	His	Thr	Val	Met	Ile	Gly	Asp	Arg	Met	Asp	Thr	Asp	Val	Lys			
200						205						210						
tct	ggg	ttg	gaa	gcc	ggc	ctg	agc	acc	gtg	ctg	gtt	cga	agc	gga	att	787		
Ser	Gly	Leu	Glu	Ala	Gly	Leu	Ser	Thr	Val	Leu	Val	Arg	Ser	Gly	Ile			
215						220						225						
tcc	gac	gac	gcc	gag	atc	cgc	cgc	tac	ccc	ttc	cgc	cca	act	cac	gtg	835		
Ser	Asp	Asp	Ala	Glu	Ile	Arg	Arg	Tyr	Pro	Phe	Arg	Pro	Thr	His	Val			
230						235						240			245			
atc	aat	tcc	atc	gcc	gat	ctt	gcc	gat	tgc	tgg	gac	gat	cct	ttc	ggg	883		
Ile	Asn	Ser	Ile	Ala	Asp													



tagtattctg taggtcatgg cat

948

&lt;210&gt; 162

&lt;211&gt; 275

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 162

Met Thr Val Asn Ile Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile  
 1 5 10 15

Lys Glu Gly Glu Ile Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu  
 20 25 30

Thr Asp Asn Asn Val Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe  
 35 40 45

Thr Pro Arg Asp Leu Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile  
 50 55 60

Pro Pro Glu Arg Ile Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu  
 65 70 75 80

Lys Ser Gln Val Lys Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly  
 85 90 95

Leu Thr Thr Ala Leu His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn  
 100 105 110

Pro Glu Phe Val Val Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala  
 115 120 125

Ile Thr Thr Ala Ile Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys  
 130 135 140

Thr Asn Pro Asp Val Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala  
 145 150 155 160

Thr Gly Ser Val Ala Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro  
 165 170 175

Tyr Tyr Ile Gly Lys Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn  
 180 185 190

Thr Ile Gly Ala His Ser Glu His Thr Val Met Ile Gly Asp Arg Met  
 195 200 205

Asp Thr Asp Val Lys Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu  
 210 215 220

Val Arg Ser Gly Ile Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe  
 225 230 235 240

Arg Pro Thr His Val Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp  
 245 250 255

Asp Asp Pro Phe Gly Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln  
 260 265 270

Phe Thr Asp  
275

<210> 163  
<211> 948  
<212> DNA  
<213> *Corynebacterium glutamicum*

<220>  
<221> CDS  
<222> (101)..(925)  
<223> FRXA01468

<400> 163  
tgccaaggat ttgaccaccg tgcaggattt gattgacttt attaacacca ataaggctga 60

ttagcgggaa aatttcgccc aaaacagggg caatggtggt atg aca gtg aac att 115  
Met Thr Val Asn Ile  
1 5

tca tat ctg acc gac atg gac ggc gtc ctc atc aaa gag ggc gag ata 163  
Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile Lys Glu Gly Glu Ile  
10 15 20

att ccg ggt gca gat cgt ttt ctt cag tct ctc acc gat aac aat gtg 211  
Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu Thr Asp Asn Asn Val  
25 30 35

gag ttt atg gtt ttg acc aac aac tcc att ttc acc ccg agg gat ctt 259  
Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe Thr Pro Arg Asp Leu  
40 45 50

tct gca cgt ctt aag act tcc ggt ttg gat atc ccg ccg gag cgt att 307  
Ser Ala Arg Leu Lys Thr Ser Ser Gly Leu Asp Ile Pro Pro Glu Arg Ile  
55 60 65

tgg act tct gca acc gcc act gct cac ttc ctg aaa tcc cag gtc aag 355  
Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu Lys Ser Gln Val Lys  
70 75 80 85

gag ggc aca gcc tat gtt gtt ggc gag tcc ggt ctg acc act gcg ttg 403  
Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly Leu Thr Thr Ala Leu  
90 95 100

cat acc gcg ggt tgg att ttg acg gat gca aat cct gag ttt gtt gtc 451  
His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn Pro Glu Phe Val Val  
105 110 115

ctg ggc gaa acc cgc aca tat tcc ttc gag gca atc act act gcg ata 499  
Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala Ile Thr Thr Ala Ile  
120 125 130

aat ctg att ttg ggt ggc gct cgc ttt att tgc acc aac ccg gat gtc 547  
Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys Thr Asn Pro Asp Val  
135 140 145

act gga cct tca cca agt ggc att ttg cct gct act ggc tct gtc gcc 595  
Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala Thr Gly Ser Val Ala  
150 155 160 165

gca ctt att acc gca gct act ggc gct gag cct tat tac atc ggc aag 643  
 Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro Tyr Tyr Ile Gly Lys  
 170 175 180  
  
 cca aac cct gtg atg atg cgc agt gcg ctg aac acc atc ggg gcg cat 691  
 Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn Thr Ile Gly Ala His  
 185 190 195  
  
 tcc gag cac act gtc atg atc ggc gac cgc atg gac acc gac gtg aaa 739  
 Ser Glu His Thr Val Met Ile Gly Asp Arg Met Asp Thr Asp Val Lys  
 200 205 210  
  
 tct ggt ttg gaa gcc gcc ctg agc acc gtg ctg gtt cga agc gga att 787  
 Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu Val Arg Ser Gly Ile  
 215 220 225  
  
 tcc gac gac gcc gag atc cgc cgc tac ccc ttc cgc cca act cac gtg 835  
 Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe Arg Pro Thr His Val  
 230 235 240 245  
  
 atc aat tcc atc gcc gat ctt gcc gat tgc tgg gac gat cct ttc ggt 883  
 Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp Asp Asp Pro Phe Gly  
 250 255 260  
  
 gac ggt gca ttt cac gta cca gat gag cag cag ttc act gac 925  
 Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln Phe Thr Asp  
 265 270 275  
  
 tagtattctg taggtcatgg cat 948

&lt;210&gt; 164

&lt;211&gt; 275

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 164

Met Thr Val Asn Ile Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile  
 1 5 10 15  
  
 Lys Glu Gly Glu Ile Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu  
 20 25 30  
  
 Thr Asp Asn Asn Val Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe  
 35 40 45  
  
 Thr Pro Arg Asp Leu Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile  
 50 55 60  
  
 Pro Pro Glu Arg Ile Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu  
 65 70 75 80  
  
 Lys Ser Gln Val Lys Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly  
 85 90 95  
  
 Leu Thr Thr Ala Leu His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn  
 100 105 110  
  
 Pro Glu Phe Val Val Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala  
 115 120 125

Ile Thr Thr Ala Ile Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys  
 130 135 140

Thr Asn Pro Asp Val Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala  
 145 150 155 160

Thr Gly Ser Val Ala Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro  
 165 170 175

Tyr Tyr Ile Gly Lys Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn  
 180 185 190

Thr Ile Gly Ala His Ser Glu His Thr Val Met Ile Gly Asp Arg Met  
 195 200 205

Asp Thr Asp Val Lys Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu  
 210 215 220

Val Arg Ser Gly Ile Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe  
 225 230 235 240

Arg Pro Thr His Val Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp  
 245 250 255

Asp Asp Pro Phe Gly Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln  
 260 265 270

Phe Thr Asp  
 275

<210> 165  
 <211> 1128  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1105)  
 <223> RXA00794

<400> 165  
 gcgggttgat acagcccaag cgccgataca ttataaatgc gcctagatac gtgcaaccca 60  
 cgtaaccagg tcagatcaag tgccccagga ggcccttcag atg aac cta aag aac 115  
 Met Asn Leu Lys Asn  
 1 5

ccc gaa acg cca gac cgt aac ctt gct atg gag ctg gtg cga gtt acg 163  
 Pro Glu Thr Pro Asp Arg Asn Leu Ala Met Glu Leu Val Arg Val Thr  
 10 15 20

gaa gca gct gca ctg gct tct gga cgt tgg gtt gga cgt ggc atg aag 211  
 Glu Ala Ala Ala Leu Ala Ser Gly Arg Trp Val Gly Arg Gly Met Lys  
 25 30 35

aat gaa ggc gac ggt gcc gct gtt gac gcc atg cgc cag ctc atc aac 259  
 Asn Glu Gly Asp Gly Ala Ala Val Asp Ala Met Arg Gln Leu Ile Asn  
 40 45 50

tca gtg acc atg aag ggc gtc gtt gtt atc ggc gag ggc gaa aaa gac 307

Ser	Val	Thr	Met	Lys	Gly	Val	Val	Val	Ile	Gly	Glu	Gly	Glu	Lys	Asp		
55						60					65						
gaa	gct	cca	atg	ctg	tac	aac	ggc	gaa	gag	gtc	gga	acc	ggc	ttt	gga	355	
Glu	Ala	Pro	Met	Leu	Tyr	Asn	Gly	Glu	Glu	Val	Gly	Thr	Gly	Phe	Gly		
70					75					80					85		
cct	gag	gtt	gat	atc	gca	gtt	gac	cca	gtt	gac	ggc	acc	acc	ctg	atg	403	
Pro	Glu	Val	Asp	Ile	Ala	Val	Asp	Pro	Val	Asp	Gly	Thr	Thr	Leu	Met		
				90					95					100			
gct	gag	ggc	cgc	ccc	aac	gca	att	tcc	att	ctc	gca	gct	gca	gag	cgt	451	
Ala	Glu	Gly	Arg	Pro	Asn	Ala	Ile	Ser	Ile	Leu	Ala	Ala	Ala	Glu	Arg		
			105					110					115				
ggc	acc	atg	tac	gat	cca	tcc	tcc	gtc	ttc	tac	atg	aag	aag	atc	gcc	499	
Gly	Thr	Met	Tyr	Asp	Pro	Ser	Ser	Val	Phe	Tyr	Met	Lys	Lys	Ile	Ala		
		120					125					130					
gtg	gga	cct	gag	gcc	gca	ggc	aag	atc	gac	atc	gaa	gct	cca	gtt	gcc	547	
Val	Gly	Pro	Glu	Ala	Ala	Gly	Lys	Ile	Asp	Ile	Glu	Ala	Pro	Val	Ala		
	135					140					145						
cac	aac	atc	aac	gcg	gtg	gca	aag	tcc	aag	gga	atc	aac	cct	tcc	gac	595	
His	Asn	Ile	Asn	Ala	Val	Ala	Lys	Ser	Lys	Gly	Ile	Asn	Pro	Ser	Asp		
150					155					160					165		
gtc	acc	gtt	gtc	gtg	ctt	gac	cgt	cct	cgc	cac	atc	gaa	ctg	atc	gca	643	
Val	Thr	Val	Val	Val	Leu	Asp	Arg	Pro	Arg	His	Ile	Glu	Leu	Ile	Ala		
				170					175					180			
gac	att	cgt	cgt	gca	ggc	gca	aag	gtt	cgt	ctc	atc	tcc	gac	ggc	gac	691	
Asp	Ile	Arg	Arg	Ala	Gly	Ala	Lys	Val	Arg	Leu	Ile	Ser	Asp	Gly	Asp		
			185					190					195				
gtt	gca	ggc	gca	gtt	gca	gca	gct	cag	gat	tcc	aac	tcc	gtg	gac	atc	739	
Val	Ala	Gly	Ala	Val	Ala	Ala	Ala	Gln	Asp	Ser	Asn	Ser	Val	Asp	Ile		
		200					205					210					
atg	atg	ggc	acc	ggc	gga	acc	cca	gaa	ggc	atc	atc	act	gcg	tgc	gcc	787	
Met	Met	Gly	Thr	Gly	Gly	Thr	Pro	Glu	Gly	Ile	Ile	Thr	Ala	Cys	Ala		
	215					220					225						
atg	aag	tgc	atg	ggc	gaa	atc	cag	ggc	atc	ctg	gcc	cca	atg	aac		835	
Met	Lys	Cys	Met	Gly	Gly	Glu	Ile	Gln	Gly	Ile	Leu	Ala	Pro	Met	Asn		
230					235					240					245		
gat	ttc	gag	cgc	cag	aag	gca	cac	gac	gct	ggc	ctg	gtt	ctt	gat	cag	883	
Asp	Phe	Glu	Arg	Gln	Lys	Ala	His	Asp	Ala	Gly	Leu	Val	Leu	Asp	Gln		
				250					255					260			
gtt	ctg	cac	acc	aac	gat	ctg	gtg	agc	tcc	gac	aac	tgc	tac	ttc	gtg	931	
Val	Leu	His	Thr	Asn	Asp	Leu	Val	Ser	Ser	Asp	Asn	Cys	Tyr	Phe	Val		
			265					270					275				
gca	acc	ggc	gtg	acc	aac	ggc	gac	atg	ctc	cgt	ggc	gtt	tcc	tac	cgc	979	
Ala	Thr	Gly	Val	Thr	Asn	Gly	Asp	Met	Leu	Arg	Gly	Val	Ser	Tyr	Arg		
		280					285					290					
gca	aac	ggc	gca	acc	acc	cgt	tcc	ctg	gtt	atg	cgc	gca	aag	tca	ggc	1027	
Ala	Asn	Gly	Ala	Thr	Thr	Arg	Ser	Leu	Val	Met	Arg	Ala	Lys	Ser	Gly		

295                      300                      305  
 acc atc cgc cac atc gag tct gtc cac cag ctg tcc aag ctg cag gaa 1075  
 Thr Ile Arg His Ile Glu Ser Val His Gln Leu Ser Lys Leu Gln Glu  
 310                      315                      320                      325  
 tac tcc gtg gtt gac tac acc acc gcg acc taagagctct tagttcgaaa 1125  
 Tyr Ser Val Val Asp Tyr Thr Thr Ala Thr  
 330                      335  
 aac 1128  
  
 <210> 166  
 <211> 335  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
  
 <400> 166  
 Met Asn Leu Lys Asn Pro Glu Thr Pro Asp Arg Asn Leu Ala Met Glu  
 1                      5                      10                      15  
 Leu Val Arg Val Thr Glu Ala Ala Ala Leu Ala Ser Gly Arg Trp Val  
 20                      25                      30  
 Gly Arg Gly Met Lys Asn Glu Gly Asp Gly Ala Ala Val Asp Ala Met  
 35                      40                      45  
 Arg Gln Leu Ile Asn Ser Val Thr Met Lys Gly Val Val Val Ile Gly  
 50                      55                      60  
 Glu Gly Glu Lys Asp Glu Ala Pro Met Leu Tyr Asn Gly Glu Glu Val  
 65                      70                      75                      80  
 Gly Thr Gly Phe Gly Pro Glu Val Asp Ile Ala Val Asp Pro Val Asp  
 85                      90                      95  
 Gly Thr Thr Leu Met Ala Glu Gly Arg Pro Asn Ala Ile Ser Ile Leu  
 100                      105                      110  
 Ala Ala Ala Glu Arg Gly Thr Met Tyr Asp Pro Ser Ser Val Phe Tyr  
 115                      120                      125  
 Met Lys Lys Ile Ala Val Gly Pro Glu Ala Ala Gly Lys Ile Asp Ile  
 130                      135                      140  
 Glu Ala Pro Val Ala His Asn Ile Asn Ala Val Ala Lys Ser Lys Gly  
 145                      150                      155                      160  
 Ile Asn Pro Ser Asp Val Thr Val Val Val Leu Asp Arg Pro Arg His  
 165                      170                      175  
 Ile Glu Leu Ile Ala Asp Ile Arg Arg Ala Gly Ala Lys Val Arg Leu  
 180                      185                      190  
 Ile Ser Asp Gly Asp Val Ala Gly Ala Val Ala Ala Ala Gln Asp Ser  
 195                      200                      205  
 Asn Ser Val Asp Ile Met Met Gly Thr Gly Gly Thr Pro Glu Gly Ile  
 210                      215                      220

Ile Thr Ala Cys Ala Met Lys Cys Met Gly Gly Glu Ile Gln Gly Ile  
 225 230 235 240

Leu Ala Pro Met Asn Asp Phe Glu Arg Gln Lys Ala His Asp Ala Gly  
 245 250 255

Leu Val Leu Asp Gln Val Leu His Thr Asn Asp Leu Val Ser Ser Asp  
 260 265 270

Asn Cys Tyr Phe Val Ala Thr Gly Val Thr Asn Gly Asp Met Leu Arg  
 275 280 285

Gly Val Ser Tyr Arg Ala Asn Gly Ala Thr Thr Arg Ser Leu Val Met  
 290 295 300

Arg Ala Lys Ser Gly Thr Ile Arg His Ile Glu Ser Val His Gln Leu  
 305 310 315 320

Ser Lys Leu Gln Glu Tyr Ser Val Val Asp Tyr Thr Thr Ala Thr  
 325 330 335

<210> 167  
 <211> 1035  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1012)  
 <223> RXN02920

<400> 167  
 tgcattgcaga ttatctgtcc aactacgccca gccgcgcgta aagcgcgggc ctgctggtgg 60

cggtgtggcgt cgaaaagcat ttttaaagga gtttaagacg atg aag ttt gtt atg 115  
 Met Lys Phe Val Met  
 1 5

tat ccg cat ttg tgg gag tcc acg acc gct gtc att gag ggt ggc gga 163  
 Tyr Pro His Leu Trp Glu Ser Thr Thr Ala Val Ile Glu Gly Gly Gly  
 10 15 20

cat gag cgg gtt gag gat att aaa gat gca gac ttc att ttc ttt aat 211  
 His Glu Arg Val Glu Asp Ile Lys Asp Ala Asp Phe Ile Phe Phe Asn  
 25 30 35

ggt tca gcg ccg gag ttc ccg gat ttg ccg gag aac atc aag ttc gtg 259  
 Gly Ser Ala Pro Glu Phe Pro Asp Leu Pro Glu Asn Ile Lys Phe Val  
 40 45 50

cag gcc tcc atg gcg ggt att gat gcg ctg gtc aag cgt ggt gtc gtc 307  
 Gln Ala Ser Met Ala Gly Ile Asp Ala Leu Val Lys Arg Gly Val Val  
 55 60 65

aat gag aag gca cgt tgg gca aac gcg gct ggc ctg tac gct gac acc 355  
 Asn Glu Lys Ala Arg Trp Ala Asn Ala Ala Gly Leu Tyr Ala Asp Thr  
 70 75 80 85

gtt gct gag tcc acc att ggt tta att ctg gcg cag atg cac atg cat 403  
 Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His

90													95				100				
gcg	acg	act	cgt	ttg	gct	aag	tcg	tgg	agc	gtg	cgg	cct	gag	gtg	gaa	451					
Ala	Thr	Thr	Arg	Leu	Ala	Lys	Ser	Trp	Ser	Val	Arg	Pro	Glu	Val	Glu						
			105				110						115								
aac	aac	aag	tca	tgg	ctg	cat	gac	aat	aaa	act	gtc	gct	att	ttg	ggc	499					
Asn	Asn	Lys	Ser	Trp	Leu	His	Asp	Asn	Lys	Thr	Val	Ala	Ile	Leu	Gly						
			120				125						130								
gcc	ggg	ggc	att	ggc	gtg	cgt	ctg	ctg	gaa	atg	ctc	aag	ccg	ttc	aac	547					
Ala	Gly	Gly	Ile	Gly	Val	Arg	Leu	Leu	Glu	Met	Leu	Lys	Pro	Phe	Asn						
			135				140						145								
gtg	aag	acc	att	gcg	gtt	aat	aac	tct	ggg	cgt	ccg	gtg	gaa	ggg	gca	595					
Val	Lys	Thr	Ile	Ala	Val	Asn	Asn	Ser	Gly	Arg	Pro	Val	Glu	Gly	Ala						
			150				155						160								
gat	gaa	acc	ttc	gcc	atg	gat	aag	gct	gag	cac	gtg	tgg	gct	gag	gct	643					
Asp	Glu	Thr	Phe	Ala	Met	Asp	Lys	Ala	Glu	His	Val	Trp	Ala	Glu	Ala						
			170				175						180								
gat	gtg	ttt	gtg	ctc	atc	ctg	ccg	ctg	act	gat	gcc	act	tat	cag	atc	691					
Asp	Val	Phe	Val	Leu	Ile	Leu	Pro	Leu	Thr	Asp	Ala	Thr	Tyr	Gln	Ile						
			185				190						195								
gtc	aat	gca	gaa	act	ttg	ggc	aag	atg	aag	cct	tct	gcc	gtg	gtg	gtc	739					
Val	Asn	Ala	Glu	Thr	Leu	Gly	Lys	Met	Lys	Pro	Ser	Ala	Val	Val	Val						
			200				205						210								
aat	gtg	ggg	cgt	ggc	ccg	ctg	atc	aac	acc	gat	gat	ctg	gtg	gat	gca	787					
Asn	Val	Gly	Arg	Gly	Pro	Leu	Ile	Asn	Thr	Asp	Asp	Leu	Val	Asp	Ala						
			215				220						225								
ttg	aac	aac	ggc	acc	att	gcg	ggg	gct	gcg	ctg	gac	gtt	acc	gat	cct	835					
Leu	Asn	Asn	Gly	Thr	Ile	Ala	Gly	Ala	Ala	Leu	Asp	Val	Thr	Asp	Pro						
			230				235						240								
gag	cca	ctt	cct	gac	agc	cac	ccg	ctg	tgg	gag	atg	gac	aat	gtg	gtt	883					
Glu	Pro	Leu	Pro	Asp	Ser	His	Pro	Leu	Trp	Glu	Met	Asp	Asn	Val	Val						
			250				255						260								
atc	act	cct	cat	act	gca	aac	acg	aat	gag	agg	att	cgt	gct	ttg	acc	931					
Ile	Thr	Pro	His	Thr	Ala	Asn	Thr	Asn	Glu	Arg	Ile	Arg	Ala	Leu	Thr						
			265				270						275								
ggc	gaa	ctc	acc	ttg	cgc	aac	att	gag	ttg	ttt	gag	gca	ggc	gag	cag	979					
Gly	Glu	Leu	Thr	Leu	Arg	Asn	Ile	Glu	Leu	Phe	Glu	Ala	Gly	Glu	Gln						
			280				285						290								
atg	gcc	acc	gag	gtc	gat	gtg	gtg	gct	ggc	tac	taggcctttt	atgggtgtgat				1032					
Met	Ala	Thr	Glu	Val	Asp	Val	Val	Ala	Gly	Tyr											
			295				300														
ccg																1035					

```
<210> 168
<211> 304
<212> PRT
<213> Corynebacterium glutamicum
```



&lt;400&gt; 168

```

Met Lys Phe Val Met Tyr Pro His Leu Trp Glu Ser Thr Thr Ala Val
 1           5           10           15

Ile Glu Gly Gly Gly His Glu Arg Val Glu Asp Ile Lys Asp Ala Asp
      20           25           30

Phe Ile Phe Phe Asn Gly Ser Ala Pro Glu Phe Pro Asp Leu Pro Glu
      35           40           45

Asn Ile Lys Phe Val Gln Ala Ser Met Ala Gly Ile Asp Ala Leu Val
 50           55           60

Lys Arg Gly Val Val Asn Glu Lys Ala Arg Trp Ala Asn Ala Ala Gly
 65           70           75           80

Leu Tyr Ala Asp Thr Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala
      85           90           95

Gln Met His Met His Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val
      100           105           110

Arg Pro Glu Val Glu Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr
      115           120           125

Val Ala Ile Leu Gly Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met
      130           135           140

Leu Lys Pro Phe Asn Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg
145           150           155           160

Pro Val Glu Gly Ala Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His
      165           170           175

Val Trp Ala Glu Ala Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp
      180           185           190

Ala Thr Tyr Gln Ile Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro
      195           200           205

Ser Ala Val Val Val Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp
      210           215           220

Asp Leu Val Asp Ala Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu
225           230           235           240

Asp Val Thr Asp Pro Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu
      245           250           255

Met Asp Asn Val Val Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg
      260           265           270

Ile Arg Ala Leu Thr Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe
      275           280           285

Glu Ala Gly Glu Gln Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr
      290           295           300

```

```
<210> 169
<211> 779
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (52) .. (756)  
<223> FRXA02379
```

<400> 169																	
tcg	cagg	cctc	cat	ggc	gggt	att	gat	gcgc	tggt	caag	cgc	tggt	gtc	gtc	aat	aga	57
															Met	Arg	
															1		
aag	cac	cgt	tgg	gca	aac	gcg	gct	ggc	ctg	tac	gct	gac	acc	gtt	gct	105	
Lys	His	Arg	Trp	Ala	Asn	Ala	Ala	Gly	Leu	Tyr	Ala	Asp	Thr	Val	Ala		
		5					10					15					
gag	tcc	acc	att	ggc	tta	att	ctg	gcg	cag	atg	cac	atg	cat	gcg	acg	153	
Glu	Ser	Thr	Ile	Gly	Leu	Ile	Leu	Ala	Gln	Met	His	Met	His	Ala	Thr		
	20					25					30						
act	cgt	ttg	gct	aag	tcg	tgg	agc	gtg	cgg	cct	gag	gtg	gaa	aac	aac	201	
Thr	Arg	Leu	Ala	Lys	Ser	Trp	Ser	Val	Arg	Pro	Glu	Val	Glu	Asn	Asn		
	35				40					45					50		
aag	tca	tgg	ctg	cat	gac	aat	aaa	act	gtc	gct	att	ttg	ggc	gcc	ggt	249	
Lys	Ser	Trp	Leu	His	Asp	Asn	Lys	Thr	Val	Ala	Ile	Leu	Gly	Ala	Gly		
				55				:	60					65			
ggc	att	ggc	gtg	cgt	ctg	ctg	gaa	atg	ctc	aag	ccg	ttc	aac	gtg	aag	297	
Gly	Ile	Gly	Val	Arg	Leu	Leu	Glu	Met	Leu	Lys	Pro	Phe	Asn	Val	Lys		
			70					75					80				
acc	att	gcg	ggt	aat	aac	tct	ggc	cgt	ccg	gtg	gaa	ggc	gca	gat	gaa	345	
Thr	Ile	Ala	Val	Asn	Asn	Ser	Gly	Arg	Pro	Val	Glu	Gly	Ala	Asp	Glu		
		85					90					95					
acc	ttc	gcc	atg	gat	aag	gct	gag	cac	gtg	tgg	gct	gag	gct	gat	gtg	393	
Thr	Phe	Ala	Met	Asp	Lys	Ala	Glu	His	Val	Trp	Ala	Glu	Ala	Asp	Val		
	100					105					110						
ttt	gtg	ctc	atc	ctg	ccg	ctg	act	gat	gcc	act	tat	cag	atc	gtc	aat	441	
Phe	Val	Leu	Ile	Leu	Pro	Leu	Thr	Asp	Ala	Thr	Tyr	Gln	Ile	Val	Asn		
	115				120					125					130		
gca	gaa	act	ttg	ggc	aag	atg	aag	cct	tct	gcc	gtg	gtg	gtc	aat	gtg	489	
Ala	Glu	Thr	Leu	Gly	Lys	Met	Lys	Pro	Ser	Ala	Val	Val	Val	Asn	Val		
				135				140						145			
ggg	cgt	ggc	ccg	ctg	atc	aac	acc	gat	gat	ctg	gtg	gat	gca	ttg	aac	537	
Gly	Arg	Gly	Pro	Leu	Ile	Asn	Thr	Asp	Asp	Leu	Val	Asp	Ala	Leu	Asn		
			150					155					160				
aac	ggc	acc	att	gcg	ggc	gct	gcg	ctg	gac	gtt	acc	gat	cct	gag	cca	585	
Asn	Gly	Thr	Ile	Ala	Gly	Ala	Ala	Leu	Asp	Val	Thr	Asp	Pro	Glu	Pro		
		165				170						175					

ctt cct gac agc cac ccg ctg tgg gag atg gac aat gtg gtt atc act 633  
 Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val Ile Thr  
 180 185 190  
  
 cct cat act gca aac acg aat gag agg att cgt gct ttg acc ggc gaa 681  
 Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr Gly Glu  
 195 200 205 210  
  
 ctc acc ttg cgc aac att gag ttg ttt gag gca ggc gag cag atg gcc 729  
 Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln Met Ala  
 215 220 225  
  
 acc gag gtc gat gtg gtg gct ggc tac taggcctttt atggtgtgat 776  
 Thr Glu Val Asp Val Val Ala Gly Tyr  
 230 235  
  
 ccg 779

<210> 170  
 <211> 235  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 170  
 Met Arg Lys His Arg Trp Ala Asn Ala Ala Gly Leu Tyr Ala Asp Thr  
 1 5 10 15  
  
 Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His  
 20 25 30  
  
 Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val Arg Pro Glu Val Glu  
 35 40 45  
  
 Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr Val Ala Ile Leu Gly  
 50 55 60  
  
 Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met Leu Lys Pro Phe Asn  
 65 70 75 80  
  
 Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg Pro Val Glu Gly Ala  
 85 90 95  
  
 Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His Val Trp Ala Glu Ala  
 100 105 110  
  
 Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp Ala Thr Tyr Gln Ile  
 115 120 125  
  
 Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro Ser Ala Val Val Val  
 130 135 140  
  
 Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp Asp Leu Val Asp Ala  
 145 150 155 160  
  
 Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu Asp Val Thr Asp Pro  
 165 170 175  
  
 Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val  
 180 185 190

Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr  
 195 200 205  
 Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln  
 210 215 220  
 Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr  
 225 230 235

<210> 171  
 <211> 792  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(769)  
 <223> RXN02688

<400> 171  
 gtgcggaaga cagcacgccc caaaccgacc aactagctaa gctacacaag gcggacgaat 60  
 ggggttcgctc agcaagcgaa ggaaggaaac ttaactagcc atg gcc ggc cgg att 115  
 Met Ala Gly Arg Ile  
 1 5  
 att ttg cta cga cac ggg cag act cac aac aac gtc aaa cac ctc ctg 163  
 Ile Leu Leu Arg His Gly Gln Thr His Asn Asn Val Lys His Leu Leu  
 10 15 20  
 gac acc cgc cca cca gga gct gaa ctc acc gac ctg ggc cgt aaa caa 211  
 Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp Leu Gly Arg Lys Gln  
 25 30 35  
 gcc ctt gaa gtt ggc cac gaa cta gcc acc tac tcc ggt gag cgc ctc 259  
 Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr Ser Gly Glu Arg Leu  
 40 45 50  
 gcc cat gtg tac agc tcc atc gtg ttg cgc gcc caa caa acc gcc gtg 307  
 Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala Gln Gln Thr Ala Val  
 55 60 65  
 ctt gcc acc tct acc ttt gaa aaa gct cgc gac atg cag tcc ggt gcg 355  
 Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp Met Gln Ser Gly Ala  
 70 75 80 85  
 att cca ctc gac gtt gtg gaa ggc att cag gaa atc aac gtc ggc gac 403  
 Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu Ile Asn Val Gly Asp  
 90 95 100  
 ttt gaa atg cgc ggc gat gaa gaa gcc cac atg aat tac tcc cgc gca 451  
 Phe Glu Met Arg Gly Asp Glu Glu Ala His Met Asn Tyr Ser Arg Ala  
 105 110 115  
 ctc aac ggc tgg ctt cac ggg gat cct gcc gct ggt ctt ccc ggc ggt 499  
 Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala Gly Leu Pro Gly Gly  
 120 125 130  
 gag acc tac aaa gac gtg ctg aac cgc tac cag ccg act ctt gat cga 547  
 Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln Pro Thr Leu Asp Arg

135	140	145	
atc atg gac agc cac gac ctt gac gac gac cgc gac gtt gcc gtt gtc			595
Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg Asp Val Ala Val Val			
150	155	160	165
agc cac ggc gcc gtc atc cgc atc gtg gca aca cac gca act ggt gtg			643
Ser His Gly Ala Val Ile Arg Ile Val Ala Thr His Ala Thr Gly Val			
	170	175	180
gat ccc aac ttt gcg ttc aac acc tac ctg ggc aac tgc cgc ttc gtg			691
Asp Pro Asn Phe Ala Phe Asn Thr Tyr Leu Gly Asn Cys Arg Phe Val			
	185	190	195
gtg ctg gag cca aac ggt aag aaa ttc agc caa tgg gat gtt gtg cgc			739
Val Leu Glu Pro Asn Gly Lys Lys Phe Ser Gln Trp Asp Val Val Arg			
	200	205	210
tgg act gac agc cca ctg cca tgg cag gag taattgagac caaaggctcg			789
Trp Thr Asp Ser Pro Leu Pro Trp Gln Glu			
	215	220	
gat			792
<210> 172			
<211> 223			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 172			
Met Ala Gly Arg Ile Ile Leu Leu Arg His Gly Gln Thr His Asn Asn			
1	5	10	15
Val Lys His Leu Leu Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp			
	20	25	30
Leu Gly Arg Lys Gln Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr			
	35	40	45
Ser Gly Glu Arg Leu Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala			
	50	55	60
Gln Gln Thr Ala Val Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp			
	65	70	75
Met Gln Ser Gly Ala Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu			
	85	90	95
Ile Asn Val Gly Asp Phe Glu Met Arg Gly Asp Glu Glu Ala His Met			
	100	105	110
Asn Tyr Ser Arg Ala Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala			
	115	120	125
Gly Leu Pro Gly Gly Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln			
	130	135	140
Pro Thr Leu Asp Arg Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg			
	145	150	155
			160

Asp Val Ala Val Val Ser His Gly Ala Val Ile Arg Ile Val Ala Thr  
 165 170 175

His Ala Thr Gly Val Asp Pro Asn Phe Ala Phe Asn Thr Tyr Leu Gly  
 180 185 190

Asn Cys Arg Phe Val Val Leu Glu Pro Asn Gly Lys Lys Phe Ser Gln  
 195 200 205

Trp Asp Val Val Arg Trp Thr Asp Ser Pro Leu Pro Trp Gln Glu  
 210 215 220

<210> 173

<211> 336

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(313)

<223> RXN03087

<400> 173

gttgccgcca gccgttccag ggcgcttgag ctgggtcagcg acatcgcaat gatcaaccag 60

gaatacctgg aaaagagctg atattgatag ggtttaagtc atg aag atc tac gca 115  
 Met Lys Ile Tyr Ala  
 1 5

cct ttt gct gga atc gtc cac tat ttt gtc gat gaa ggc gat ccc gtg 163  
 Pro Phe Ala Gly Ile Val His Tyr Phe Val Asp Glu Gly Asp Pro Val  
 10 15 20

gaa acc ggc atg caa ctg gga acg gta gaa acc atc aaa ctc gag gca 211  
 Glu Thr Gly Met Gln Leu Gly Thr Val Glu Thr Ile Lys Leu Glu Ala  
 25 30 35

cca atc atg gca ccg gga cct ggc atc gta gct aag gtt tct ttt gat 259  
 Pro Ile Met Ala Pro Gly Pro Gly Ile Val Ala Lys Val Ser Phe Asp  
 40 45 50

gat ttc tcc gac gtc acc ggc ggc gat gaa ctc ctc gaa ttg gag gca 307  
 Asp Phe Ser Asp Val Thr Gly Gly Asp Glu Leu Leu Glu Leu Glu Ala  
 55 60 65

aag aac taatgggtca aacccgcatc att 336  
 Lys Asn  
 70

<210> 174

<211> 71

<212> PRT

<213> Corynebacterium glutamicum

<400> 174

Met Lys Ile Tyr Ala Pro Phe Ala Gly Ile Val His Tyr Phe Val Asp  
 1 5 10 15

Glu Gly Asp Pro Val Glu Thr Gly Met Gln Leu Gly Thr Val Glu Thr

20 25 30  
 Ile Lys Leu Glu Ala Pro Ile Met Ala Pro Gly Pro Gly Ile Val Ala  
 35 40 45  
 Lys Val Ser Phe Asp Asp Phe Ser Asp Val Thr Gly Gly Asp Glu Leu  
 50 55 60  
 Leu Glu Leu Glu Ala Lys Asn  
 65 70  
  
 <210> 175  
 <211> 310  
 <212> DNA  
 <213> Corynebacterium glutamicum  
  
 <220>  
 <221> CDS  
 <222> (101)..(310)  
 <223> RXN03186  
  
 <400> 175  
 ttcggtgcact tcggcgtgtc acaattaggt acgaccaaga atgggaccgg gaaaccggga 60  
  
 cgtataaacg aaataaaaca ttccaacagg aggtgtggaa atg gcc gat caa gca 115  
 Met Ala Asp Gln Ala  
 1 5  
  
 aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163  
 Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg  
 10 15 20  
  
 gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211  
 Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn  
 25 30 35  
  
 gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259  
 Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu  
 40 45 50  
  
 cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307  
 Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys  
 55 60 65  
  
 cgc 310  
 Arg  
 70

<210> 176  
 <211> 70  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 176  
 Met Ala Asp Gln Ala Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn  
 1 5 10 15  
  
 Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp  
 20 25 30

Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln  
                   35                  40                  45  
 Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu  
           50                  55                  60  
 Arg Ala Ser Ala Lys Arg  
       65                  70

<210> 177  
 <211> 302  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(279)  
 <223> RXN03187

<400> 177  
 gtt gca gtg tct gac ttc tcc act gat ctg cca aac cag atc cgt gaa 48  
 Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu  
       1                  5                  10                  15  
 tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc ttc ggt ttc 96  
 Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe  
                   20                  25                  30  
 tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc gac gct gag 144  
 Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu  
           35                  40                  45  
 tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa ggc aag atc 192  
 Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile  
       50                  55                  60  
 gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag ttg gat gat 240  
 Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp  
       65                  70                  75                  80  
 cct acg agt gtt tcc gta gat cca aac gct cct gag gaa taaatcacct 289  
 Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu  
                   85                  90  
 caagggacag ata 302

<210> 178  
 <211> 93  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 178  
 Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu  
       1                  5                  10                  15  
 Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe  
           20                  25                  30



Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu  
                   35                                  40                                  45

Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile  
                   50                                  55                                  60

Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp  
                   65                                  70                                  75                                  80

Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu  
                                   85                                  90

<210> 179  
 <211> 1953  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1930)  
 <223> RXN02591

<400> 179  
 atgtgtccgt tgtctcacct aaagtttttaa ctagtctctgt atctgaaagc tacgctaggg 60

ggcgagaact ctgtcgaatg acacaaaatc tggagaagta atg act act gct gca 115  
   Met Thr Thr Ala Ala  
   1  5

atc agg ggc ctt cag ggc gag gcg ccg acc aag aat aag gaa ctg ctg 163  
 Ile Arg Gly Leu Gln Gly Glu Ala Pro Thr Lys Asn Lys Glu Leu Leu  
                                   10                                  15                                  20

aac tgg atc gca gac gcc gtc gag ctc ttc cag cct gag gct gtt gtg 211  
 Asn Trp Ile Ala Asp Ala Val Glu Leu Phe Gln Pro Glu Ala Val Val  
                                   25                                  30                                  35

ttc gtt gat gga tcc cag gct gag tgg gat cgc atg gcg gag gat ctt 259  
 Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg Met Ala Glu Asp Leu  
                                   40                                  45                                  50

gtt gaa gcc ggt acc ctc atc aag ctc aac gag gaa aag cgt ccg aac 307  
 Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu Glu Lys Arg Pro Asn  
                                   55                                  60                                  65

agc tac cta gct cgt tcc aac cca tct gac gtt gcg cgc gtt gag tcc 355  
 Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val Ala Arg Val Glu Ser  
                                   70                                  75                                  80                                  85

cgc acc ttc atc tgc tcc gag aag gaa gaa gat gct ggc cca acc aac 403  
 Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp Ala Gly Pro Thr Asn  
                                   90                                  95                                  100

aac tgg gct cca cca cag gca atg aag gac gaa atg tcc aag cat tac 451  
 Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu Met Ser Lys His Tyr  
                                   105                                  110                                  115

gct ggt tcc atg aag ggg cgc acc atg tac gtc gtg cct ttc tgc atg 499  
 Ala Gly Ser Met Lys Gly Arg Thr Met Tyr Val Val Pro Phe Cys Met  
                                   120                                  125                                  130

ggt cca atc agc gat ccg gac cct aag ctt ggt gtg cag ctc act gac	547
Gly Pro Ile Ser Asp Pro Asp Pro Lys Leu Gly Val Gln Leu Thr Asp	
135 140 145	
tcc gag tac gtt gtc atg tcc atg cgc atc atg acc cgc atg ggt att	595
Ser Glu Tyr Val Val Met Ser Met Arg Ile Met Thr Arg Met Gly Ile	
150 155 160 165	
gaa gcg ctg gac aag atc ggc gcg aac ggc agc ttc gtc agg tgc ctc	643
Glu Ala Leu Asp Lys Ile Gly Ala Asn Gly Ser Phe Val Arg Cys Leu	
170 175 180	
cac tcc gtt ggt gct cct ttg gag cca ggc cag gaa gac gtt gca tgg	691
His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln Glu Asp Val Ala Trp	
185 190 195	
cct tgc aac gac acc aag tac atc acc cag ttc cca gag acc aag gaa	739
Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe Pro Glu Thr Lys Glu	
200 205 210	
att tgg tcc tac ggt tcc ggc tac ggc gga aac gca atc ctg gca aag	787
Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn Ala Ile Leu Ala Lys	
215 220 225	
aag tgc tac gca ctg cgt atc gca tct gtc atg gct cgc gaa gaa gga	835
Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met Ala Arg Glu Glu Gly	
230 235 240 245	
tgg atg gct gag cac atg ctc atc ctg aag ctg atc aac cca gag ggc	883
Trp Met Ala Glu His Met Leu Ile Leu Lys Leu Ile Asn Pro Glu Gly	
250 255 260	
aag gcg tac cac atc gca gca gca ttc cca tct gct tgt ggc aag acc	931
Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser Ala Cys Gly Lys Thr	
265 270 275	
aac ctc gcc atg atc act cca acc atc cca ggc tgg acc gct cag gtt	979
Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly Trp Thr Ala Gln Val	
280 285 290	
gtt ggc gac gac atc gct tgg ctg aag ctg cgc gag gac ggc ctc tac	1027
Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg Glu Asp Gly Leu Tyr	
295 300 305	
gca gtt aac cca gaa aat ggt ttc ttc ggt gtt gct cca ggc acc aac	1075
Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val Ala Pro Gly Thr Asn	
310 315 320 325	
tac gca tcc aac cca atc gcg atg aag acc atg gaa cca ggc aac acc	1123
Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met Glu Pro Gly Asn Thr	
330 335 340	
ctg ttc acc aac gtg gca ctc acc gac gac ggc gac atc tgg tgg gaa	1171
Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly Asp Ile Trp Trp Glu	
345 350 355	
ggc atg gac ggc gac gcc cca gct cac ctc att gac tgg atg ggc aac	1219
Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile Asp Trp Met Gly Asn	
360 365 370	

gac tgg acc cca gag tcc gac gaa aac gct gct cac cct aac tcc cgt Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala His Pro Asn Ser Arg 375 380 385	1267
tac tgc gta gca atc gac cag tcc cca gca gca gca cct gag ttc aac Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala Ala Pro Glu Phe Asn 390 395 400 405	1315
gac tgg gaa ggc gtc aag atc gac gca atc ctc ttc ggt gga cgt cgc Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu Phe Gly Gly Arg Arg 410 415 420	1363
gca gac acc gtc cca ctg gtt acc cag acc tac gac tgg gag cac ggc Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr Asp Trp Glu His Gly 425 430 435	1411
acc atg gtt ggt gca ctg ctc gca tcc ggt cag acc gca gct tcc gca Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln Thr Ala Ala Ser Ala 440 445 450	1459
gaa gca aag gtc ggc aca ctc cgc cac gac cca atg gca atg ctc cca Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro Met Ala Met Leu Pro 455 460 465	1507
ttc att ggc tac aac gct ggt gaa tac ctg cag aac tgg att gac atg Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln Asn Trp Ile Asp Met 470 475 480 485	1555
ggt aac aag ggt ggc gac aag atg cca tcc atc ttc ctg gtc aac tgg Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile Phe Leu Val Asn Trp 490 495 500	1603
ttc cgc cgt ggc gaa gat gga cgc ttc ctg tgg cct ggc ttc ggc gac Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp Pro Gly Phe Gly Asp 505 510 515	1651
aac tct cgc gtt ctg aag tgg gtc atc gac cgc atc gaa ggc cac gtt Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg Ile Glu Gly His Val 520 525 530	1699
ggc gca gac gag acc gtt gtt gga cac acc gct aag gcc gaa gac ctc Gly Ala Asp Glu Thr Val Val Gly His Thr Ala Lys Ala Glu Asp Leu 535 540 545	1747
gac ctc gac ggc ctc gac acc cca att gag gat gtc aag gaa gca ctg Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp Val Lys Glu Ala Leu 550 555 560 565	1795
acc gct cct gca gag cag tgg gca aac gac gtt gaa gac aac gcc gag Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val Glu Asp Asn Ala Glu 570 575 580	1843
tac ctc act ttc ctc gga cca cgt gtt cct gca gag gtt cac agc cag Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala Glu Val His Ser Gln 585 590 595	1891
ttc gat gct ctg aag gcc cgc att tca gca gct cac gct taaagttcac Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala His Ala 600 605 610	1940
gcttaagaac tgc	1953

&lt;210&gt; 180

&lt;211&gt; 610

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 180

Met Thr Thr Ala Ala Ile Arg Gly Leu Gln Gly Glu Ala Pro Thr Lys  
 1 5 10 15

Asn Lys Glu Leu Leu Asn Trp Ile Ala Asp Ala Val Glu Leu Phe Gln  
 20 25 30

Pro Glu Ala Val Val Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg  
 35 40 45

Met Ala Glu Asp Leu Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu  
 50 55 60

Glu Lys Arg Pro Asn Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val  
 65 70 75 80

Ala Arg Val Glu Ser Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp  
 85 90 95

Ala Gly Pro Thr Asn Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu  
 100 105 110

Met Ser Lys His Tyr Ala Gly Ser Met Lys Gly Arg Thr Met Tyr Val  
 115 120 125

Val Pro Phe Cys Met Gly Pro Ile Ser Asp Pro Asp Pro Lys Leu Gly  
 130 135 140

Val Gln Leu Thr Asp Ser Glu Tyr Val Val Met Ser Met Arg Ile Met  
 145 150 155 160

Thr Arg Met Gly Ile Glu Ala Leu Asp Lys Ile Gly Ala Asn Gly Ser  
 165 170 175

Phe Val Arg Cys Leu His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln  
 180 185 190

Glu Asp Val Ala Trp Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe  
 195 200 205

Pro Glu Thr Lys Glu Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn  
 210 215 220

Ala Ile Leu Ala Lys Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met  
 225 230 235 240

Ala Arg Glu Glu Gly Trp Met Ala Glu His Met Leu Ile Leu Lys Leu  
 245 250 255

Ile Asn Pro Glu Gly Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser  
 260 265 270

Ala Cys Gly Lys Thr Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly  
 275 280 285

Trp Thr Ala Gln Val Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg  
 290 295 300  
 Glu Asp Gly Leu Tyr Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val  
 305 310 315 320  
 Ala Pro Gly Thr Asn Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met  
 325 330 335  
 Glu Pro Gly Asn Thr Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly  
 340 345 350  
 Asp Ile Trp Trp Glu Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile  
 355 360 365  
 Asp Trp Met Gly Asn Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala  
 370 375 380  
 His Pro Asn Ser Arg Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala  
 385 390 395 400  
 Ala Pro Glu Phe Asn Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu  
 405 410 415  
 Phe Gly Gly Arg Arg Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr  
 420 425 430  
 Asp Trp Glu His Gly Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln  
 435 440 445  
 Thr Ala Ala Ser Ala Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro  
 450 455 460  
 Met Ala Met Leu Pro Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln  
 465 470 475 480  
 Asn Trp Ile Asp Met Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile  
 485 490 495  
 Phe Leu Val Asn Trp Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp  
 500 505 510  
 Pro Gly Phe Gly Asp Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg  
 515 520 525  
 Ile Glu Gly His Val Gly Ala Asp Glu Thr Val Val Gly His Thr Ala  
 530 535 540  
 Lys Ala Glu Asp Leu Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp  
 545 550 555 560  
 Val Lys Glu Ala Leu Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val  
 565 570 575  
 Glu Asp Asn Ala Glu Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala  
 580 585 590  
 Glu Val His Ser Gln Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala  
 595 600 605

His Ala  
610

<210> 181  
<211> 1305  
<212> DNA  
<213> *Corynebacterium glutamicum*

<220>  
<221> CDS  
<222> (101)..(1282)  
<223> RXS01260

<400> 181  
ctaaacgtgg gctgcattcc ttccaaagtc tctgatcaaa aacgctgaag ttgcccatatc 60  
ctttacccat gagaagaaga ccttcggcat caatggcgaa gtg acc ttc aac tat 115  
Val Thr Phe Asn Tyr  
1 5  
gag gat gct cac aag cgt tcc cgt ggc gtt tcc gac aag atc gtt gga 163  
Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly  
10 15 20  
ggc gtt cat tac ttg atg aag aag aac aag atc atc gaa att cat ggt 211  
Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Ile Glu Ile His Gly  
25 30 35  
ctt gga aac ttc aag gat gct aag act ctt gag gtc acc gac ggt aag 259  
Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu Val Thr Asp Gly Lys  
40 45 50  
gat gct ggc aag acc atc acc ttt gat gac tgc atc atc gca acc ggt 307  
Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly  
55 60 65  
tcg gta gtc aac acc ctc cgt ggc gtt gac ttc tca gag aac gtt gtg 355  
Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe Ser Glu Asn Val Val  
70 75 80 85  
tct ttt gaa gag cag att ctt aac cct gtt gcg cca aag aag atg gtc 403  
Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val  
90 95 100  
att gtt ggt gca ggc gca att gga atg gaa ttc gcc tac gtt ctt ggt 451  
Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly  
105 110 115  
aac tac ggt gta gat gta acc gtc atc gag ttc atg gat cgt gtg ctt 499  
Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe Met Asp Arg Val Leu  
120 125 130  
cca aat gaa gat gct gaa gtc tcc aag gtt att gca aag gcc tac aag 547  
Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys  
135 140 145  
aag atg ggc gtt aag ctt ctt cct ggc cat gca acc act gct gtt cgg 595  
Lys Met Gly Val Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg  
150 155 160 165

gac aac ggt gac ttt gtc gag gtt gat tac cag aag aag ggc tct gac	643
Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp	
170 175 180	
aag aca gag act ctt act gtt gat cga gtc atg gtt tcc gtt ggt ttc	691
Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met Val Ser Val Gly Phe	
185 190 195	
cgt cca cgc gtt gag gga ttt ggt ctt gaa aac act ggc gtt aag ctc	739
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu	
200 205 210	
acc gag cgt ggc gca atc gag atc gat gat tac atg cgt acc aac gtc	787
Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr Met Arg Thr Asn Val	
215 220 225	
gat ggc att tac gcc atc ggt gac gtg acc gcc aag ctt cag ctt gct	835
Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala	
230 235 240 245	
cac gtc gca gaa gca cag ggc att gtt gcc gca gag act att gct ggt	883
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly	
250 255 260	
gca gaa act cag act ctt ggt gat tac atg atg atg cca cgt gca acc	931
Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr	
265 270 275	
ttc tgc aac cca cag gtt tct tcc ttt ggt tac acc gaa gag cag gcc	979
Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr Thr Glu Glu Gln Ala	
280 285 290	
aag gag aag tgg cca gat cgt gag atc aag gtt gct tcc ttc cca ttc	1027
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe	
295 300 305	
tct gca aac ggt aaa gca gtt ggc ctg gca gaa act gat ggt ttc gca	1075
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala	
310 315 320 325	
aag atc gtt gct gat gca gaa ttc ggt gag ctg ctc ggt gca cac ctg	1123
Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Ala His Leu	
330 335 340	
gtt gga gca aat gca tca gag ctc atc aat gaa ttg gtg ctt gct cag	1171
Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu Leu Val Leu Ala Gln	
345 350 355	
aac tgg gat ctc acc act gaa gag atc tct cgt agc gtc cat att cac	1219
Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His	
360 365 370	
cca acg cta tct gag gca gtt aag gaa gct gca cac ggt atc tct gga	1267
Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Ser Gly	
375 380 385	
cac atg atc aac ttc tagaatccac ctgcttggtgccc ctg	1305
His Met Ile Asn Phe	
390	

<210> 182  
 <211> 394  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 182

Val	Thr	Phe	Asn	Tyr	Glu	Asp	Ala	His	Lys	Arg	Ser	Arg	Gly	Val	Ser
1				5					10					15	
Asp	Lys	Ile	Val	Gly	Gly	Val	His	Tyr	Leu	Met	Lys	Lys	Asn	Lys	Ile
			20					25					30		
Ile	Glu	Ile	His	Gly	Leu	Gly	Asn	Phe	Lys	Asp	Ala	Lys	Thr	Leu	Glu
			35				40					45			
Val	Thr	Asp	Gly	Lys	Asp	Ala	Gly	Lys	Thr	Ile	Thr	Phe	Asp	Asp	Cys
	50					55					60				
Ile	Ile	Ala	Thr	Gly	Ser	Val	Val	Asn	Thr	Leu	Arg	Gly	Val	Asp	Phe
65					70					75					80
Ser	Glu	Asn	Val	Val	Ser	Phe	Glu	Glu	Gln	Ile	Leu	Asn	Pro	Val	Ala
			85						90					95	
Pro	Lys	Lys	Met	Val	Ile	Val	Gly	Ala	Gly	Ala	Ile	Gly	Met	Glu	Phe
			100					105					110		
Ala	Tyr	Val	Leu	Gly	Asn	Tyr	Gly	Val	Asp	Val	Thr	Val	Ile	Glu	Phe
		115					120					125			
Met	Asp	Arg	Val	Leu	Pro	Asn	Glu	Asp	Ala	Glu	Val	Ser	Lys	Val	Ile
	130					135					140				
Ala	Lys	Ala	Tyr	Lys	Lys	Met	Gly	Val	Lys	Leu	Leu	Pro	Gly	His	Ala
145					150					155					160
Thr	Thr	Ala	Val	Arg	Asp	Asn	Gly	Asp	Phe	Val	Glu	Val	Asp	Tyr	Gln
			165						170					175	
Lys	Lys	Gly	Ser	Asp	Lys	Thr	Glu	Thr	Leu	Thr	Val	Asp	Arg	Val	Met
			180					185					190		
Val	Ser	Val	Gly	Phe	Arg	Pro	Arg	Val	Glu	Gly	Phe	Gly	Leu	Glu	Asn
		195					200					205			
Thr	Gly	Val	Lys	Leu	Thr	Glu	Arg	Gly	Ala	Ile	Glu	Ile	Asp	Asp	Tyr
	210					215					220				
Met	Arg	Thr	Asn	Val	Asp	Gly	Ile	Tyr	Ala	Ile	Gly	Asp	Val	Thr	Ala
225				230						235					240
Lys	Leu	Gln	Leu	Ala	His	Val	Ala	Glu	Ala	Gln	Gly	Ile	Val	Ala	Ala
			245						250					255	
Glu	Thr	Ile	Ala	Gly	Ala	Glu	Thr	Gln	Thr	Leu	Gly	Asp	Tyr	Met	Met
		260						265					270		
Met	Pro	Arg	Ala	Thr	Phe	Cys	Asn	Pro	Gln	Val	Ser	Ser	Phe	Gly	Tyr
		275					280					285			
Thr	Glu	Glu	Gln	Ala	Lys	Glu	Lys	Trp	Pro	Asp	Arg	Glu	Ile	Lys	Val



290 295 300

Ala Ser Phe Pro Phe Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu  
 305 310 315 320

Thr Asp Gly Phe Ala Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu  
 325 330 335

Leu Gly Ala His Leu Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu  
 340 345 350

Leu Val Leu Ala Gln Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg  
 355 360 365

Ser Val His Ile His Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala  
 370 375 380

His Gly Ile Ser Gly His Met Ile Asn Phe  
 385 390

<210> 183  
 <211> 294  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(271)  
 <223> RXS01261

<400> 183  
 gtgggtgttt ttcattttct tccactctaa aattaagtat ggaaaaccaa ccgcacccgg 60

atgcacgaca atgaccact aaacacgtat ccttgaatgc gtg act gaa cat tat 115  
 Val Thr Glu His Tyr  
 1 5

gac gta gta gta ctc gga gcc ggc ccc ggt ggc tat gtc tcc gcc atc 163  
 Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly Tyr Val Ser Ala Ile  
 10 15 20

cgt gca gcg cag ctt ggc aag aag gtt gct gta att gag aag cag tac 211  
 Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr  
 25 30 35

tgg ggt ggt gtt tgc cta aac gtg ggc tgc att cct tcc aaa gtc tct 259  
 Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Val Ser  
 40 45 50

gat caa aaa cgc tgaagttgcc cataccttta ccc 294  
 Asp Gln Lys Arg  
 55

<210> 184  
 <211> 57  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 184

Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly  
 1 5 10 15  
 Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val  
 20 25 30  
 Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile  
 35 40 45  
 Pro Ser Lys Val Ser Asp Gln Lys Arg  
 50 55

<210> 185  
 <211> 1650  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1627)  
 <223> RXA02640

<400> 185  
 accaacgacg acgccggtgt agcagatgta ttggagtggt ggttctaata ggtggtgtta 60  
 aaacactgct tagtggccca atacgtgcaa aaataaggcc atg aga atc tca aag 115  
 Met Arg Ile Ser Lys  
 1 5  
 gcc aat gcg tat gtt gca gcg att gac caa ggc acc act tcc act cgg 163  
 Ala Asn Ala Tyr Val Ala Ala Ile Asp Gln Gly Thr Thr Ser Thr Arg  
 10 15 20  
 tgc atc ttc att gat gcc caa gga aaa gtg gtg tct tct gct tcc aag 211  
 Cys Ile Phe Ile Asp Ala Gln Gly Lys Val Val Ser Ser Ala Ser Lys  
 25 30 35  
 gag cac cgc caa atc ttc cca caa cag ggc tgg gta gag cac gat cct 259  
 Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp Val Glu His Asp Pro  
 40 45 50  
 gaa gaa att tgg gac aac att cga tct gtc gtc agc cag gcg atg gtc 307  
 Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val Ser Gln Ala Met Val  
 55 60 65  
 tcc att gac atc acc cca cac gag gtt gca tcg ctg gga gtc acc aac 355  
 Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser Leu Gly Val Thr Asn  
 70 75 80 85  
 cag cgc gaa acc acc gtg gtg tgg gac aag cac acc ggc gaa cct gtc 403  
 Gln Arg Glu Thr Thr Val Val Trp Asp Lys His Thr Gly Glu Pro Val  
 90 95 100  
 tac aac gca atc gtg tgg caa gac acc cgc acc tct gac att tgc cta 451  
 Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr Ser Asp Ile Cys Leu  
 105 110 115  
 gag atc gcg ggc gaa gaa ggc cag gaa aag tgg ctt gac cgc acc ggc 499  
 Glu Ile Ala Gly Glu Glu Gly Gln Glu Lys Trp Leu Asp Arg Thr Gly  
 120 125 130

ctg ctg atc aac tcc tac cca tcg ggg ccc aaa atc aag tgg att ctc	547
Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys Ile Lys Trp Ile Leu	
135 140 145	
gac aac gtt gag gga gct cgc gaa cgc gcc gaa aag ggc gac ctt ttg	595
Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu Lys Gly Asp Leu Leu	
150 155 160 165	
ttt ggc acc atg gat acc tgg gtg ctg tgg aac ctg acc ggc ggt gtc	643
Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn Leu Thr Gly Gly Val	
170 175 180	
cgc ggc gac gac ggt gat gat gcc atc cac gtc acc gat gtc acc aac	691
Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val Thr Asp Val Thr Asn	
185 190 195	
gca tcc cgc aca cta ttg atg gat ctc cgc acg caa cag tgg gat cca	739
Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr Gln Gln Trp Asp Pro	
200 205 210	
gaa cta tgc gaa gcc cta gac att ccg atg tcc atg ctc cct gag att	787
Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser Met Leu Pro Glu Ile	
215 220 225	
cgt ccc tcc gtc gga gaa ttc cgc tcc gtg cgc cac cgc gga acc cta	835
Arg Pro Ser Val Gly Gln Phe Arg Ser Val Arg His Arg Gly Thr Leu	
230 235 240 245	
gcc gac gtc ccg att act ggc gtg ctc ggc gac cag caa gcg gcc ctt	883
Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp Gln Gln Ala Ala Leu	
250 255 260	
ttt ggt cag ggc gga ttc cac gaa ggt gct gct aaa aat acc tac ggc	931
Phe Gly Gln Gly Gly Phe His Glu Gly Ala Ala Lys Asn Thr Tyr Gly	
265 270 275	
acc ggc ctc ttc ctg ctg atg aac acc ggc acc tcg ttg aag att tcc	979
Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr Ser Leu Lys Ile Ser	
280 285 290	
gag cac ggc ctg ctg tcc acc atc gcc tat caa cgg gaa gga tcc gct	1027
Glu His Gly Leu Leu Ser Thr Ile Ala Tyr Gln Arg Glu Gly Ser Ala	
295 300 305	
ccg gtc tac gcg ctg gaa ggt tcc gta tcc atg ggc ggt tcc ttg gtg	1075
Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met Gly Gly Ser Leu Val	
310 315 320 325	
cag tgg ctg cgc gac aac cta cag cta atc ccc aac gca cca gcg att	1123
Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro Asn Ala Pro Ala Ile	
330 335 340	
gaa aac ctc gcc cga gaa gtc gaa gac aac ggt ggc gtt cat gtt gtc	1171
Glu Asn Leu Ala Arg Glu Val Glu Asp Asn Gly Gly Val His Val Val	
345 350 355	
cca gca ttc acc gga ctg ttc gca cca cgt tgg cgc ccc gat gct cgt	1219
Pro Ala Phe Thr Gly Leu Phe Ala Pro Arg Trp Arg Pro Asp Ala Arg	
360 365 370	

ggc gtc att aca ggc ctc acc cgt ttt gcc aac cgc aaa cac atc gcc 1267  
 Gly Val Ile Thr Gly Leu Thr Arg Phe Ala Asn Arg Lys His Ile Ala  
 375 380 385  
 cgc gca gtc ctt gaa gcc aac gcc ttc caa acc cgc gaa gtt gtg gac 1315  
 Arg Ala Val Leu Glu Ala Asn Ala Phe Gln Thr Arg Glu Val Val Asp  
 390 395 400 405  
 gcc atg gcc aaa gac gca ggc aaa gcc ctc gaa tcc ctc cgc gtc gac 1363  
 Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Glu Ser Leu Arg Val Asp  
 410 415 420  
 ggt gcg atg gtg gaa aat gac ctc ctc atg caa atg caa gcc gac ttc 1411  
 Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln Met Gln Ala Asp Phe  
 425 430 435  
 ctc ggc atc gac gtc caa cgt ctc gag gac gta gaa acc acc gcc gtc 1459  
 Leu Gly Ile Asp Val Gln Arg Leu Glu Asp Val Glu Thr Thr Ala Val  
 440 445 450  
 ggc gtc gca ttc gct gca ggt ctc ggc tct gga ttc ttc aaa aca act 1507  
 Gly Val Ala Phe Ala Ala Gly Leu Gly Ser Gly Phe Phe Lys Thr Thr  
 455 460 465  
 gac gag atc gaa aaa ctt att gca gtg aag aaa gtc tgg aac cct gac 1555  
 Asp Glu Ile Glu Lys Leu Ile Ala Val Lys Lys Val Trp Asn Pro Asp  
 470 475 480 485  
 atg agc gaa gaa gag cgc gaa cgt cgc tat gcc gaa tgg aat agg gca 1603  
 Met Ser Glu Glu Glu Arg Glu Arg Arg Tyr Ala Glu Trp Asn Arg Ala  
 490 495 500  
 gtg gag cat tct tat gac cag gcc tagctgattt gggtcggcct tta 1650  
 Val Glu His Ser Tyr Asp Gln Ala  
 505

&lt;210&gt; 186

&lt;211&gt; 509

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 186

Met Arg Ile Ser Lys Ala Asn Ala Tyr Val Ala Ala Ile Asp Gln Gly  
 1 5 10 15  
 Thr Thr Ser Thr Arg Cys Ile Phe Ile Asp Ala Gln Gly Lys Val Val  
 20 25 30  
 Ser Ser Ala Ser Lys Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp  
 35 40 45  
 Val Glu His Asp Pro Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val  
 50 55 60  
 Ser Gln Ala Met Val Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser  
 65 70 75 80  
 Leu Gly Val Thr Asn Gln Arg Glu Thr Thr Val Val Trp Asp Lys His  
 85 90 95

Thr Gly Glu Pro Val Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr  
 100 105 110  
 Ser Asp Ile Cys Leu Glu Ile Ala Gly Glu Glu Gly Gln Glu Lys Trp  
 115 120 125  
 Leu Asp Arg Thr Gly Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys  
 130 135 140  
 Ile Lys Trp Ile Leu Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu  
 145 150 155 160  
 Lys Gly Asp Leu Leu Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn  
 165 170 175  
 Leu Thr Gly Gly Val Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val  
 180 185 190  
 Thr Asp Val Thr Asn Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr  
 195 200 205  
 Gln Gln Trp Asp Pro Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser  
 210 215 220  
 Met Leu Pro Glu Ile Arg Pro Ser Val Gly Glu Phe Arg Ser Val Arg  
 225 230 235 240  
 His Arg Gly Thr Leu Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp  
 245 250 255  
 Gln Gln Ala Ala Leu Phe Gly Gln Gly Gly Phe His Glu Gly Ala Ala  
 260 265 270  
 Lys Asn Thr Tyr Gly Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr  
 275 280 285  
 Ser Leu Lys Ile Ser Glu His Gly Leu Leu Ser Thr Ile Ala Tyr Gln  
 290 295 300  
 Arg Glu Gly Ser Ala Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met  
 305 310 315 320  
 Gly Gly Ser Leu Val Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro  
 325 330 335  
 Asn Ala Pro Ala Ile Glu Asn Leu Ala Arg Glu Val Glu Asp Asn Gly  
 340 345 350  
 Gly Val His Val Val Pro Ala Phe Thr Gly Leu Phe Ala Pro Arg Trp  
 355 360 365  
 Arg Pro Asp Ala Arg Gly Val Ile Thr Gly Leu Thr Arg Phe Ala Asn  
 370 375 380  
 Arg Lys His Ile Ala Arg Ala Val Leu Glu Ala Asn Ala Phe Gln Thr  
 385 390 395 400  
 Arg Glu Val Val Asp Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Glu  
 405 410 415  
 Ser Leu Arg Val Asp Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln

420								425				430			
Met	Gln	Ala	Asp	Phe	Leu	Gly	Ile	Asp	Val	Gln	Arg	Leu	Glu	Asp	Val
435							440				445				
Glu	Thr	Thr	Ala	Val	Gly	Val	Ala	Phe	Ala	Ala	Gly	Leu	Gly	Ser	Gly
450				455				460							
Phe	Phe	Lys	Thr	Thr	Asp	Glu	Ile	Glu	Lys	Leu	Ile	Ala	Val	Lys	Lys
465					470			475				480			
Val	Trp	Asn	Pro	Asp	Met	Ser	Glu	Glu	Glu	Arg	Glu	Arg	Arg	Tyr	Ala
				485		490								495	
Glu	Trp	Asn	Arg	Ala	Val	Glu	His	Ser	Tyr	Asp	Gln	Ala			
500				505											

```
<210> 187
<211> 1119
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1096)  
<223> RXN01025
```

<400> 187																		
gggcagcagc	ggcaggtttc	caggaggttt	ccatgcgggt	ggcttgggac	atgggctaac												60	
ctgagacggt	taaatatcgt	tttcgaaagg	tgggtttcgc	gtg	gtt	tct	gta	agc										115
				Val	Val	Ser	Val	Ser										
					1			5										
gtg	atg	ggt	gca	ggt	tcc	tgg	gga	acc	acg	ttg	gcc	aag	gtc	ttc	tct		163	
Val	Met	Gly	Ala	Gly	Ser	Trp	Gly	Thr	Thr	Leu	Ala	Lys	Val	Phe	Ser			
				10				15						20				
gat	gct	ggc	aac	gct	gtg	acg	ttg	tgg	gcg	agg	cgg	gaa	gag	ttg	gca		211	
Asp	Ala	Gly	Asn	Ala	Val	Thr	Leu	Trp	Ala	Arg	Arg	Glu	Glu	Leu	Ala			
			25					30					35					
agc	acc	atc	cgt	gac	agc	cat	gaa	aac	cgt	gat	tac	ctt	ccg	ggg	att		259	
Ser	Thr	Ile	Arg	Asp	Ser	His	Glu	Asn	Arg	Asp	Tyr	Leu	Pro	Gly	Ile			
		40					45					50						
acg	ttg	ccg	gag	tcg	ctg	cag	gtc	aca	tca	tcg	gca	acg	gag	gct	tta		307	
Thr	Leu	Pro	Glu	Ser	Leu	Gln	Val	Thr	Ser	Ser	Ala	Thr	Glu	Ala	Leu			
	55					60					65							
gag	ggc	gca	gcc	att	gtg	gtg	ttg	gcg	att	cct	tcg	cag	gcg	ttg	cgt		355	
Glu	Gly	Ala	Ala	Ile	Val	Val	Leu	Ala	Ile	Pro	Ser	Gln	Ala	Leu	Arg			
70					75					80					85			
ggc	aat	ttg	gcg	gag	tgg	aaa	gag	acg	atc	ccg	cag	gat	gcg	acc	ttg		403	
Gly	Asn	Leu	Ala	Glu	Trp	Lys	Glu	Thr	Ile	Pro	Gln	Asp	Ala	Thr	Leu			
				90					95					100				
gtg	tcc	ttg	gct	aaa	ggt	att	gaa	aag	ggc	acg	cac	ctg	cgg	atg	agt		451	
Val	Ser	Leu	Ala	Lys	Gly	Ile	Glu	Lys	Gly	Thr	His	Leu	Arg	Met	Ser			

105										110										115										
gaa	gtg	atc	gcg	gag	gtg	acg	gaa	gcg	gat	cct	tca	cgc	atc	gcg	gtg	499														
Glu	Val	Ile	Ala	Glu	Val	Thr	Glu	Ala	Asp	Pro	Ser	Arg	Ile	Ala	Val															
120					125					130																				
ttg	tcg	ggg	cca	aac	ctt	gct	cgt	gag	atc	gcg	gag	ggg	cag	cct	gca	547														
Leu	Ser	Gly	Pro	Asn	Leu	Ala	Arg	Glu	Ile	Ala	Glu	Gly	Gln	Pro	Ala															
135					140					145																				
gct	acg	gtg	att	gct	tgc	cct	gat	gaa	aac	cga	gcg	aaa	ctt	gtg	cag	595														
Ala	Thr	Val	Ile	Ala	Cys	Pro	Asp	Glu	Asn	Arg	Ala	Lys	Leu	Val	Gln															
150					155					160					165															
gct	gca	gtg	gct	gcg	ccg	tat	ttc	cgc	ccg	tac	acc	aac	act	gat	gtg	643														
Ala	Ala	Val	Ala	Ala	Pro	Tyr	Phe	Arg	Pro	Tyr	Thr	Asn	Thr	Asp	Val															
170					175					180																				
gtg	ggc	act	gaa	atc	ggt	ggt	gcg	tgt	aag	aac	gtc	atc	gcg	ctg	gcc	691														
Val	Gly	Thr	Glu	Ile	Gly	Gly	Ala	Cys	Lys	Asn	Val	Ile	Ala	Leu	Ala															
185					190					195																				
tgt	ggt	att	tcc	cat	ggt	tac	ggc	ctg	ggt	gag	aac	acc	aat	gca	tcg	739														
Cys	Gly	Ile	Ser	His	Gly	Tyr	Gly	Leu	Gly	Glu	Asn	Thr	Asn	Ala	Ser															
200					205					210																				
ttg	att	act	cgt	ggc	ctt	gca	gag	atc	gca	cgc	ctc	ggt	gcc	aca	ttg	787														
Leu	Ile	Thr	Arg	Gly	Leu	Ala	Glu	Ile	Ala	Arg	Leu	Gly	Ala	Thr	Leu															
215					220					225																				
ggt	gcg	gat	gcg	aag	act	ttt	tct	ggc	ctt	gcg	gga	atg	ggc	gac	ttg	835														
Gly	Ala	Asp	Ala	Lys	Thr	Phe	Ser	Gly	Leu	Ala	Gly	Met	Gly	Asp	Leu															
230					235					240					245															
gtg	gct	acg	tgt	tca	tca	ccg	ctg	tcg	cgt	aac	cgc	agc	ttc	ggt	gag	883														
Val	Ala	Thr	Cys	Ser	Ser	Pro	Leu	Ser	Arg	Asn	Arg	Ser	Phe	Gly	Glu															
250					255					260																				
cgt	ttg	ggt	cag	ggt	gaa	tcc	cta	gag	aag	gct	cgc	gag	gca	acc	aat	931														
Arg	Leu	Gly	Gln	Gly	Glu	Ser	Leu	Glu	Lys	Ala	Arg	Glu	Ala	Thr	Asn															
265					270					275																				
ggt	cag	gtt	gcg	gag	ggt	gtt	att	tcc	tcg	cag	tcg	att	ttt	gat	ctt	979														
Gly	Gln	Val	Ala	Glu	Gly	Val	Ile	Ser	Ser	Gln	Ser	Ile	Phe	Asp	Leu															
280					285					290																				
gcc	acc	aag	ctt	ggt	gtg	gag	atg	ccg	atc	acc	cag	gct	gtc	tac	ggt	1027														
Ala	Thr	Lys	Leu	Gly	Val	Glu	Met	Pro	Ile	Thr	Gln	Ala	Val	Tyr	Gly															
295					300					305																				
gtg	tgc	cac	cga	gat	atg	aaa	gta	act	gac	atg	att	gtg	gct	ctc	atg	1075														
Val	Cys	His	Arg	Asp	Met	Lys	Val	Thr	Asp	Met	Ile	Val	Ala	Leu	Met															
310					315					320					325															
ggc	agg	tct	aag	aag	gct	gag	tagtcttagg	ttgtaagctt	caa							1119														
Gly	Arg	Ser	Lys	Lys	Ala	Glu																								
330																														

&lt;210&gt; 188

&lt;211&gt; 332

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 188

Val Val Ser Val Ser Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu  
 1 5 10 15  
 Ala Lys Val Phe Ser Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg  
 20 25 30  
 Arg Glu Glu Leu Ala Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp  
 35 40 45  
 Tyr Leu Pro Gly Ile Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser  
 50 55 60  
 Ala Thr Glu Ala Leu Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro  
 65 70 75 80  
 Ser Gln Ala Leu Arg Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro  
 85 90 95  
 Gln Asp Ala Thr Leu Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr  
 100 105 110  
 His Leu Arg Met Ser Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro  
 115 120 125  
 Ser Arg Ile Ala Val Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala  
 130 135 140  
 Glu Gly Gln Pro Ala Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg  
 145 150 155 160  
 Ala Lys Leu Val Gln Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr  
 165 170 175  
 Thr Asn Thr Asp Val Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn  
 180 185 190  
 Val Ile Ala Leu Ala Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu  
 195 200 205  
 Asn Thr Asn Ala Ser Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg  
 210 215 220  
 Leu Gly Ala Thr Leu Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala  
 225 230 235 240  
 Gly Met Gly Asp Leu Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn  
 245 250 255  
 Arg Ser Phe Gly Glu Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala  
 260 265 270  
 Arg Glu Ala Thr Asn Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln  
 275 280 285  
 Ser Ile Phe Asp Leu Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr  
 290 295 300



Gln Ala Val Tyr Gly Val Cys His Arg Asp Met Lys Val Thr Asp Met  
305 310 315 320

Ile Val Ala Leu Met Gly Arg Ser Lys Lys Ala Glu  
325 330

<210> 189  
<211> 1015  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1015)  
<223> FRXA01025

<400> 189  
gggcagcagc ggcagggttc cagraggttt ccatgcgggt ggcttggrac wtgggctaac 60  
ctgaracggt taaatatcgt ttctgaaagg tgggtttcgc gtg gtt tct gta agc 115  
Val Val Ser Val Ser  
1 5  
gtg atg ggt gca ggt tcc tgg gga acc acg ttg gcc aag gtc ttc tct 163  
Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu Ala Lys Val Phe Ser  
10 15 20  
gat gct ggc aac gct gtg acg ttg tgg gcg agg cgg gaa gag ttg gca 211  
Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg Arg Glu Glu Leu Ala  
25 30 35  
agc acc atc cgt gac agc cat gaa aac cgt gat tac ctt ccg ggg att 259  
Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp Tyr Leu Pro Gly Ile  
40 45 50  
acg ttg ccg gag tgc ctg cag gtc aca tca tgc gca acg gag gct tta 307  
Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser Ala Thr Glu Ala Leu  
55 60 65  
gag ggc gca gcc att gtg gtg ttg gcg att cct tgc cag gcg ttg cgt 355  
Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro Ser Gln Ala Leu Arg  
70 75 80 85  
ggc aat ttg gcg gag tgg aaa gag acg atc ccg cag gat gcg acc ttg 403  
Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro Gln Asp Ala Thr Leu  
90 95 100  
gtg tcc ttg gct aaa ggt att gaa aag ggc acg cac ctg cgg atg agt 451  
Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr His Leu Arg Met Ser  
105 110 115  
gaa gtg atc gcg gag gtg acg gaa gcg gat cct tca cgc atc gcg gtg 499  
Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro Ser Arg Ile Ala Val  
120 125 130  
ttg tgc ggg cca aac ctt gct cgt gag atc gcg gag ggg cag cct gca 547  
Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala Glu Gly Gln Pro Ala  
135 140 145  
gct acg gtg att gct tgc cct gat gaa aac cga gcg aaa ctt gtg cag 595

Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg Ala Lys Leu Val Gln  
 150 155 160 165

gct gca gtg gct gcg ccg tat ttc cgc ccg tac acc aac act gat gtg 643  
 Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr Thr Asn Thr Asp Val  
 170 175 180

gtg ggc act gaa atc ggt ggt gcg tgt aag aac gtc atc gcg ctg gcc 691  
 Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn Val Ile Ala Leu Ala  
 185 190 195

tgt ggt att tcc cat ggt tac ggc ctg ggt gag aac acc aat gca tcg 739  
 Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu Asn Thr Asn Ala Ser  
 200 205 210

ttg att act cgt ggc ctt gca gag atc gca cgc ctc ggt gcc aca ttg 787  
 Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg Leu Gly Ala Thr Leu  
 215 220 225

ggt gcg gat gcg aag act ttt tct ggc ctt gcg gga atg ggc gac ttg 835  
 Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala Gly Met Gly Asp Leu  
 230 235 240 245

gtg gct acg tgt tca tca ccg ctg tcg cgt aac cgc agc ttc ggt gag 883  
 Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn Arg Ser Phe Gly Glu  
 250 255 260

cgt ttg ggt cag ggt gaa tcc cta gag aag gct cgc gag gca acc aat 931  
 Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala Arg Glu Ala Thr Asn  
 265 270 275

ggt cag gtt gcg gag ggt gtt att tcc tcg cag tcg att ttt gat ctt 979  
 Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln Ser Ile Phe Asp Leu  
 280 285 290

gcc acc aag ctt ggt gtg gag atg ccg atc acc cag 1015  
 Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr Gln  
 295 300 305

&lt;210&gt; 190

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 190

Val Val Ser Val Ser Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu  
 1 5 10 15

Ala Lys Val Phe Ser Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg  
 20 25 30

Arg Glu Glu Leu Ala Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp  
 35 40 45

Tyr Leu Pro Gly Ile Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser  
 50 55 60

Ala Thr Glu Ala Leu Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro  
 65 70 75 80

```
<210> 191
<211> 1809
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1786)  
<223> RXA01851
```

```
<400> 191
ttgtggcctt tttgcagggg aaacttattt aaataattca taagtaaaaa accgtcaatt 60

cacgatgtgg gttggcgggt ttcctattag gctcactttt atg acg agc gca cac    115
                Met Thr Ser Ala His
```

	1	5	
ttt gaa tcc cgc cgg att ggc cct ccg ctt cgc gat aat tat gac gtc	163		
Phe Glu Ser Arg Arg Ile Gly Pro Pro Leu Arg Asp Asn Tyr Asp Val			
10 15 20			
att gtg att ggc ggt ggt atc tca ggt gta cag att gcg cga cat gct	211		
Ile Val Ile Gly Gly Gly Ile Ser Gly Val Gln Ile Ala Arg His Ala			
25 30 35			
caa ggc cgc ggt tta cgc act gtg atg ttt gag gcc aga gat tat tct	259		
Gln Gly Arg Gly Leu Arg Thr Val Met Phe Glu Ala Arg Asp Tyr Ser			
40 45 50			
tct gga aca tca tcg aca acc tcc aag atg att cat ggt ggt ttg cgc	307		
Ser Gly Thr Ser Ser Thr Thr Ser Lys Met Ile His Gly Gly Leu Arg			
55 60 65			
tat ttg gag cag tac gat ttc ggc gtg gtc cag gaa gcc gtg aag gaa	355		
Tyr Leu Glu Gln Tyr Asp Phe Gly Val Val Gln Glu Ala Val Lys Glu			
70 75 80 85			
cgc cgg tac cta ggt atc gcc gct ccg cat ttg gtg gct cca cgc agt	403		
Arg Arg Tyr Leu Gly Ile Ala Ala Pro His Leu Val Ala Pro Arg Ser			
90 95 100			
ttc atg ctc acg gcg ttt gat tgg tca gag ccg aaa gcc cct atg ttg	451		
Phe Met Leu Thr Ala Phe Asp Trp Ser Glu Pro Lys Ala Pro Met Leu			
105 110 115			
ggt gct ggt gtg gcg ttg tat gaa acg atg gcg tgg cag cgt aac cag	499		
Gly Ala Gly Val Ala Leu Tyr Glu Thr Met Ala Trp Gln Arg Asn Gln			
120 125 130			
ggg caa tcg aag gaa aac cac tcg ccg cgt ttc cgg tgg att cct aaa	547		
Gly Gln Ser Lys Glu Asn His Ser Pro Arg Phe Arg Trp Ile Pro Lys			
135 140 145			
aat gca ctg ctc aag gaa gtc ccg tgg ctt gac ccg gag ggc ttg aag	595		
Asn Ala Leu Leu Lys Glu Val Pro Trp Leu Asp Pro Glu Gly Leu Lys			
150 155 160 165			
gga gcg tgg cgc cac gat gat acg ttg aat ctc cat gca gaa cga ctc	643		
Gly Ala Trp Arg His Asp Asp Thr Leu Asn Leu His Ala Glu Arg Leu			
170 175 180			
ctc ctc gcg gtg att aaa gct ttt gcg gca gat ggc gga acg gcg atc	691		
Leu Leu Ala Val Ile Lys Ala Phe Ala Ala Asp Gly Gly Thr Ala Ile			
185 190 195			
aac cac gcc aaa gtc act cgc att ctc cgg aac gtg gaa gaa ggc cgc	739		
Asn His Ala Lys Val Thr Arg Ile Leu Arg Asn Val Glu Glu Gly Arg			
200 205 210			
gtc aag ggt gta gaa gtg act gat cag gtc acc aac acc acg cat gag	787		
Val Lys Gly Val Glu Val Thr Asp Gln Val Thr Asn Thr Thr His Glu			
215 220 225			
gtg aat gcc cct gtg gtg atc aac gct gcg ggt ccg tgg gtt gcg cag	835		
Val Asn Ala Pro Val Val Ile Asn Ala Ala Gly Pro Trp Val Ala Gln			
230 235 240 245			

gcg ttg ggt gat ttg gcg gag gta acc aag ttg aag gtg cgc caa tcc	883
Ala Leu Gly Asp Leu Ala Glu Val Thr Lys Leu Lys Val Arg Gln Ser	
250 255 260	
aag gga gtg cat ttg ctc act ggt gat ttg ggc agc cag agt ggc gtg	931
Lys Gly Val His Leu Leu Thr Gly Asp Leu Gly Ser Gln Ser Gly Val	
265 270 275	
ttt gtg cgt ggc aaa aac ggc aag cat gtg atc gtg aat ccg tgg atg	979
Phe Val Arg Gly Lys Asn Gly Lys His Val Ile Val Asn Pro Trp Met	
280 285 290	
ggg cgc acc ctt att ggt cca acc gac acc atg att gac ggt gac gct	1027
Gly Arg Thr Leu Ile Gly Pro Thr Asp Thr Met Ile Asp Gly Asp Ala	
295 300 305	
gat gat gcg gct gca gat gaa agc gat atc gat ttg ctg ctt gag acc	1075
Asp Asp Ala Ala Ala Asp Glu Ser Asp Ile Asp Leu Leu Leu Glu Thr	
310 315 320 325	
atc gat tcg gta cgc gct aca ccg ctt gat cgc aaa gag atc atc tcc	1123
Ile Asp Ser Val Arg Ala Thr Pro Leu Asp Arg Lys Glu Ile Ile Ser	
330 335 340	
acg ctg gtg ggt gtg cgc ccg ctt gtt gat gac ggc acc gac acc tac	1171
Thr Leu Val Gly Val Arg Pro Leu Val Asp Asp Gly Thr Asp Thr Tyr	
345 350 355	
acg tcc tct cgc cgt ttc gat att tcc gat cac gcc aac gtc ggc att	1219
Thr Ser Ser Arg Arg Phe Asp Ile Ser Asp His Ala Asn Val Gly Ile	
360 365 370	
gat ggt ttg gtg tct gtc tct ggc ggc aag tgg acc act tcc cgc gtg	1267
Asp Gly Leu Val Ser Val Ser Gly Gly Lys Trp Thr Thr Ser Arg Val	
375 380 385	
atg ggg tac aag gtg att gag cat gtg gtg gag cac caa gct gcg gtg	1315
Met Gly Tyr Lys Val Ile Glu His Val Val Glu His Gln Ala Ala Val	
390 395 400 405	
tta cct ccg ctg cgc cac ttt gac tcc agg cag atg ccg ttg agt act	1363
Leu Pro Pro Leu Arg His Phe Asp Ser Arg Gln Met Pro Leu Ser Thr	
410 415 420	
tct ttt ggc gcg tat gag tcc gtg gct gat tcc ttt gag tca gcg ctt	1411
Ser Phe Gly Ala Tyr Glu Ser Val Ala Asp Ser Phe Glu Ser Ala Leu	
425 430 435	
cgc agc cac ccc gag ctg gat gtg gat gat gaa atc cgc gtg cat ctg	1459
Arg Ser His Pro Glu Leu Asp Val Asp Asp Glu Ile Arg Val His Leu	
440 445 450	
gcc aga ctg tat gga act gag cat gaa aaa gtg ctg gat ctc gtc gca	1507
Ala Arg Leu Tyr Gly Thr Glu His Glu Lys Val Leu Asp Leu Val Ala	
455 460 465	
aag caa ccc gac ctg ggg cgc cga ctt gac cca gac aac ctt gat atc	1555
Lys Gln Pro Asp Leu Gly Arg Arg Leu Asp Pro Asp Asn Leu Asp Ile	
470 475 480 485	

gcg gcg cag gcc gtt ttt gct gtc gcc gag gag gcg gcc gtc gac ctg 1603  
 Ala Ala Gln Ala Val Phe Ala Val Ala Glu Glu Ala Ala Val Asp Leu  
 490 495 500

gcg gac gtg ctg gat cgt cgc atc gtg ctc ggc acg ctg ggt tat gtg 1651  
 Ala Asp Val Leu Asp Arg Arg Ile Val Leu Gly Thr Leu Gly Tyr Val  
 505 510 515

caa ccg gct gcc gtg cgt gcg acg gcc gaa gca atg gcg cag gtc acc 1699  
 Gln Pro Ala Ala Val Arg Ala Thr Ala Glu Ala Met Ala Gln Val Thr  
 520 525 530

ggg tgg tca gct gag ctt atc gac gcc cag tgc cag tcc tac ctc gcc 1747  
 Gly Trp Ser Ala Glu Leu Ile Asp Ala Gln Cys Gln Ser Tyr Leu Ala  
 535 540 545

aag caa gac aaa atc caa gcc gtg tta aag ccg tac cgc taacactccg 1796  
 Lys Gln Asp Lys Ile Gln Ala Val Leu Lys Pro Tyr Arg  
 550 555 560

tcacgcacac cgg 1809

<210> 192  
 <211> 562  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 192  
 Met Thr Ser Ala His Phe Glu Ser Arg Arg Ile Gly Pro Pro Leu Arg  
 1 5 10 15

Asp Asn Tyr Asp Val Ile Val Ile Gly Gly Gly Ile Ser Gly Val Gln  
 20 25 30

Ile Ala Arg His Ala Gln Gly Arg Gly Leu Arg Thr Val Met Phe Glu  
 35 40 45

Ala Arg Asp Tyr Ser Ser Gly Thr Ser Ser Thr Thr Ser Lys Met Ile  
 50 55 60

His Gly Gly Leu Arg Tyr Leu Glu Gln Tyr Asp Phe Gly Val Val Gln  
 65 70 75 80

Glu Ala Val Lys Glu Arg Arg Tyr Leu Gly Ile Ala Ala Pro His Leu  
 85 90 95

Val Ala Pro Arg Ser Phe Met Leu Thr Ala Phe Asp Trp Ser Glu Pro  
 100 105 110

Lys Ala Pro Met Leu Gly Ala Gly Val Ala Leu Tyr Glu Thr Met Ala  
 115 120 125

Trp Gln Arg Asn Gln Gly Gln Ser Lys Glu Asn His Ser Pro Arg Phe  
 130 135 140

Arg Trp Ile Pro Lys Asn Ala Leu Leu Lys Glu Val Pro Trp Leu Asp  
 145 150 155 160

Pro Glu Gly Leu Lys Gly Ala Trp Arg His Asp Asp Thr Leu Asn Leu  
 165 170 175

His Ala Glu Arg Leu Leu Leu Ala Val Ile Lys Ala Phe Ala Ala Asp  
 180 185 190  
 Gly Gly Thr Ala Ile Asn His Ala Lys Val Thr Arg Ile Leu Arg Asn  
 195 200 205  
 Val Glu Glu Gly Arg Val Lys Gly Val Glu Val Thr Asp Gln Val Thr  
 210 215 220  
 Asn Thr Thr His Glu Val Asn Ala Pro Val Val Ile Asn Ala Ala Gly  
 225 230 235 240  
 Pro Trp Val Ala Gln Ala Leu Gly Asp Leu Ala Glu Val Thr Lys Leu  
 245 250 255  
 Lys Val Arg Gln Ser Lys Gly Val His Leu Leu Thr Gly Asp Leu Gly  
 260 265 270  
 Ser Gln Ser Gly Val Phe Val Arg Gly Lys Asn Gly Lys His Val Ile  
 275 280 285  
 Val Asn Pro Trp Met Gly Arg Thr Leu Ile Gly Pro Thr Asp Thr Met  
 290 295 300  
 Ile Asp Gly Asp Ala Asp Asp Ala Ala Ala Asp Glu Ser Asp Ile Asp  
 305 310 315 320  
 Leu Leu Leu Glu Thr Ile Asp Ser Val Arg Ala Thr Pro Leu Asp Arg  
 325 330 335  
 Lys Glu Ile Ile Ser Thr Leu Val Gly Val Arg Pro Leu Val Asp Asp  
 340 345 350  
 Gly Thr Asp Thr Tyr Thr Ser Ser Arg Arg Phe Asp Ile Ser Asp His  
 355 360 365  
 Ala Asn Val Gly Ile Asp Gly Leu Val Ser Val Ser Gly Gly Lys Trp  
 370 375 380  
 Thr Thr Ser Arg Val Met Gly Tyr Lys Val Ile Glu His Val Val Glu  
 385 390 395 400  
 His Gln Ala Ala Val Leu Pro Pro Leu Arg His Phe Asp Ser Arg Gln  
 405 410 415  
 Met Pro Leu Ser Thr Ser Phe Gly Ala Tyr Glu Ser Val Ala Asp Ser  
 420 425 430  
 Phe Glu Ser Ala Leu Arg Ser His Pro Glu Leu Asp Val Asp Asp Glu  
 435 440 445  
 Ile Arg Val His Leu Ala Arg Leu Tyr Gly Thr Glu His Glu Lys Val  
 450 455 460  
 Leu Asp Leu Val Ala Lys Gln Pro Asp Leu Gly Arg Arg Leu Asp Pro  
 465 470 475 480  
 Asp Asn Leu Asp Ile Ala Ala Gln Ala Val Phe Ala Val Ala Glu Glu  
 485 490 495

Ala Ala Val Asp Leu Ala Asp Val Leu Asp Arg Arg Ile Val Leu Gly  
                   500                  505                  510

Thr Leu Gly Tyr Val Gln Pro Ala Val Arg Ala Thr Ala Glu Ala  
           515                  520                  525

Met Ala Gln Val Thr Gly Trp Ser Ala Glu Leu Ile Asp Ala Gln Cys  
       530                  535                  540

Gln Ser Tyr Leu Ala Lys Gln Asp Lys Ile Gln Ala Val Leu Lys Pro  
 545                  550                  555                  560

Tyr Arg

<210> 193  
 <211> 900  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(877)  
 <223> RXA01242

<400> 193  
 cgccggcaac caaatgaggc ttttgggcgt tggacagtga gacaatgggt aagaaattcg 60

gacatatatta gtaaatggc tttttgcttt aaggagtgc atg tac gca gag gag 115  
   Met Tyr Ala Glu Glu  
   1                  5

cgc cgt cga cag att gcc tca tta acg gca gtt gag gga cgt gta aat 163  
 Arg Arg Arg Gln Ile Ala Ser Leu Thr Ala Val Glu Gly Arg Val Asn  
                   10                  15                  20

gtc aca gaa tta gcg ggc cga ttc gat gtc act gca gag acg att cga 211  
 Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr Ala Glu Thr Ile Arg  
                   25                  30                  35

cga gac ctt gcg gtg cta gac cgc gag gga att gtt cac cgc gtt cac 259  
 Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile Val His Arg Val His  
                   40                  45                  50

ggt ggc gca gta gcc acc caa tct ttc caa acc aca gag ttg agc ttg 307  
 Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr Thr Glu Leu Ser Leu  
                   55                  60                  65

gat act cgt ttc agg tct gca tcg tca gca aag tac tcc att gcc aag 355  
 Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys Tyr Ser Ile Ala Lys  
                   70                  75                  80                  85

gca gcg atg cag ttc ctg ccc gct gag cat ggc gga ctg ttc ctc gat 403  
 Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly Gly Leu Phe Leu Asp  
                   90                  95                  100

gcg gga act act gtt act gct ttg gcc gat ctc att tct gag cat cct 451  
 Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu Ile Ser Glu His Pro  
                   105                  110                  115



agc tcc aag cag tgg tcg atc gtg acc aac tgc ctc ccc atc gca ctt 499  
 Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys Leu Pro Ile Ala Leu  
 120 125 130

aat ctg gcc aac gcc ggg ctt gat gat gtc cag ctg ctt gga gga agc 547  
 Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln Leu Leu Gly Gly Ser  
 135 140 145

gtt cgc gcg atc acc cag gct gtt gtg ggt gac act gcg ctt cgt act 595  
 Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp Thr Ala Leu Arg Thr  
 150 155 160 165

ctc gcg ctg atg cgt gcg gat gta gtg ttc atc ggc acc aac gcg ttg 643  
 Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile Gly Thr Asn Ala Leu  
 170 175 180

acg ttg gat cac gga ttg tct acg gcc gat tcc caa gag gct gcc atg 691  
 Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser Gln Glu Ala Ala Met  
 185 190 195

aaa tct gcg atg atc acc aac gcc cac aag gtg gtg gtg ttg tgt gac 739  
 Lys Ser Ala Met Ile Thr Asn Ala His Lys Val Val Val Leu Cys Asp  
 200 205 210

tcc acc aag atg ggc acc gac tac ctc gtg agc ttt ggc gca atc agc 787  
 Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser Phe Gly Ala Ile Ser  
 215 220 225

gat atc gat gtg gtg gtc acc gat gcg ggt gca cca gca agt ttc gtt 835  
 Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala Pro Ala Ser Phe Val  
 230 235 240 245

gag cag ttg cga gaa cgc gat gta gaa gtt gtg att gca gaa 877  
 Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val Ile Ala Glu  
 250 255

tgattcttac agtcaactgca agt 900

&lt;210&gt; 194

&lt;211&gt; 259

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 194

Met Tyr Ala Glu Glu Arg Arg Arg Gln Ile Ala Ser Leu Thr Ala Val  
1 5 10 15

Glu Gly Arg Val Asn Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr  
20 25 30

Ala Glu Thr Ile Arg Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile  
35 40 45

Val His Arg Val His Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr  
50 55 60

Thr Glu Leu Ser Leu Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys  
65 70 75 80

Tyr Ser Ile Ala Lys Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly

85										90					95						
Gly	Leu	Phe	Leu	Asp	Ala	Gly	Thr	Thr	Val	Thr	Ala	Leu	Ala	Asp	Leu						
			100					105					110								
Ile	Ser	Glu	His	Pro	Ser	Ser	Lys	Gln	Trp	Ser	Ile	Val	Thr	Asn	Cys						
		115					120					125									
Leu	Pro	Ile	Ala	Leu	Asn	Leu	Ala	Asn	Ala	Gly	Leu	Asp	Asp	Val	Gln						
	130					135					140										
Leu	Leu	Gly	Gly	Ser	Val	Arg	Ala	Ile	Thr	Gln	Ala	Val	Val	Gly	Asp						
145					150					155				160							
Thr	Ala	Leu	Arg	Thr	Leu	Ala	Leu	Met	Arg	Ala	Asp	Val	Val	Phe	Ile						
			165					170						175							
Gly	Thr	Asn	Ala	Leu	Thr	Leu	Asp	His	Gly	Leu	Ser	Thr	Ala	Asp	Ser						
		180					185						190								
Gln	Glu	Ala	Ala	Met	Lys	Ser	Ala	Met	Ile	Thr	Asn	Ala	His	Lys	Val						
	195						200					205									
Val	Val	Leu	Cys	Asp	Ser	Thr	Lys	Met	Gly	Thr	Asp	Tyr	Leu	Val	Ser						
	210					215					220										
Phe	Gly	Ala	Ile	Ser	Asp	Ile	Asp	Val	Val	Val	Thr	Asp	Ala	Gly	Ala						
225					230					235				240							
Pro	Ala	Ser	Phe	Val	Glu	Gln	Leu	Arg	Glu	Arg	Asp	Val	Glu	Val	Val						
			245					250					255								

Ile Ala Glu

<210> 195  
 <211> 969  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(946)  
 <223> RXA02288

<400> 195  
 aacaacaatc taacgccatc atgtttataaa aaagcaagac ctaacataaa aatgtagaa 60.  
 agtgctggat ctaacaacat ttccgtggta actttttcac atg tcc caa gtg att 115  
 Met Ser Gln Val Ile  
 1 5  
 ccc gcc agc tca caa gaa aag cgt cgt gag cgc atc gtt tct tat gtc 163  
 Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg Ile Val Ser Tyr Val  
 10 15 20  
 acc cgt cat gga ttc gct cgt gtt gaa gca tta gct gag ctt ttt gag 211  
 Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu Ala Glu Leu Phe Glu  
 25 30 35

gtc agc gca atg acc att cac cgt gat ttg gag gcg ctg gct gca gac	259
Val Ser Ala Met Thr Ile His Arg Asp Leu Glu Ala Leu Ala Ala Asp	
40 45 50	
aat ttg gtg gag cgc att agg ggt ggc gcg cgt tcg gtg tcg ccg tcg	307
Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg Ser Val Ser Pro Ser	
55 60 65	
atg agt gag ttg gca gtg gag cag cgt cgg cat ttg cat cgc act gtt	355
Met Ser Glu Leu Ala Val Glu Gln Arg Arg His Leu His Arg Thr Val	
70 75 80 85	
aaa gag gcg ttg tgt act gca gca gca cgg ttg att ccg gag ggc gct	403
Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu Ile Pro Glu Gly Ala	
90 95 100	
gtg gtg gcg att gat gat tcc acc acg ttg gag tct ttg gtt gag aag	451
Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu Ser Leu Val Glu Lys	
105 110 115	
ttg ccg cag cgg tca cca tcg gcg ttg att acg cat tct ttg aag aca	499
Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr His Ser Leu Lys Thr	
120 125 130	
atg gcg gat cat cgt gtg cgc gcc ggg atg agc gat atc cgt ttg att	547
Met Ala Asp His Arg Val Arg Ala Gly Met Ser Asp Ile Arg Leu Ile	
135 140 145	
gcg tgt gcg gga ttg tat ttc gcg gag act gat tct ttc ttg ggc aag	595
Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp Ser Phe Leu Gly Lys	
150 155 160 165	
gca act tca gcg cag ttg aat gag ctg tcg gcg gat att tct ttt gtt	643
Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala Asp Ile Ser Phe Val	
170 175 180	
tct acg act gcg gtg cgc gct acg ggg gag gtt ccg gcg ctg ttt cat	691
Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val Pro Ala Leu Phe His	
185 190 195	
cct gat atg gag gct gct gat acg aag cgg gcg ttg att ggg att ggt	739
Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala Leu Ile Gly Ile Gly	
200 205 210	
agc gtg cgt gtg ttg gtg gtg gat tct agt aaa ttt ggt tcg gct ggt	787
Ser Val Arg Val Leu Val Val Asp Ser Ser Lys Phe Gly Ser Ala Gly	
215 220 225	
gtg ttc aag gtt gct tcg att gag gag ttt gac cac atc atc att gat	835
Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp His Ile Ile Ile Asp	
230 235 240 245	
cag cag tgc acc cgt gag cag cgg gat ctt ttg cgt aat tcg cgc gcg	883
Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu Arg Asn Ser Arg Ala	
250 255 260	
cag atc cat gtg att gac cac aat ggt gat gaa att ttg gat acc cca	931
Gln Ile His Val Ile Asp His Asn Gly Asp Glu Ile Leu Asp Thr Pro	
265 270 275	
acg gaa gag gat ttt taagatggct ttggttcttg gaa	969

Thr Glu Glu Asp Phe  
280

<210> 196

<211> 282

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 196

Met Ser Gln Val Ile Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg  
1 5 10 15

Ile Val Ser Tyr Val Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu  
20 25 30

Ala Glu Leu Phe Glu Val Ser Ala Met Thr Ile His Arg Asp Leu Glu  
35 40 45

Ala Leu Ala Ala Asp Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg  
50 55 60

Ser Val Ser Pro Ser Met Ser Glu Leu Ala Val Glu Gln Arg Arg His  
65 70 75 80

Leu His Arg Thr Val Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu  
85 90 95

Ile Pro Glu Gly Ala Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu  
100 105 110

Ser Leu Val Glu Lys Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr  
115 120 125

His Ser Leu Lys Thr Met Ala Asp His Arg Val Arg Ala Gly Met Ser  
130 135 140

Asp Ile Arg Leu Ile Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp  
145 150 155 160

Ser Phe Leu Gly Lys Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala  
165 170 175

Asp Ile Ser Phe Val Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val  
180 185 190

Pro Ala Leu Phe His Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala  
195 200 205

Leu Ile Gly Ile Gly Ser Val Arg Val Leu Val Val Asp Ser Ser Lys  
210 215 220

Phe Gly Ser Ala Gly Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp  
225 230 235 240

His Ile Ile Ile Asp Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu  
245 250 255

Arg Asn Ser Arg Ala Gln Ile His Val Ile Asp His Asn Gly Asp Glu  
260 265 270

Ile Leu Asp Thr Pro Thr Glu Glu Asp Phe  
275 280

<210> 197  
<211> 887  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (1)..(864)  
<223> RXN01891

<400> 197  
ggt ggc cac tat ggt ttg cct ttc gct cgc tcc act gtc ctc ttc tac 48  
Gly Gly His Tyr Gly Leu Pro Phe Ala Arg Ser Thr Val Leu Phe Tyr  
1 5 10 15  
tac aac aag gat ctg tgg gct aag gct ggc ctg gaa gat cgt ggc cca 96  
Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly Pro  
20 25 30  
gag tca tgg gaa gag ttc tcc gag tgg ggt cca aag ctg cag gaa gcg 144  
Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu Ala  
35 40 45  
atg gac agt ggt ttc gca cac ggt tgg gga gat gca acc aac tac ctt 192  
Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr Leu  
50 55 60  
tct tgg act ttc gaa ggc cca atg tgg tcc ctc ggc ggc aac tac tct 240  
Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr Ser  
65 70 75 80  
gaa ggt tgg gag tcc cgt ctg act acc cca gag acc atc cgt gca gtt 288  
Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala Val  
85 90 95  
gag tgg ctc aag tcc acc gtt gat gaa ggt ttc gca acc gtc tcc acc 336  
Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser Thr  
100 105 110  
gac gtc acc aac gag ttc gca acc ggc ctg atc ggt tca tgc atc cag 384  
Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile Gln  
115 120 125  
tcc acc ggt gat ctg tct tcg gtt gcc ggc gct gca agc ttc gac tgg 432  
Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp Trp  
130 135 140  
ggc gta gca gca ctt cct aac cca acc ggc gag ggc gct tgc cca acc 480  
Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro Thr  
145 150 155 160  
ggt ggc gca ggc ctg gga atc cca tct ggc atc tct gag cag cgt cag 528  
Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg Gln  
165 170 175  
gac aac gcc ctg aag ttc atc gac ttc ctc acc aac gcc gcg aac act 576  
Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn Thr

180	185	190	
ggc tac tgg tcc cgc gag acc ggt tat gtt cca gtt cgt aag gat gct			624
Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp Ala			
195	200	205	
gca tct gat cca gat cac gca gca ttc ctc gag gag aac cct gca tac			672
Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala Tyr			
210	215	220	
aac gtt gca gtg gag cag ctt cct gat acc cgt tcc cag gac aac ttc			720
Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn Phe			
225	230	235	240
cgc gtg ctg ctg cca aac ggt gac cgc acc atc ggt gac gca ctg gag			768
Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu Glu			
245	250	255	
aag atc tgc ctg act ggt gca gac atc gat gtc acc ctg gct gag gtt			816
Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu Val			
260	265	270	
gag acc aag ctg aac acc atc tac acc cgc gac atc gaa cca ctt att			864
Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu Ile			
275	280	285	
taatccgagc acttcagcta cac			887

&lt;210&gt; 198

&lt;211&gt; 288

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 198

Gly Gly His Tyr Gly Leu Pro Phe Ala Arg Ser Thr Val Leu Phe Tyr
1 5 10 15

Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly Pro
20 25 30

Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu Ala
35 40 45

Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr Leu
50 55 60

Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr Ser
65 70 75 80

Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala Val
85 90 95

Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser Thr
100 105 110

Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile Gln
115 120 125

Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp Trp
130 135 140

Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro Thr  
 145 150 155 160  
 Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg Gln  
 165 170 175  
 Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn Thr  
 180 185 190  
 Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp Ala  
 195 200 205  
 Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala Tyr  
 210 215 220  
 Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn Phe  
 225 230 235 240  
 Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu Glu  
 245 250 255  
 Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu-Ala Glu Val  
 260 265 270  
 Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu Ile  
 275 280 285

<210> 199  
 <211> 842  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(819)  
 <223> FRXA01891

<400> 199  
 tac tac aac aag gat ctg tgg gct aag gct ggc ctg gaa gat cgt ggc 48  
 Tyr Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly  
 1 5 10 15  
 cca gag tca tgg gaa gag ttc tcc gag tgg ggt cca aag ctg cag gaa 96  
 Pro Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu  
 20 25 30  
 gcg atg gac agt ggt ttc gca cac ggt tgg gga gat gca acc aac tac 144  
 Ala Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr  
 35 40 45  
 ctt tct tgg act ttc gaa ggc cca atg tgg tcc ctc ggc ggc aac tac 192  
 Leu Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr  
 50 55 60  
 tct gaa ggt tgg gag tcc cgt ctg act acc cca gag acc atc cgt gca 240  
 Ser Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala

65	70	75	80	
ggt gag tgg ctc aag tcc acc gtt gat gaa ggt ttc gca acc gtc tcc				288
Val Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser				
	85	90	95	
acc gac gtc acc aac gag ttc gca acc ggc ctg atc ggt tca tgc atc				336
Thr Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile				
	100	105	110	
cag tcc acc ggt gat ctg tct tcg gtt gcc ggc gct gca agc ttc gac				384
Gln Ser Thr Gly Asp Leu Ser Val Ala Gly Ala Ala Ser Phe Asp				
	115	120	125	
tgg ggc gta gca gca ctt cct aac cca acc ggc gag ggc gct tgc cca				432
Trp Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro				
	130	135	140	
acc ggt ggc gca ggc ctg gga atc cca tct ggc atc tct gag cag cgt				480
Thr Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg				
	145	150	155	160
cag gac aac gcc ctg aag ttc atc gac ttc ctc acc aac gcc gcg aac				528
Gln Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn				
	165	170	175	
act ggc tac tgg tcc cgc gag acc ggt tat gtt cca gtt cgt aag gat				576
Thr Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp				
	180	185	190	
gct gca tct gat cca gat cac gca gca ttc ctc gag gag aac cct gca				624
Ala Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala				
	195	200	205	
tac aac gtt gca gtg gag cag ctt cct gat acc cgt tcc cag gac aac				672
Tyr Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn				
	210	215	220	
ttc cgc gtg ctg ctg cca aac ggt gac cgc acc atc ggt gac gca ctg				720
Phe Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu				
	225	230	235	240
gag aag atc tgc ctg act ggt gca gac atc gat gtc acc ctg gct gag				768
Glu Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu				
	245	250	255	
ggt gag acc aag ctg aac acc atc tac acc cgc gac atc gaa cca ctt				816
Val Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu				
	260	265	270	
att taatccgagc acttcagcta cac				842
Ile				

&lt;210&gt; 200

&lt;211&gt; 273

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 200



Tyr Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly  
 1 5 10 15  
 Pro Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu  
 20 25 30  
 Ala Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr  
 35 40 45  
 Leu Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr  
 50 55 60  
 Ser Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala  
 65 70 75 80  
 Val Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser  
 85 90 95  
 Thr Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile  
 100 105 110  
 Gln Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp  
 115 120 125  
 Trp Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro  
 130 135 140  
 Thr Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg  
 145 150 155 160  
 Gln Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn  
 165 170 175  
 Thr Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp  
 180 185 190  
 Ala Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala  
 195 200 205  
 Tyr Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn  
 210 215 220  
 Phe Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu  
 225 230 235 240  
 Glu Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu  
 245 250 255  
 Val Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu  
 260 265 270

Ile

&lt;210&gt; 201

&lt;211&gt; 776

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (7)..(753)

&lt;223&gt; RXA02414

&lt;400&gt; 201

```

tttaccatg agt tac aac agc ccg tat aac aac acg aat ttc agc acc act 51
  Met Ser Tyr Asn Ser Pro Tyr Asn Asn Thr Asn Phe Ser Thr Thr
    1             5             10             15

ggc gcg ttc caa cct gct ggt ggg ccg gtg aag ccg tgg aat aag ccc 99
Gly Ala Phe Gln Pro Ala Gly Gly Pro Val Lys Pro Trp Asn Lys Pro
                20             25             30

gat gcc agc ctg aat cag cag ctg aaa aac aaa tcc cgt gtg cgc aca 147
Asp Ala Ser Leu Asn Gln Gln Leu Lys Asn Lys Ser Arg Val Arg Thr
                35             40             45

ggg ctt acc atc gcc atc ggt tat gta gtg gtg att tgg gcg gtg cat 195
Gly Leu Thr Ile Ala Ile Gly Tyr Val Val Val Ile Trp Ala Val His
                50             55             60

ttg gca tcc atc gtc att gcg ctg ctc act ggc ttc aac ctg acc aac 243
Leu Ala Ser Ile Val Ile Ala Leu Leu Thr Gly Phe Asn Leu Thr Asn
                65             70             75

ttt ggt att cat ccg ctg gat acc agt gca ctg tgg ggt att ttc acc 291
Phe Gly Ile His Pro Leu Asp Thr Ser Ala Leu Trp Gly Ile Phe Thr
                80             85             90             95

tca ccg ctg ttg cat gga agc ttc agc cac ctc att gga aat acc gtt 339
Ser Pro Leu Leu His Gly Ser Phe Ser His Leu Ile Gly Asn Thr Val
                100             105             110

cca ggc ttt ata ttc agt ttc ctc atc ggt atg agt ggc aag cgc gtg 387
Pro Gly Phe Ile Phe Ser Phe Leu Ile Gly Met Ser Gly Lys Arg Val
                115             120             125

ttc tgg gaa gtc acg att atc gca ggt ctc atc ggc ggt ctt ggt aca 435
Phe Trp Glu Val Thr Ile Ile Ala Gly Leu Ile Gly Gly Leu Gly Thr
                130             135             140

tgg att ttc ggt gga atc ggc acc aac cac atc ggt gcg tcc ggc ctg 483
Trp Ile Phe Gly Gly Ile Gly Thr Asn His Ile Gly Ala Ser Gly Leu
                145             150             155

att tat ggc tgg ctt ggc tac ctg atc gtg cgt gga att ttc aac aag 531
Ile Tyr Gly Trp Leu Gly Tyr Leu Ile Val Arg Gly Ile Phe Asn Lys
                160             165             170             175

gat att aaa cag ttc ctg ctt ggc ata gtt ttg gcg ttc att tac tcc 579
Asp Ile Lys Gln Phe Leu Leu Gly Ile Val Leu Ala Phe Ile Tyr Ser
                180             185             190

ggg ttg ttc tgg ggt ctg cta cct act caa atc ggt gtg tcc tgg cag 627
Gly Leu Phe Trp Gly Leu Leu Pro Thr Gln Ile Gly Val Ser Trp Gln
                195             200             205

ggc cac ctt ttc ggt gca ctt ggt gga atc ggt gcg ggt gct ttt atc 675
Gly His Leu Phe Gly Ala Leu Gly Gly Ile Gly Ala Gly Ala Phe Ile
                210             215             220

```

gcc tcg gat gac ccg gca gcg ttg aaa gcg aag aag caa cag aag aaa 723  
 Ala Ser Asp Asp Pro Ala Ala Leu Lys Ala Lys Lys Gln Gln Lys Lys  
 225 230 235

tta gaa aag caa caa cgc caa aga ggc tta tagttttcac ctacgcgacta 773  
 Leu Glu Lys Gln Gln Arg Gln Arg Gly Leu  
 240 245

cac 776

<210> 202

<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 202

Met Ser Tyr Asn Ser Pro Tyr Asn Asn Thr Asn Phe Ser Thr Thr Gly  
 1 5 10 15

Ala Phe Gln Pro Ala Gly Gly Pro Val Lys Pro Trp Asn Lys Pro Asp  
 20 25 30

Ala Ser Leu Asn Gln Gln Leu Lys Asn Lys Ser Arg Val Arg Thr Gly  
 35 40 45

Leu Thr Ile Ala Ile Gly Tyr Val Val Val Ile Trp Ala Val His Leu  
 50 55 60

Ala Ser Ile Val Ile Ala Leu Leu Thr Gly Phe Asn Leu Thr Asn Phe  
 65 70 75 80

Gly Ile His Pro Leu Asp Thr Ser Ala Leu Trp Gly Ile Phe Thr Ser  
 85 90 95

Pro Leu Leu His Gly Ser Phe Ser His Leu Ile Gly Asn Thr Val Pro  
 100 105 110

Gly Phe Ile Phe Ser Phe Leu Ile Gly Met Ser Gly Lys Arg Val Phe  
 115 120 125

Trp Glu Val Thr Ile Ile Ala Gly Leu Ile Gly Gly Leu Gly Thr Trp  
 130 135 140

Ile Phe Gly Gly Ile Gly Thr Asn His Ile Gly Ala Ser Gly Leu Ile  
 145 150 155 160

Tyr Gly Trp Leu Gly Tyr Leu Ile Val Arg Gly Ile Phe Asn Lys Asp  
 165 170 175

Ile Lys Gln Phe Leu Leu Gly Ile Val Leu Ala Phe Ile Tyr Ser Gly  
 180 185 190

Leu Phe Trp Gly Leu Leu Pro Thr Gln Ile Gly Val Ser Trp Gln Gly  
 195 200 205

His Leu Phe Gly Ala Leu Gly Gly Ile Gly Ala Gly Ala Phe Ile Ala  
 210 215 220

Ser Asp Asp Pro Ala Ala Leu Lys Ala Lys Lys Gln Gln Lys Lys Leu  
 225 230 235 240

Glu Lys Gln Gln Arg Gln Arg Gly Leu  
245

<210> 203  
<211> 840  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(817)  
<223> RXN01580

<400> 203  
cggtaaacgc ctcattaaag tccaatgccca tgctcataac actaacagtt aaccgtgcgg 60  
tcaactttgc tccctatcct taaaaagccc acagaaaagg atg tat aag aat atg 115  
Met Tyr Lys Asn Met 5  
cac att gtt gcc cat cgc ggt gcg gaa gat ctg cac ctc gaa aac acc 163  
His Ile Val Ala His Arg Gly Ala Glu Asp Leu His Leu Glu Asn Thr 20  
atg acc gct ttc cag gct gcc gcg ccc gct gac gct ttt gag ctg gat 211  
Met Thr Ala Phe Gln Ala Ala Pro Ala Asp Ala Phe Glu Leu Asp 35  
atc cac gcc acc gct gac aat cag gtc gtc gtt atc cac gac cgc acc 259  
Ile His Ala Thr Ala Asp Asn Gln Val Val Val Ile His Asp Arg Thr 50  
gca gcg cgt gtt gcc gcg cca gat tcc ctg cac cgc gac acc ccg gtt 307  
Ala Ala Arg Val Ala Ala Pro Asp Ser Leu His Arg Asp Thr Pro Val 65  
gcg cgc tta agc gcc gcg caa atc aag gag ata acg ctt atc gac gga 355  
Ala Arg Leu Ser Ala Ala Gln Ile Lys Glu Ile Thr Leu Ile Asp Gly 85  
tcc ccc gta cca acc ctg gag gaa gtt cta ctc cag acg agc ctg ccg 403  
Ser Pro Val Pro Thr Leu Glu Glu Val Leu Leu Gln Thr Ser Leu Pro 100  
atc caa gtg gaa atc aaa tct gcc ggt gca gtt cca gca gcc gca gca 451  
Ile Gln Val Glu Ile Lys Ser Ala Gly Ala Val Pro Ala Ala Ala Ala 115  
tta ttg cag aaa tac cca gag cac ctg gag cgc ctg ctg ttc atc agt 499  
Leu Leu Gln Lys Tyr Pro Glu His Leu Glu Arg Leu Leu Phe Ile Ser 130  
ttc atc gat gca gca ctg gtg gaa atc gtg gat cga ctg cca gaa gct 547  
Phe Ile Asp Ala Ala Leu Val Glu Ile Val Asp Arg Leu Pro Glu Ala 145  
cgc gtg gga atc ttg cgc gat gcg tcc atg gat gat ctg cgc att ctt 595  
Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp Asp Leu Arg Ile Leu 165

gat tac atc ccg cta aaa aat gtg ggc gcg atc ttg ccc tcg tgg aaa 643  
Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile Leu Pro Ser Trp Lys  
170 175 180  
  
gca cta aac gtg gcg tca att gct gat cta cat acc aag gga atc aag 691  
Ala Leu Asn Val Ala Ser Ile Ala Asp Leu His Thr Lys Gly Ile Lys  
185 190 195  
  
gtt ggc tgc tgg aca att cgg gat gaa aat gcg ttt ggg atc gca caa 739  
Val Gly Cys Trp Thr Ile Arg Asp Glu Asn Ala Phe Gly Ile Ala Gln  
200 205 210  
  
caa gct ggc gtt gat tac gcc act gtt agc gat ccc tct cgt ttc ctc 787  
Gln Ala Gly Val Asp Tyr Ala Thr Val Ser Asp Pro Ser Arg Phe Leu  
215 220 225  
  
gcg ccc tcc cct gct ggg gag ttg cac tgg taaataatct agtgaccaga 837  
Ala Pro Ser Pro Ala Gly Glu Leu His Trp  
230 235  
  
ctg 840

<210> 204  
<211> 239  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 204  
Met Tyr Lys Asn Met His Ile Val Ala His Arg Gly Ala Glu Asp Leu  
1 5 10 15  
  
His Leu Glu Asn Thr Met Thr Ala Phe Gln Ala Ala Ala Pro Ala Asp  
20 25 30  
  
Ala Phe Glu Leu Asp Ile His Ala Thr Ala Asp Asn Gln Val Val Val  
35 40 45  
  
Ile His Asp Arg Thr Ala Ala Arg Val Ala Ala Pro Asp Ser Leu His  
50 55 60  
  
Arg Asp Thr Pro Val Ala Arg Leu Ser Ala Ala Gln Ile Lys Glu Ile  
65 70 75 80  
  
Thr Leu Ile Asp Gly Ser Pro Val Pro Thr Leu Glu Glu Val Leu Leu  
85 90 95  
  
Gln Thr Ser Leu Pro Ile Gln Val Glu Ile Lys Ser Ala Gly Ala Val  
100 105 110  
  
Pro Ala Ala Ala Ala Leu Leu Gln Lys Tyr Pro Glu His Leu Glu Arg  
115 120 125  
  
Leu Leu Phe Ile Ser Phe Ile Asp Ala Ala Leu Val Glu Ile Val Asp  
130 135 140  
  
Arg Leu Pro Glu Ala Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp  
145 150 155 160  
  
Asp Leu Arg Ile Leu Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile

	165		170		175	
Leu Pro Ser Trp Lys Ala Leu Asn Val Ala Ser Ile Ala Asp Leu His						
	180		185		190	
Thr Lys Gly Ile Lys Val Gly Cys Trp Thr Ile Arg Asp Glu Asn Ala						
	195		200		205	
Phe Gly Ile Ala Gln Gln Ala Gly Val Asp Tyr Ala Thr Val Ser Asp						
	210		215		220	
Pro Ser Arg Phe Leu Ala Pro Ser Pro Ala Gly Glu Leu His Trp						
	225		230		235	

<210> 205  
 <211> 1314  
 <212> DNA  
 <213> Corynebacterium glutamicum  
  
 <220>  
 <221> CDS  
 <222> (101)..(1291)  
 <223> RXA01436  
  
 <400> 205.

```

gcctaaacaa accagtcaac gacctttccc gtggcgcaac agtccctgac atcgtcaaca 60

cagtagccat cacagcaatt caggcaggag gacgcagcta atg gca ttg gca ctt 115
                                         Met Ala Leu Ala Leu
                                         1 5

gtt ttg aac tcc ggt tca tct tcc atc aaa ttc cag ctg gtc aac ccc 163
Val Leu Asn Ser Gly Ser Ser Ser Ile Lys Phe Gln Leu Val Asn Pro
                        10 15 20

gaa aac tct gcc atc gac gag cca tat gtt tct ggt ctt gtg gag cag 211
Glu Asn Ser Ala Ile Asp Glu Pro Tyr Val Ser Gly Leu Val Glu Gln
                        25 30 35

att ggt gag cca aac ggc cgc atc gta ctc aaa ata gag ggt gaa aaa 259
Ile Gly Glu Pro Asn Gly Arg Ile Val Leu Lys Ile Glu Gly Glu Lys
                        40 45 50

tat acc cta gag aca ccc atc gca gat cac tcc gaa ggc cta aac ctg 307
Tyr Thr Leu Glu Thr Pro Ile Ala Asp His Ser Glu Gly Leu Asn Leu
                        55 60 65

gcg ttc gat ctc atg gac cag cac aac tgt ggt cct tcc caa ctg gaa 355
Ala Phe Asp Leu Met Asp Gln His Asn Cys Gly Pro Ser Gln Leu Glu
                        70 75 80 85

atc acc gca gtt gga cac cgc gtg gtc cac ggc gga atc ttg ttc tcc 403
Ile Thr Ala Val Gly His Arg Val Val His Gly Gly Ile Leu Phe Ser
                        90 95 100

gca ccg gaa ctt atc act gat gaa atc gtg gaa atg atc cgc gat ctc 451
Ala Pro Glu Leu Ile Thr Asp Glu Ile Val Glu Met Ile Arg Asp Leu
                        105 110 115

att cca ctc gca cca ctg cac aac cct gca aac gtt gac ggc att gat 499
  
```

Ile	Pro	Leu	Ala	Pro	Leu	His	Asn	Pro	Ala	Asn	Val	Asp	Gly	Ile	Asp	
		120					125					130				
gtt	gct	cga	aaa	att	ctc	ccc	gat	gtc	cca	cac	gta	gct	gtc	ttt	gac	547
Val	Ala	Arg	Lys	Ile	Leu	Pro	Asp	Val	Pro	His	Val	Ala	Val	Phe	Asp	
		135				140					145					
acc	ggt	ttc	ttc	cac	tca	ctt	cca	cca	gca	gct	gcg	ctg	tat	gcc	atc	595
Thr	Gly	Phe	Phe	His	Ser	Leu	Pro	Pro	Ala	Ala	Ala	Leu	Tyr	Ala	Ile	
		150				155					160				165	
aac	aag	gat	gtc	gca	gct	gaa	cac	gga	atc	agg	cgc	tat	ggt	ttc	cac	643
Asn	Lys	Asp	Val	Ala	Ala	Glu	His	Gly	Ile	Arg	Arg	Tyr	Gly	Phe	His	
				170					175					180		
ggc	acc	tcc	cat	gaa	ttt	gtg	tcc	aag	cgc	gtg	gtg	gaa	att	ctg	gaa	691
Gly	Thr	Ser	His	Glu	Phe	Val	Ser	Lys	Arg	Val	Val	Glu	Ile	Leu	Glu	
			185					190						195		
aag	ccc	acc	gaa	gac	atc	aac	acc	atc	acc	ttc	cac	ctg	ggc	aac	ggc	739
Lys	Pro	Thr	Glu	Asp	Ile	Asn	Thr	Ile	Thr	Phe	His	Leu	Gly	Asn	Gly	
		200					205					210				
gca	tcc	atg	gct	gct	gtt	caa	ggc	ggc	cgt	gcg	gta	gat	act	tcc	atg	787
Ala	Ser	Met	Ala	Ala	Val	Gln	Gly	Gly	Arg	Ala	Val	Asp	Thr	Ser	Met	
		215				220					225					
ggc	atg	aca	cct	ctc	gcg	ggc	ctt	gtc	atg	ggc	acc	cga	agc	ggc	gac	835
Gly	Met	Thr	Pro	Leu	Ala	Gly	Leu	Val	Met	Gly	Thr	Arg	Ser	Gly	Asp	
		230				235				240					245	
att	gat	cca	ggc	atc	gtc	ttc	cac	ctt	tcc	cgc	acc	gct	ggc	atg	agc	883
Ile	Asp	Pro	Gly	Ile	Val	Phe	His	Leu	Ser	Arg	Thr	Ala	Gly	Met	Ser	
				250					255					260		
atc	gat	gag	atc	gat	aat	ctg	ctg	aac	aaa	aag	tcg	ggt	gta	aag	gga	931
Ile	Asp	Glu	Ile	Asp	Asn	Leu	Leu	Asn	Lys	Lys	Ser	Gly	Val	Lys	Gly	
			265					270					275			
ctt	tcc	ggt	gtt	aat	gat	ttc	cgt	gaa	ctg	cgg	gaa	atg	atc	gac	aac	979
Leu	Ser	Gly	Val	Asn	Asp	Phe	Arg	Glu	Leu	Arg	Glu	Met	Ile	Asp	Asn	
		280					285					290				
aat	gat	caa	gat	gcc	tgg	tcc	gcg	tac	aac	att	tac	ata	cac	caa	ctc	1027
Asn	Asp	Gln	Asp	Ala	Trp	Ser	Ala	Tyr	Asn	Ile	Tyr	Ile	His	Gln	Leu	
		295				300					305					
cgc	cgc	tac	ctc	ggc	tcc	tac	atg	gtg	gca	ctg	gga	cgg	gta	gac	acc	1075
Arg	Arg	Tyr	Leu	Gly	Ser	Tyr	Met	Val	Ala	Leu	Gly	Arg	Val	Asp	Thr	
		310			315					320					325	
atc	gtg	ttc	acc	gcc	ggc	gtc	ggc	gaa	aat	gcc	cag	ttt	gtc	cgt	gag	1123
Ile	Val	Phe	Thr	Ala	Gly	Val	Gly	Glu	Asn	Ala	Gln	Phe	Val	Arg	Glu	
				330				335						340		
gat	gcc	ttg	gca	ggc	ttg	gaa	atg	tac	gga	att	gag	atc	gat	cca	gag	1171
Asp	Ala	Leu	Ala	Gly	Leu	Glu	Met	Tyr	Gly	Ile	Glu	Ile	Asp	Pro	Glu	
			345					350					355			
cgt	aac	gca	ttg	cca	aac	gat	ggc	cct	cga	ttg	att	tcc	acc	gat	gcc	1219
Arg	Asn	Ala	Leu	Pro	Asn	Asp	Gly	Pro	Arg	Leu	Ile	Ser	Thr	Asp	Ala	

360                                      365                                      370  
 tcc aag gtg aag gtg ttt gtt att cca act aat gaa gag tta gct atc 1267  
 Ser Lys Val Lys Val Phe Val Ile Pro Thr Asn Glu Glu Leu Ala Ile  
 375                                      380                                      385  
 gct agg tac gcg gtg aag ttc gct tagctctcct ggtaggatac cac 1314  
 Ala Arg Tyr Ala Val Lys Phe Ala  
 390                                      395  
  
 <210> 206  
 <211> 397  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
  
 <400> 206  
 Met Ala Leu Ala Leu Val Leu Asn Ser Gly Ser Ser Ser Ile Lys Phe  
 1                                      5                                      10                                      15  
 Gln Leu Val Asn Pro Glu Asn Ser Ala Ile Asp Glu Pro Tyr Val Ser  
 20                                      25                                      30  
 Gly Leu Val Glu Gln Ile Gly Glu Pro Asn Gly Arg Ile Val Leu Lys  
 35                                      40                                      45  
 Ile Glu Gly Glu Lys Tyr Thr Leu Glu Thr Pro Ile Ala Asp His Ser  
 50                                      55                                      60  
 Glu Gly Leu Asn Leu Ala Phe Asp Leu Met Asp Gln His Asn Cys Gly  
 65                                      70                                      75                                      80  
 Pro Ser Gln Leu Glu Ile Thr Ala Val Gly His Arg Val Val His Gly  
 85                                      90                                      95  
 Gly Ile Leu Phe Ser Ala Pro Glu Leu Ile Thr Asp Glu Ile Val Glu  
 100                                      105                                      110  
 Met Ile Arg Asp Leu Ile Pro Leu Ala Pro Leu His Asn Pro Ala Asn  
 115                                      120                                      125  
 Val Asp Gly Ile Asp Val Ala Arg Lys Ile Leu Pro Asp Val Pro His  
 130                                      135                                      140  
 Val Ala Val Phe Asp Thr Gly Phe Phe His Ser Leu Pro Pro Ala Ala  
 145                                      150                                      155                                      160  
 Ala Leu Tyr Ala Ile Asn Lys Asp Val Ala Ala Glu His Gly Ile Arg  
 165                                      170                                      175  
 Arg Tyr Gly Phe His Gly Thr Ser His Glu Phe Val Ser Lys Arg Val  
 180                                      185                                      190  
 Val Glu Ile Leu Glu Lys Pro Thr Glu Asp Ile Asn Thr Ile Thr Phe  
 195                                      200                                      205  
 His Leu Gly Asn Gly Ala Ser Met Ala Ala Val Gln Gly Gly Arg Ala  
 210                                      215                                      220  
 Val Asp Thr Ser Met Gly Met Thr Pro Leu Ala Gly Leu Val Met Gly  
 225                                      230                                      235                                      240





acc gaa ggc gga cta ctc agc aag aaa tct gat ggg cgc tac caa ttg 307  
 Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp Gly Arg Tyr Gln Leu  
 55 60 65

ggc tta cgt atc tgg gaa ctc gcc caa aat aca gga cgg cag tta cgc 355  
 Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr Gly Arg Gln Leu Arg  
 70 75 80 85

gac act gca cgc ccg ttc atc caa gag ctc tac tca ctt act tcc gag 403  
 Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr Ser Leu Thr Ser Glu  
 90 95 100

act gcg cag cta gtg gtc cgc gat aaa gat gaa gca ctt ttg att gac 451  
 Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu Ala Leu Leu Ile Asp  
 105 110 115

cga gcc tac ggc acg aag aaa att cca cgc tcg gct cga gtc ggt ggt 499  
 Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser Ala Arg Val Gly Gly  
 120 125 130

cga cta cct ctg aac tcc act gcg gtt ggc aag att ctc ctt gcg ttt 547  
 Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys Ile Leu Leu Ala Phe  
 135 140 145

gat gag cca tgg gta aaa cag tcc tat ctc aag ctg cca ctc aac gcc 595  
 Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys Leu Pro Leu Asn Ala  
 150 155 160 165

tcc acc cca aag aca att gtg aat ccc gac gtc ttg gct gcg cag ctg 643  
 Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val Leu Ala Ala Gln Leu  
 170 175 180

aaa caa att cac tcg caa ggc ttt gcc atc aca cat gac gag caa cga 691  
 Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr His Asp Glu Gln Arg  
 185 190 195

atc ggc ggc gca tcg atc gcc gta ccg gtc tgg cat aca gga aaa ctg 739  
 Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp His Thr Gly Lys Leu  
 200 205 210

gga gca gca ctg ggg ttg gtg gtt ccc acc gca cag gct gca aat ctt 787  
 Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala Gln Ala Ala Asn Leu  
 215 220 225

gag cgc tat ctc ccg atc ctt cag gcg aca agt cag aga att aca aaa 835  
 Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser Gln Arg Ile Thr Lys  
 230 235 240 245

gca acc gcg ctc att cct ttg gac aca ctt ttg gct tca cac aaa aat 883  
 Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu Ala Ser His Lys Asn  
 250 255 260

gca gaa cga aaa ggc gat acc taaaccgcc ctccatctgc ata 927  
 Ala Glu Arg Lys Gly Asp Thr  
 265

&lt;210&gt; 208

&lt;211&gt; 268

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 208

```

Met Ala Gly Gly Asn Arg Glu Pro Gly Arg Thr Val Thr Ser Lys Val
 1           5           10           15

Ile Ala Val Leu Gly Ala Phe Glu His Thr Met Arg Pro Leu Gly Val
      20           25           30

Thr Glu Ile Ala Glu Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg
      35           40           45

Leu Val Ser Glu Leu Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp
      50           55           60

Gly Arg Tyr Gln Leu Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr
      65           70           75           80

Gly Arg Gln Leu Arg Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr
      85           90           95

Ser Leu Thr Ser Glu Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu
      100           105           110

Ala Leu Leu Ile Asp Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser
      115           120           125

Ala Arg Val Gly Gly Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys
      130           135           140

Ile Leu Leu Ala Phe Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys
      145           150           155           160

Leu Pro Leu Asn Ala Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val
      165           170           175

Leu Ala Ala Gln Leu Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr
      180           185           190

His Asp Glu Gln Arg Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp
      195           200           205

His Thr Gly Lys Leu Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala
      210           215           220

Gln Ala Ala Asn Leu Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser
      225           230           235           240

Gln Arg Ile Thr Lys Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu
      245           250           255

Ala Ser His Lys Asn Ala Glu Arg Lys Gly Asp Thr
      260           265

```

&lt;210&gt; 209

&lt;211&gt; 1158

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1135)

&lt;223&gt; RXA00246

&lt;400&gt; 209

ttgcaaggat tgtaatttaa ggcacatcta tgtcgggtgtg aaattacatg tgccagaaga 60

gcaatttgcc aagtaatcca agcgagaagg agtgagtttt atg acc act gct gca 115  
 Met Thr Thr Ala Ala  
 1 5

ccc caa gaa ttt acc gct gct gtt gtt gaa aaa ttc ggt cat gac gtg 163  
 Pro Gln Glu Phe Thr Ala Ala Val Val Glu Lys Phe Gly His Asp Val  
 10 15 20

acc gtg aag gat att gac ctt cca aag cca ggg cca cac cag gca ttg 211  
 Thr Val Lys Asp Ile Asp Leu Pro Lys Pro Gly Pro His Gln Ala Leu  
 25 30 35

gtg aag gta ctc acc tcc ggc atc tgc cac acc gac ctc cac gcc ttg 259  
 Val Lys Val Leu Thr Ser Gly Ile Cys His Thr Asp Leu His Ala Leu  
 40 45 50

gag ggc gat tgg cca gta aag ccg gaa cca cca ttc gta cca gga cac 307  
 Glu Gly Asp Trp Pro Val Lys Pro Glu Pro Pro Phe Val Pro Gly His  
 55 60 65

gaa ggt gta ggt gaa gtt gtt gag ctc gga cca ggt gaa cac gat gtg 355  
 Glu Gly Val Gly Glu Val Val Glu Leu Gly Pro Gly Glu His Asp Val  
 70 75 80 85

aag gtc ggc gat att gtc ggc aat gcg tgg ctc tgg tca gcg tgt ggc 403  
 Lys Val Gly Asp Ile Val Gly Asn Ala Trp Leu Trp Ser Ala Cys Gly  
 90 95 100

acc tgc gaa tac tgc atc acc ggc agg gaa act cag tgc aac gaa gct 451  
 Thr Cys Glu Tyr Cys Ile Thr Gly Arg Glu Thr Gln Cys Asn Glu Ala  
 105 110 115

gag tat ggt ggc tac acc caa aat gga tcc ttc ggc cag tac atg ctg 499  
 Glu Tyr Gly Gly Tyr Thr Gln Asn Gly Ser Phe Gly Gln Tyr Met Leu  
 120 125 130

gtg gat acc cgt tac gcc gct cgc atc cca gac ggc gtg gac tac ctc 547  
 Val Asp Thr Arg Tyr Ala Ala Arg Ile Pro Asp Gly Val Asp Tyr Leu  
 135 140 145

gaa gca gca cca att ctg tgt gca ggc gtg act gtc tac aag gca ctc 595  
 Glu Ala Ala Pro Ile Leu Cys Ala Gly Val Thr Val Tyr Lys Ala Leu  
 150 155 160 165

aaa gtc tct gaa acc cgc ccg ggc caa ttc atg gtg atc tcc ggt gtc 643  
 Lys Val Ser Glu Thr Arg Pro Gly Gln Phe Met Val Ile Ser Gly Val  
 170 175 180

ggc gga ctt ggc cac atc gca gtc caa tac gca gcg gcg atg ggc atg 691  
 Gly Gly Leu Gly His Ile Ala Val Gln Tyr Ala Ala Ala Met Gly Met  
 185 190 195

cgt gtc att gcg gta gat att gcc gat gac aag ctg gaa ctt gcc cgt 739  
 Arg Val Ile Ala Val Asp Ile Ala Asp Asp Lys Leu Glu Leu Ala Arg  
 200 205 210

aag cac ggt gcg gaa ttt acc gtg aat gcg cgt aat gaa gat tca ggc 787  
 Lys His Gly Ala Glu Phe Thr Val Asn Ala Arg Asn Glu Asp Ser Gly  
 215 220 225  
  
 gaa gct gta cag aag tac acc aac ggt ggc gca cac ggc gtg ctt gtg 835  
 Glu Ala Val Gln Lys Tyr Thr Asn Gly Gly Ala His Gly Val Leu Val  
 230 235 240 245  
  
 act gca gtt cac gag gca gca ttc ggc cag gca ctg gat atg gct cga 883  
 Thr Ala Val His Glu Ala Ala Phe Gly Gln Ala Leu Asp Met Ala Arg  
 250 255 260  
  
 cgt gca gga aca att gtg ttc aac ggt ctg cca ccg gga gag ttc cca 931  
 Arg Ala Gly Thr Ile Val Phe Asn Gly Leu Pro Pro Gly Glu Phe Pro  
 265 270 275  
  
 gca tcc gtg ttc aac atc gta ttc aag ggc ctg acc atc cgt gga tcc 979  
 Ala Ser Val Phe Asn Ile Val Phe Lys Gly Leu Thr Ile Arg Gly Ser  
 280 285 290  
  
 ctc gtg gga acc cgc caa gac ttg gcc gaa gcg ctc gat ttc ttt gca 1027  
 Leu Val Gly Thr Arg Gln Asp Leu Ala Glu Ala Leu Asp Phe Phe Ala  
 295 300 305  
  
 cgc gga cta atc aag cca acc gtg agt gag tgc tcc ctc gat gag gtc 1075  
 Arg Gly Leu Ile Lys Pro Thr Val Ser Glu Cys Ser Leu Asp Glu Val  
 310 315 320 325  
  
 aat ggt gtg ctt gac cgc atg cga aac ggc aag atc gat ggt cgt gtg 1123  
 Asn Gly Val Leu Asp Arg Met Arg Asn Gly Lys Ile Asp Gly Arg Val  
 330 335 340  
  
 gcg att cgt ttc taacggattg tgttgaaact gct 1158  
 Ala Ile Arg Phe  
 345

&lt;210&gt; 210

&lt;211&gt; 345

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 210

Met Thr Thr Ala Ala Pro Gln Glu Phe Thr Ala Ala Val Val Glu Lys  
 1 5 10 15  
  
 Phe Gly His Asp Val Thr Val Lys Asp Ile Asp Leu Pro Lys Pro Gly  
 20 25 30  
  
 Pro His Gln Ala Leu Val Lys Val Leu Thr Ser Gly Ile Cys His Thr  
 35 40 45  
  
 Asp Leu His Ala Leu Glu Gly Asp Trp Pro Val Lys Pro Glu Pro Pro  
 50 55 60  
  
 Phe Val Pro Gly His Glu Gly Val Gly Glu Val Val Glu Leu Gly Pro  
 65 70 75 80  
  
 Gly Glu His Asp Val Lys Val Gly Asp Ile Val Gly Asn Ala Trp Leu  
 85 90 95

Trp Ser Ala Cys Gly Thr Cys Glu Tyr Cys Ile Thr Gly Arg Glu Thr  
                   100                  105                  110  
 Gln Cys Asn Glu Ala Glu Tyr Gly Gly Tyr Thr Gln Asn Gly Ser Phe  
                   115                  120                  125  
 Gly Gln Tyr Met Leu Val Asp Thr Arg Tyr Ala Ala Arg Ile Pro Asp  
                   130                  135                  140  
 Gly Val Asp Tyr Leu Glu Ala Ala Pro Ile Leu Cys Ala Gly Val Thr  
                   145                  150                  155                  160  
 Val Tyr Lys Ala Leu Lys Val Ser Glu Thr Arg Pro Gly Gln Phe Met  
                   165                  170                  175  
 Val Ile Ser Gly Val Gly Gly Leu Gly His Ile Ala Val Gln Tyr Ala  
                   180                  185                  190  
 Ala Ala Met Gly Met Arg Val Ile Ala Val Asp Ile Ala Asp Asp Lys  
                   195                  200                  205  
 Leu Glu Leu Ala Arg Lys His Gly Ala Glu Phe Thr Val Asn Ala Arg  
                   210                  215                  220  
 Asn Glu Asp Ser Gly Glu Ala Val Gln Lys Tyr Thr Asn Gly Gly Ala  
                   225                  230                  235                  240  
 His Gly Val Leu Val Thr Ala Val His Glu Ala Ala Phe Gly Gln Ala  
                   245                  250                  255  
 Leu Asp Met Ala Arg Arg Ala Gly Thr Ile Val Phe Asn Gly Leu Pro  
                   260                  265                  270  
 Pro Gly Glu Phe Pro Ala Ser Val Phe Asn Ile Val Phe Lys Gly Leu  
                   275                  280                  285  
 Thr Ile Arg Gly Ser Leu Val Gly Thr Arg Gln Asp Leu Ala Glu Ala  
                   290                  295                  300  
 Leu Asp Phe Phe Ala Arg Gly Leu Ile Lys Pro Thr Val Ser Glu Cys  
                   305                  310                  315                  320  
 Ser Leu Asp Glu Val Asn Gly Val Leu Asp Arg Met Arg Asn Gly Lys  
                   325                  330                  335  
 Ile Asp Gly Arg Val Ala Ile Arg Phe  
                   340                  345

<210> 211  
 <211> 723  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(700)  
 <223> RXA01571

<400> 211

```

aaactacctg ctgagagctt tgtaatttac ggtgtggttg tggaggggtg cgtcgagaag 60

cgctcgtagg cgcttttgat ttttcggtag gctaactggg gtg agt atc tca gta 115
Val Ser Ile Ser Val
1 5

aaa gca cta caa aag tcc ggc cca gaa gca cct ttc gag gtc aag atc 163
Lys Ala Leu Gln Lys Ser Gly Pro Glu Ala Pro Phe Glu Val Lys Ile
10 15 20

att gaa cgc cgt gac cca cgc gca gat gat gtg gtt att gat atc aaa 211
Ile Glu Arg Arg Asp Pro Arg Ala Asp Asp Val Val Ile Asp Ile Lys
25 30 35

gct gcg ggc atc tgc cac agc gat atc cac acc atc cgc aac gaa tgg 259
Ala Ala Gly Ile Cys His Ser Asp Ile His Thr Ile Arg Asn Glu Trp
40 45 50

ggc gag gcg cac ttc ccg ctc acc gtc ggc cac gaa atc gca ggc gtt 307
Gly Glu Ala His Phe Pro Leu Thr Val Gly His Glu Ile Ala Gly Val
55 60 65

gtc tct gcg gtt gga tcc gat gta acc aaa tgg aaa gtc ggc gac cgc 355
Val Ser Ala Val Gly Ser Asp Val Thr Lys Trp Lys Val Gly Asp Arg
70 75 80 85

gtg ggc gtc ggc tgc ctc gtt aac tcc tgc ggc gaa tgc gaa cag tgc 403
Val Gly Val Gly Cys Leu Val Asn Ser Cys Gly Glu Cys Glu Gln Cys
90 95 100

gtc gca gga ttt gaa aac aac tgc ctt cgc gga aac gtc gga acc tac 451
Val Ala Gly Phe Glu Asn Asn Cys Leu Arg Gly Asn Val Gly Thr Tyr
105 110 115

aac tct aac gac gtc gac ggc acc atc acc caa ggc ggc tac gct gaa 499
Asn Ser Asn Asp Val Asp Gly Thr Ile Thr Gln Gly Gly Tyr Ala Glu
120 125 130

aag gta gtg gtc aac gaa cgt ttc ctg tgc agc atc cca gag gaa ctt 547
Lys Val Val Val Asn Glu Arg Phe Leu Cys Ser Ile Pro Glu Glu Leu
135 140 145

aac ttc gat gtc gca gca cca ctg ctg tgc gca ggc atc acc acc tac 595
Asn Phe Asp Val Ala Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr
150 155 160 165

tcc cca atc gct cgc tgg aac gtt aaa gaa ggc gac aaa gta gca gtc 643
Ser Pro Ile Ala Arg Trp Asn Val Lys Glu Gly Asp Lys Val Ala Val
170 175 180

atg ggc ctc ggc ggg act cgg aca cat ggg tgt cca gat cgc tgc agc 691
Met Gly Leu Gly Gly Thr Arg Thr His Gly Cys Pro Asp Arg Cys Ser
185 190 195

caa ggg tgc tgagggtacc gttctgtccc gtt 723
Gln Gly Cys
200

```

&lt;210&gt; 212

&lt;211&gt; 200

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 212

Val Ser Ile Ser Val Lys Ala Leu Gln Lys Ser Gly Pro Glu Ala Pro  
 1 5 10 15

Phe Glu Val Lys Ile Ile Glu Arg Arg Asp Pro Arg Ala Asp Asp Val  
 20 25 30

Val Ile Asp Ile Lys Ala Ala Gly Ile Cys His Ser Asp Ile His Thr  
 35 40 45

Ile Arg Asn Glu Trp Gly Glu Ala His Phe Pro Leu Thr Val Gly His  
 50 55 60

Glu Ile Ala Gly Val Val Ser Ala Val Gly Ser Asp Val Thr Lys Trp  
 65 70 75 80

Lys Val Gly Asp Arg Val Gly Val Gly Cys Leu Val Asn Ser Cys Gly  
 85 90 95

Glu Cys Glu Gln Cys Val Ala Gly Phe Glu Asn Asn Cys Leu Arg Gly  
 100 105 110

Asn Val Gly Thr Tyr Asn Ser Asn Asp Val Asp Gly Thr Ile Thr Gln  
 115 120 125

Gly Gly Tyr Ala Glu Lys Val Val Val Asn Glu Arg Phe Leu Cys Ser  
 130 135 140

Ile Pro Glu Glu Leu Asn Phe Asp Val Ala Ala Pro Leu Leu Cys Ala  
 145 150 155 160

Gly Ile Thr Thr Tyr Ser Pro Ile Ala Arg Trp Asn Val Lys Glu Gly  
 165 170 175

Asp Lys Val Ala Val Met Gly Leu Gly Gly Thr Arg Thr His Gly Cys  
 180 185 190

Pro Asp Arg Cys Ser Gln Gly Cys  
 195 200

&lt;210&gt; 213

&lt;211&gt; 615

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(592)

&lt;223&gt; RXA01572

&lt;400&gt; 213

ctgctgtgcg caggcatcac cacctactcc ccaatcgctc gctggaacgt taaagaaggc 60

gacaaagtag cagtcattggg cctcggcggg actcggacac atg ggt gtc cag atc 115  
 Met Gly Val Gln Ile  
 1 5



gct gca gcc aag ggt gct gag gtt acc gtt ctg tcc cgt tcc ctg cgc 163  
 Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu Ser Arg Ser Leu Arg  
                   10                  15                  20  
  
 aag gca gaa ctt gcc aag gaa ctc ggc gca gct cgc acg ctt gcg act 211  
 Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala Arg Thr Leu Ala Thr  
                   25                  30                  35  
  
 tct gat gag gat ttc ttc acc gaa cac gcc ggt gaa ttc gac ttc atc 259  
 Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly Glu Phe Asp Phe Ile  
                   40                  45                  50  
  
 ctc aac acc att agc gca tcc atc cca gtc gac aag tac ctg agc ctt 307  
 Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp Lys Tyr Leu Ser Leu  
                   55                  60                  65  
  
 ctc aag cca cac ggt gtc atg gct gtt gtc ggt ctg cca cca gag aag 355  
 Leu Lys Pro His Gly Val Met Ala Val Val Gly Leu Pro Pro Glu Lys  
                   70                  75                  80                  85  
  
 cag cca ctg agc ttc ggt gcg ctc atc ggc ggc gga aaa gtc ctc acc 403  
 Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly Gly Lys Val Leu Thr  
                   90                  95                  100  
  
 gga tcc aac att ggc ggc atc cct gaa acc cag gaa atg ctc gac ttc 451  
 Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln Glu Met Leu Asp Phe  
                   105                  110                  115  
  
 tgt gca aaa cac ggc ctc ggt gcg atg atc gaa act gtc ggc gtc aac 499  
 Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu Thr Val Gly Val Asn  
                   120                  125                  130  
  
 gat gtt gat gca gcc tac gac cgt gtt gtt gcc ggc gac gtt cag ttc 547  
 Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala Gly Asp Val Gln Phe  
                   135                  140                  145  
  
 cgc gtt gtc att gat act gct tcg ttt gct gag gtt gag gcg gtt 592  
 Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu Val Glu Ala Val  
                   150                  155                  160  
  
 taggtttact gaagttcaga ctt 615

&lt;210&gt; 214

&lt;211&gt; 164

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 214

Met Gly Val Gln Ile Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu  
                   1                  5                  10                  15

Ser Arg Ser Leu Arg Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala  
                   20                  25                  30

Arg Thr Leu Ala Thr Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly  
                   35                  40                  45

Glu Phe Asp Phe Ile Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp  
                   50                  55                  60

Lys Tyr Leu Ser Leu Leu Lys Pro His Gly Val Met Ala Val Val Gly  
 65 70 75 80  
 Leu Pro Pro Glu Lys Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly  
 85 90 95  
 Gly Lys Val Leu Thr Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln  
 100 105 110  
 Glu Met Leu Asp Phe Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu  
 115 120 125  
 Thr Val Gly Val Asn Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala  
 130 135 140  
 Gly Asp Val Gln Phe Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu  
 145 150 155 160  
 Val Glu Ala Val

<210> 215  
 <211> 1140  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1117)  
 <223> RXA01758

<400> 215  
 ccccttatt cagagtgatg gtctaccgga gaagtaccca gaccaatagc atcgaccaac 60  
 gatagcgcg tcagaagttc tttagtga aa gcagaaccaa atg ccc aaa tac att 115  
 Met Pro Lys Tyr Ile  
 1 5  
 gcc atg cag gta tcc gaa tcc ggt gca ccg tta gcc gcg aat ctc gtg 163  
 Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu Ala Ala Asn Leu Val  
 10 15 20  
 caa cct gct ccg ttg aaa tcg agg gaa gtc cgc gtg gaa atc gct gct 211  
 Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg Val Glu Ile Ala Ala  
 25 30 35  
 agt ggt gtg tgc cat gca gat att ggc acg gca gca gca tcg ggg aag 259  
 Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala Ala Ala Ser Gly Lys  
 40 45 50  
 cac act gtt ttt cct gtt acc cct ggt cat gag att gca gga acc atc 307  
 His Thr Val Phe Pro Val Thr Pro Gly His Glu Ile Ala Gly Thr Ile  
 55 60 65  
 gcg gaa att ggt gaa aac gta tct cgg tgg acg gtt ggt gat cgc gtt 355  
 Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr Val Gly Asp Arg Val  
 70 75 80 85  
 gca atc ggt tgg ttt ggt ggc aat tgc ggt gac tgc gct ttt tgt cgt 403  
 Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp Cys Ala Phe Cys Arg

90												95												100											
gca	ggt	gat	cct	gtg	cat	tgc	aga	gag	cgg	aag	att	cct	ggc	gtt	tct							451													
Ala	Gly	Asp	Pro	Val	His	Cys	Arg	Glu	Arg	Lys	Ile	Pro	Gly	Val	Ser																				
			105						110					115																					
tat	gcg	ggt	ggt	tgg	gca	cag	aat	att	gtt	gtt	cca	gcg	gag	gct	ctt							499													
Tyr	Ala	Gly	Gly	Trp	Ala	Gln	Asn	Ile	Val	Val	Pro	Ala	Glu	Ala	Leu																				
			120				125						130																						
gct	gcg	att	cca	gat	ggc	atg	gac	ttt	tac	gag	ccc	gcc	ccg	atg	ggc							547													
Ala	Ala	Ile	Pro	Asp	Gly	Met	Asp	Phe	Tyr	Glu	Pro	Ala	Pro	Met	Gly																				
			135				140					145																							
tgc	gca	ggt	gtg	aca	aca	ttc	aat	gcg	ttg	cga	aac	ctg	aag	ctg	gat							595													
Cys	Ala	Gly	Val	Thr	Thr	Phe	Asn	Ala	Leu	Arg	Asn	Leu	Lys	Leu	Asp																				
					155					160					165																				
ccc	ggt	gcg	gct	gtc	gcg	gtc	ttt	gga	atc	ggc	ggt	tta	gtg	cgc	cta							643													
Pro	Gly	Ala	Ala	Val	Ala	Val	Phe	Gly	Ile	Gly	Gly	Leu	Val	Arg	Leu																				
				170					175					180																					
gct	att	cag	ttt	gct	gcg	aaa	atg	ggt	tat	cga	acc	atc	acc	atc	gcc							691													
Ala	Ile	Gln	Phe	Ala	Ala	Lys	Met	Gly	Tyr	Arg	Thr	Ile	Thr	Ile	Ala																				
			185					190					195																						
cgc	ggt	tta	gag	cgt	gag	gag	cta	gct	agg	caa	ctt	ggc	gcc	aac	cac							739													
Arg	Gly	Leu	Glu	Arg	Glu	Glu	Leu	Ala	Arg	Gln	Leu	Gly	Ala	Asn	His																				
			200				205					210																							
tac	atc	gat	agc	aat	gat	ctg	cac	cct	ggc	cag	gcg	tta	ttt	gaa	ctt							787													
Tyr	Ile	Asp	Ser	Asn	Asp	Leu	His	Pro	Gly	Gln	Ala	Leu	Phe	Glu	Leu																				
			215				220					225																							
ggc	ggg	gct	gac	ttg	atc	ttg	tct	act	gcg	tcc	acc	acg	gag	cct	ctt							835													
Gly	Gly	Ala	Asp	Leu	Ile	Leu	Ser	Thr	Ala	Ser	Thr	Thr	Glu	Pro	Leu																				
					235					240					245																				
tcg	gag	ttg	tct	acc	ggt	ctt	tct	att	ggc	ggg	cag	cta	acc	att	atc							883													
Ser	Glu	Leu	Ser	Thr	Gly	Leu	Ser	Ile	Gly	Gly	Gln	Leu	Thr	Ile	Ile																				
				250					255					260																					
gga	gtt	gat	ggg	gga	gat	atc	acc	gtt	tcg	gca	gcc	caa	ttg	atg	atg							931													
Gly	Val	Asp	Gly	Gly	Asp	Ile	Thr	Val	Ser	Ala	Ala	Gln	Leu	Met	Met																				
			265					270					275																						
aac	cgt	cag	atc	atc	aca	ggt	cac	ctc	act	gga	agt	gcg	aat	gac	acg							979													
Asn	Arg	Gln	Ile	Ile	Thr	Gly	His	Leu	Thr	Gly	Ser	Ala	Asn	Asp	Thr																				
			280				285					290																							
gaa	cag	act	atg	aaa	ttt	gct	cat	ctc	cat	ggc	gtg	aaa	ccg	ctt	att							1027													
Glu	Gln	Thr	Met	Lys	Phe	Ala	His	Leu	His	Gly	Val	Lys	Pro	Leu	Ile																				
			295				300					305																							
gaa	cgg	atg	cct	ctc	gat	caa	gcc	aac	gag	gct	att	gca	cgt	att	tca							1075													
Glu	Arg	Met	Pro	Leu	Asp	Gln	Ala	Asn	Glu	Ala	Ile	Ala	Arg	Ile	Ser																				
			310			315				320					325																				
gct	ggt	aaa	cca	cgt	ttc	cgt	att	gtc	ttg	gag	ccg	aat	tca									1117													
Ala	Gly	Lys	Pro	Arg	Phe	Arg	Ile	Val	Leu	Glu	Pro	Asn	Ser																						
				330					335																										

taatgccaac agcaagccca att

1140

<210> 216

<211> 339

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

Met Pro Lys Tyr Ile Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu  
1 5 10 15

Ala Ala Asn Leu Val Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg  
20 25 30

Val Glu Ile Ala Ala Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala  
35 40 45

Ala Ala Ser Gly Lys His Thr Val Phe Pro Val Thr Pro Gly His Glu  
50 55 60

Ile Ala Gly Thr Ile Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr  
65 70 75 80

Val Gly Asp Arg Val Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp  
85 90 95

Cys Ala Phe Cys Arg Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys  
100 105 110

Ile Pro Gly Val Ser Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val  
115 120 125

Pro Ala Glu Ala Leu Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu  
130 135 140

Pro Ala Pro Met Gly Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg  
145 150 155 160

Asn Leu Lys Leu Asp Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly  
165 170 175

Gly Leu Val Arg Leu Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg  
180 185 190

Thr Ile Thr Ile Ala Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln  
195 200 205

Leu Gly Ala Asn His Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln  
210 215 220

Ala Leu Phe Glu Leu Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser  
225 230 235 240

Thr Thr Glu Pro Leu Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly  
245 250 255

Gln Leu Thr Ile Ile Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala  
260 265 270

Ala Gln Leu Met Met Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly  
 275 280 285

Ser Ala Asn Asp Thr Glu Gln Thr Met Lys Phe Ala His Leu His Gly  
 290 295 300

Val Lys Pro Leu Ile Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala  
 305 310 315 320

Ile Ala Arg Ile Ser Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu  
 325 330 335

Pro Asn Ser

<210> 217  
 <211> 1641  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1618)  
 <223> RXA02539

<400> 217  
 ggctgctaag cgtgcgaatg tgcgcgttgt cacaatcgtt gaccaagtgt cacctgacgc 60  
 acaggtagtg ctcagggtgga ggtggcccaa aggagaccca atg act gtc tac gca 115  
 Met Thr Val Tyr Ala  
 1 5

aat cca gga acc gaa ggc tcg atc gtt aac tat gaa aag cgc tac gag 163  
 Asn Pro Gly Thr Glu Gly Ser Ile Val Asn Tyr Glu Lys Arg Tyr Glu  
 10 15 20

aac tac att ggt ggc aag tgg gtt cca ccg gta gag ggc cag tac ctt 211  
 Asn Tyr Ile Gly Gly Lys Trp Val Pro Pro Val Glu Gly Gln Tyr Leu  
 25 30 35

gag aac att tca cct gtc act ggt gaa gtt ttc tgt gag gtc gca cgt 259  
 Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe Cys Glu Val Ala Arg  
 40 45 50

ggc acc gca gcg gac gtg gag ctt gca ctg gat gct gca cat gca gcc 307  
 Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp Ala Ala His Ala Ala  
 55 60 65

gct gat gcg tgg ggc aag act tct gtc gct gaa cgt gct ctg atc ctg 355  
 Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu Arg Ala Leu Ile Leu  
 70 75 80 85

cac cgc att gcg gac cgc atg gaa gag cac ctg gaa gaa atc gca gtt 403  
 His Arg Ile Ala Asp Arg Met Glu Glu His Leu Glu Glu Ile Ala Val  
 90 95 100

gca gaa acc tgg gag aac ggc aag gca gtc cgt gag act ctt gct gca 451  
 Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg Glu Thr Leu Ala Ala  
 105 110 115

gat atc cca ctg gca atc gac cac ttc cgc tac ttt gct ggc gcg atc	499
Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr Phe Ala Gly Ala Ile	
120 125 130	
cgt gct cag gaa gat cgt tcc tca cag atc gac cac aac act gtt gct	547
Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp His Asn Thr Val Ala	
135 140 145	
tac cac ttc aac gag cca atc ggt gtt gtt ggt cag atc att cct tgg	595
Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly Gln Ile Ile Pro Trp	
150 155 160 165	
aac ttc cca atc ctc atg gct acc tgg aag ctc gca ccg gca ctt gct	643
Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu Ala Pro Ala Leu Ala	
170 175 180	
gca ggt aac gcg atc gtc atg aag cca gct gag cag acc cca gca tcc	691
Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu Gln Thr Pro Ala Ser	
185 190 195	
att ttg tat ctg att aac atc atc ggc gat ctc atc cca gag ggc gtc	739
Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu Ile Pro Glu Gly Val	
200 205 210	
ctc aac atc gtc aac gga ctc ggc ggt gaa gca ggc gct gca ctg tcc	787
Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala Gly Ala Ala Leu Ser	
215 220 225	
ggc tct aat cgg att ggc aag att gct ttc acc ggt tcc acc gag gtc	835
Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr Gly Ser Thr Glu Val	
230 235 240 245	
ggc aag ctg atc aac cgc gct gca tcc gac aag atc att cct gtc acc	883
Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys Ile Ile Pro Val Thr	
250 255 260	
ctg gag ctc ggc ggt aag tcc cca tcc atc ttc ttc tcc gat gtt ctg	931
Leu Glu Leu Gly Gly Lys Ser Pro Ser Ile Phe Phe Ser Asp Val Leu	
265 270 275	
tca cag gat gac gcc ttc gca gag aag gca gtt gaa ggc ttc gcg atg	979
Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val Glu Gly Phe Ala Met	
280 285 290	
ttc gcc ctc aat cag ggt gaa gtt tgt acc tgt cct tcc cgt gca ctt	1027
Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys Pro Ser Arg Ala Leu	
295 300 305	
gtt cat gag tcc atc gct gat gaa ttc ctc gag ctt ggc gtg aag cga	1075
Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu Leu Gly Val Lys Arg	
310 315 320 325	
gtt cag aac atc aag ctg ggt aac cca ctt gat act gaa acc atg atg	1123
Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp Thr Glu Thr Met Met	
330 335 340	
ggc gct cag gcg tcc cag gag cag atg gac aag atc tcc tcc tac ctg	1171
Gly Ala Gln Ala Ser Gln Glu Gln Met Asp Lys Ile Ser Ser Tyr Leu	
345 350 355	
aag atc ggc cca gaa gaa ggc gct caa acc ctc act ggt ggc aag gtc	1219

Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu Thr Gly Gly Lys Val  
 360 365 370  
 aac aag gtt gat ggc atg gag aac ggt tac tac att gag cca acc gtt 1267  
 Asn Lys Val Asp Gly Met Glu Asn Gly Tyr Tyr Ile Glu Pro Thr Val  
 375 380 385  
 ttc cgc ggc acc aac gac atg agg atc ttc cgc gag gaa atc ttc gga 1315  
 Phe Arg Gly Thr Asn Asp Met Arg Ile Phe Arg Glu Glu Ile Phe Gly  
 390 395 400 405  
 cca gtc ctt tct gtt gct acc ttc agc gac ttc gat gag gcc atc cgt 1363  
 Pro Val Leu Ser Val Ala Thr Phe Ser Asp Phe Asp Glu Ala Ile Arg  
 410 415 420  
 att gca aac gac acc aac tac ggc ctc ggc gct ggt gtc tgg agc cgt 1411  
 Ile Ala Asn Asp Thr Asn Tyr Gly Leu Gly Ala Gly Val Trp Ser Arg  
 425 430 435  
 gac caa aac acc att tat cgt gca ggt cgc gca atc cag gct ggt cga 1459  
 Asp Gln Asn Thr Ile Tyr Arg Ala Gly Arg Ala Ile Gln Ala Gly Arg  
 440 445 450  
 gtt tgg gtc aac cag tac cac aac tac cca gcg cac tcc gct ttc ggt 1507  
 Val Trp Val Asn Gln Tyr His Asn Tyr Pro Ala His Ser Ala Phe Gly  
 455 460 465  
 gga tac aag gag tcc ggc atc ggc cgt gag aac cac ctc atg atg ctg 1555  
 Gly Tyr Lys Glu Ser Gly Ile Gly Arg Glu Asn His Leu Met Met Leu  
 470 475 480 485  
 aac cac tac cag cag acc aag aac ctg ttg gtc tcc tac gat cca aac 1603  
 Asn His Tyr Gln Gln Thr Lys Asn Leu Leu Val Ser Tyr Asp Pro Asn  
 490 495 500  
 cca acc gga ctg ttc tgatctaagc gttaagtcct aga 1641  
 Pro Thr Gly Leu Phe  
 505

&lt;210&gt; 218

&lt;211&gt; 506

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 218

Met Thr Val Tyr Ala Asn Pro Gly Thr Glu Gly Ser Ile Val Asn Tyr  
 1 5 10 15  
 Glu Lys Arg Tyr Glu Asn Tyr Ile Gly Gly Lys Trp Val Pro Pro Val  
 20 25 30  
 Glu Gly Gln Tyr Leu Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe  
 35 40 45  
 Cys Glu Val Ala Arg Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp  
 50 55 60  
 Ala Ala His Ala Ala Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu  
 65 70 75 80

Arg	Ala	Leu	Ile	Leu	His	Arg	Ile	Ala	Asp	Arg	Met	Glu	Glu	His	Leu
				85					90					95	
Glu	Glu	Ile	Ala	Val	Ala	Glu	Thr	Trp	Glu	Asn	Gly	Lys	Ala	Val	Arg
			100					105					110		
Glu	Thr	Leu	Ala	Ala	Asp	Ile	Pro	Leu	Ala	Ile	Asp	His	Phe	Arg	Tyr
		115					120					125			
Phe	Ala	Gly	Ala	Ile	Arg	Ala	Gln	Glu	Asp	Arg	Ser	Ser	Gln	Ile	Asp
		130				135					140				
His	Asn	Thr	Val	Ala	Tyr	His	Phe	Asn	Glu	Pro	Ile	Gly	Val	Val	Gly
145					150					155					160
Gln	Ile	Ile	Pro	Trp	Asn	Phe	Pro	Ile	Leu	Met	Ala	Thr	Trp	Lys	Leu
				165					170					175	
Ala	Pro	Ala	Leu	Ala	Ala	Gly	Asn	Ala	Ile	Val	Met	Lys	Pro	Ala	Glu
			180					185					190		
Gln	Thr	Pro	Ala	Ser	Ile	Leu	Tyr	Leu	Ile	Asn	Ile	Ile	Gly	Asp	Leu
		195					200					205			
Ile	Pro	Glu	Gly	Val	Leu	Asn	Ile	Val	Asn	Gly	Leu	Gly	Gly	Glu	Ala
	210					215					220				
Gly	Ala	Ala	Leu	Ser	Gly	Ser	Asn	Arg	Ile	Gly	Lys	Ile	Ala	Phe	Thr
225					230					235					240
Gly	Ser	Thr	Glu	Val	Gly	Lys	Leu	Ile	Asn	Arg	Ala	Ala	Ser	Asp	Lys
				245					250					255	
Ile	Ile	Pro	Val	Thr	Leu	Glu	Leu	Gly	Gly	Lys	Ser	Pro	Ser	Ile	Phe
			260					265					270		
Phe	Ser	Asp	Val	Leu	Ser	Gln	Asp	Asp	Ala	Phe	Ala	Glu	Lys	Ala	Val
		275					280					285			
Glu	Gly	Phe	Ala	Met	Phe	Ala	Leu	Asn	Gln	Gly	Glu	Val	Cys	Thr	Cys
	290					295					300				
Pro	Ser	Arg	Ala	Leu	Val	His	Glu	Ser	Ile	Ala	Asp	Glu	Phe	Leu	Glu
305					310					315					320
Leu	Gly	Val	Lys	Arg	Val	Gln	Asn	Ile	Lys	Leu	Gly	Asn	Pro	Leu	Asp
				325					330					335	
Thr	Glu	Thr	Met	Met	Gly	Ala	Gln	Ala	Ser	Gln	Glu	Gln	Met	Asp	Lys
			340					345					350		
Ile	Ser	Ser	Tyr	Leu	Lys	Ile	Gly	Pro	Glu	Glu	Gly	Ala	Gln	Thr	Leu
		355					360					365			
Thr	Gly	Gly	Lys	Val	Asn	Lys	Val	Asp	Gly	Met	Glu	Asn	Gly	Tyr	Tyr
	370					375					380				
Ile	Glu	Pro	Thr	Val	Phe	Arg	Gly	Thr	Asn	Asp	Met	Arg	Ile	Phe	Arg
385					390					395					400
Glu	Glu	Ile	Phe	Gly	Pro	Val	Leu	Ser	Val	Ala	Thr	Phe	Ser	Asp	Phe



312

cgc ctg ccc ggc cgc tac gga cag tca  
 Arg Leu Pro Gly Arg Tyr Gly Gln Ser  
 105 110

430

```
<210> 220
<211> 110
<212> PRT
<213> Corynebacterium glutamicum
```

```

<400> 220
Val Ser Leu Thr Phe Pro Val Ile Asn Pro Ser Asp Gly Ser Thr Ile
  1           5           10           15
Thr Glu Leu Glu Asn His Asp Ser Thr Gln Trp Met Ser Ala Leu Ser
          20           25           30
Asp Ala Val Ala Ala Gly Pro Ser Trp Ala Ala Lys Thr Pro Arg Glu
          35           40           45
Arg Ser Val Val Leu Thr Ala Ile Phe Glu Ala Leu Thr Glu Arg Ala
  50           55           60
Gln Glu Leu Ala Glu Ile Ile His Leu Glu Ala Gly Lys Ser Asp Ala
  65           70           75           80
Glu Ala Leu Gly Glu Val Ala Tyr Gly Ala Glu Tyr Phe Arg Trp Phe
          85           90           95
Ala Glu Glu Ala Val Arg Leu Pro Gly Arg Tyr Gly Gln Ser
          100          105          110

```

```
<210> 221
<211> 747
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(724)  
<223> RXN03150
```

```

<400> 221
tttaacagag tgcgtttcaa tgctgtagt gttccggcaa ttttgaatgt cgttacggtt 60

acccaaggct gaattcctga gtcaccttg tacaagatca gtg gaa gcc cag ttc 115
                                         Val Glu Ala Gln Phe
                                         1                               5

acc tct ccc ctg ctc aac aat ggg caa acc tgt ttc ctt ggt acc cga 163
Thr Ser Pro Leu Leu Asn Asn Gly Gln Thr Cys Phe Leu Gly Thr Arg
                        10                               15                        20

atc ctt gct cca aaa tca cgt tac gcg gaa gta gtc gat gca ttc acc 211
Ile Leu Ala Pro Lys Ser Arg Tyr Ala Glu Val Val Asp Ala Phe Thr
                        25                               30                        35

gct ttc gct ggc agc ctg cag gtt gga gtc acg tcc tcc cct gac act 259
Ala Phe Ala Gly Ser Leu Gln Val Gly Val Thr Ser Ser Pro Asp Thr

```

40	45	50	
cag atc gga ccg atg gcg act gcc cgg cag cgt gag cgc gtg gaa tcc			307
Gln Ile Gly Pro Met Ala Thr Ala Arg Gln Arg Glu Arg Val Glu Ser			
55	60	65	
tac att tcc caa ggc aaa aat gct gga gcc cgc atc act gtc ggt ggc			355
Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg Ile Thr Val Gly Gly			
70	75	80	85
agc cgt cca cga gat ctt gac gcc gga ttc ttc gtt gag cca aca gtg			403
Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe Val Glu Pro Thr Val			
90	95	100	
ttc gcc gat gta gac aat cgc gca gcc att gcc caa gat gaa atc ttc			451
Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala Gln Asp Glu Ile Phe			
105	110	115	
gga ccg gtg ccc tct gtt gtt tcc tac caa gac gat gaa cac gcc atc			499
Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp Asp Glu His Ala Ile			
120	125	130	
caa cta gcc aac gat tcc gaa ttc ggt ctc ggc gga act gtc tgg acg			547
Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly Gly Thr Val Trp Thr			
135	140	145	
agc gat ccc gag cgc ggc gct gca ttg gcc cgc cga gtt cac aca gga			595
Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg Arg Val His Thr Gly			
150	155	160	165
acc att ggc atc aac cgc tat atc cct gat ccc gcc gca cca ttt gga			643
Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro Ala Ala Pro Phe Gly			
170	175	180	
ggt gtg aaa aac agt ggc ctt ggc aga gaa ctc ggc ccc gaa ggt ctt			691
Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu Gly Pro Glu Gly Leu			
185	190	195	
gct tcc tac caa gaa acc caa acc att tat ctc taatccaaac tgcacctata			744
Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu			
200	205		
tat			747

&lt;210&gt; 222

&lt;211&gt; 208

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 222

Val	Glu	Ala	Gln	Phe	Thr	Ser	Pro	Leu	Leu	Asn	Asn	Gly	Gln	Thr	Cys
1				5					10					15	

Phe	Leu	Gly	Thr	Arg	Ile	Leu	Ala	Pro	Lys	Ser	Arg	Tyr	Ala	Glu	Val
			20					25					30		

Val	Asp	Ala	Phe	Thr	Ala	Phe	Ala	Gly	Ser	Leu	Gln	Val	Gly	Val	Thr
	35						40					45			

Ser	Ser	Pro	Asp	Thr	Gln	Ile	Gly	Pro	Met	Ala	Thr	Ala	Arg	Gln	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50                      55                      60  
 Glu Arg Val Glu Ser Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg  
 65                      70                      75                      80  
 Ile Thr Val Gly Gly Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe  
                     85                      90                      95  
 Val Glu Pro Thr Val Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala  
                     100                      105                      110  
 Gln Asp Glu Ile Phe Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp  
                     115                      120                      125  
 Asp Glu His Ala Ile Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly  
                     130                      135                      140  
 Gly Thr Val Trp Thr Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg  
 145                      150                      155                      160  
 Arg Val His Thr Gly Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro  
                     165                      170                      175  
 Ala Ala Pro Phe Gly Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu  
                     180                      185                      190  
 Gly Pro Glu Gly Leu Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu  
                     195                      200                      205

<210> 223  
 <211> 881  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (1)..(858)  
 <223> RXN01340

<400> 223  
 aaa gtg ggg gag atc atc gcc tcc gtc ttt gat acc ttt aat atc ccg 48  
 Lys Val Gly Glu Ile Ile Ala Ser Val Phe Asp Thr Phe Asn Ile Pro  
   1                      5                      10                      15  
 cag ggc ttg gtc tca atc atc acc acc act cga gat gca gag cta tcg 96  
 Gln Gly Leu Val Ser Ile Ile Thr Thr Thr Arg Asp Ala Glu Leu Ser  
                     20                      25                      30  
 gca gaa ctc atg gct gat cct cgc ttg gct aaa gtc acc ttc act gga 144  
 Ala Glu Leu Met Ala Asp Pro Arg Leu Ala Lys Val Thr Phe Thr Gly  
                     35                      40                      45  
 tca acc aac gtg gga cgc atc ctg gtc cgc caa tcc gcg gac cga ctg 192  
 Ser Thr Asn Val Gly Arg Ile Leu Val Arg Gln Ser Ala Asp Arg Leu  
                     50                      55                      60  
 ctg cgc acc tcc atg gaa ctc ggc gga aat gca gct ttt gtt atc gac 240

Leu Arg Thr Ser Met Glu Leu Gly Gly Asn Ala Ala Phe Val Ile Asp	
65 70 75 80	
gaa gcc gca gac ctc gac gaa gcc gta tcc ggt gcc atc gcc gca aaa	288
Glu Ala Ala Asp Leu Asp Glu Ala Val Ser Gly Ala Ile Ala Ala Lys	
85 90 95	
ctc cgc aac gcc ggc caa gta tgc atc gca gct aac cgt ttc ttg gtt	336
Leu Arg Asn Ala Gly Gln Val Cys Ile Ala Ala Asn Arg Phe Leu Val	
100 105 110	
cat gaa tcc cgc gct gcc gaa ttc acc tca aag ctg gcg aca gcc atg	384
His Glu Ser Arg Ala Ala Glu Phe Thr Ser Lys Leu Ala Thr Ala Met	
115 120 125	
cag aac act ccc att ggg ccg gtg att tct gcc cgc caa cgc gac cgg	432
Gln Asn Thr Pro Ile Gly Pro Val Ile Ser Ala Arg Gln Arg Asp Arg	
130 135 140	
atc gca gca cta gtg gat gaa gcc atc acc gac ggc gcc cgc ctc atc	480
Ile Ala Ala Leu Val Asp Glu Ala Ile Thr Asp Gly Ala Arg Leu Ile	
145 150 155 160	
atc ggt ggg gag gtc ccc gac ggc tcc ggc ttc ttc tat cca gcc acc	528
Ile Gly Gly Glu Val Pro Asp Gly Ser Gly Phe Phe Tyr Pro Ala Thr	
165 170 175	
atc ttg gcc gat gtc cct gca cag tca cgg att gtg cat gag gaa atc	576
Ile Leu Ala Asp Val Pro Ala Gln Ser Arg Ile Val His Glu Glu Ile	
180 185 190	
ttc gga cct gtg gcc acc att gcc act ttc acc gac ttg gcc gaa ggc	624
Phe Gly Pro Val Ala Thr Ile Ala Thr Phe Thr Asp Leu Ala Glu Gly	
195 200 205	
gtt gca caa gca aat tcc acc gaa ttc ggc ctc gca gcc tac gga ttc	672
Val Ala Gln Ala Asn Ser Thr Glu Phe Gly Leu Ala Ala Tyr Gly Phe	
210 215 220	
agc aac aat gtg aaa gca aca cag tac atg gcg gaa cac ttg gaa gcc	720
Ser Asn Asn Val Lys Ala Thr Gln Tyr Met Ala Glu His Leu Glu Ala	
225 230 235 240	
gga atg gtc gga atc aac aga ggc gcc atc tct gac cca gca gca cct	768
Gly Met Val Gly Ile Asn Arg Gly Ala Ile Ser Asp Pro Ala Ala Pro	
245 250 255	
ttt ggc ggc atc gga caa tcc ggc ttc ggc aga gaa ggc gga acc gaa	816
Phe Gly Gly Ile Gly Gln Ser Gly Phe Gly Arg Glu Gly Gly Thr Glu	
260 265 270	
gga atc gaa gaa tat ctc tcc gtg cgt tac ctc gct ttg ccg	858
Gly Ile Glu Glu Tyr Leu Ser Val Arg Tyr Leu Ala Leu Pro	
275 280 285	
tgacacatga gctgtccggt gaa	881

&lt;210&gt; 224

&lt;211&gt; 286

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 224

Lys Val Gly Glu Ile Ile Ala Ser Val Phe Asp Thr Phe Asn Ile Pro  
 1 5 10 15  
 Gln Gly Leu Val Ser Ile Ile Thr Thr Thr Arg Asp Ala Glu Leu Ser  
 20 25 30  
 Ala Glu Leu Met Ala Asp Pro Arg Leu Ala Lys Val Thr Phe Thr Gly  
 35 40 45  
 Ser Thr Asn Val Gly Arg Ile Leu Val Arg Gln Ser Ala Asp Arg Leu  
 50 55 60  
 Leu Arg Thr Ser Met Glu Leu Gly Gly Asn Ala Ala Phe Val Ile Asp  
 65 70 75 80  
 Glu Ala Ala Asp Leu Asp Glu Ala Val Ser Gly Ala Ile Ala Ala Lys  
 85 90 95  
 Leu Arg Asn Ala Gly Gln Val Cys Ile Ala Ala Asn Arg Phe Leu Val  
 100 105 110  
 His Glu Ser Arg Ala Ala Glu Phe Thr Ser Lys Leu Ala Thr Ala Met  
 115 120 125  
 Gln Asn Thr Pro Ile Gly Pro Val Ile Ser Ala Arg Gln Arg Asp Arg  
 130 135 140  
 Ile Ala Ala Leu Val Asp Glu Ala Ile Thr Asp Gly Ala Arg Leu Ile  
 145 150 155 160  
 Ile Gly Gly Glu Val Pro Asp Gly Ser Gly Phe Phe Tyr Pro Ala Thr  
 165 170 175  
 Ile Leu Ala Asp Val Pro Ala Gln Ser Arg Ile Val His Glu Glu Ile  
 180 185 190  
 Phe Gly Pro Val Ala Thr Ile Ala Thr Phe Thr Asp Leu Ala Glu Gly  
 195 200 205  
 Val Ala Gln Ala Asn Ser Thr Glu Phe Gly Leu Ala Ala Tyr Gly Phe  
 210 215 220  
 Ser Asn Asn Val Lys Ala Thr Gln Tyr Met Ala Glu His Leu Glu Ala  
 225 230 235 240  
 Gly Met Val Gly Ile Asn Arg Gly Ala Ile Ser Asp Pro Ala Ala Pro  
 245 250 255  
 Phe Gly Gly Ile Gly Gln Ser Gly Phe Gly Arg Glu Gly Gly Thr Glu  
 260 265 270  
 Gly Ile Glu Glu Tyr Leu Ser Val Arg Tyr Leu Ala Leu Pro  
 275 280 285

&lt;210&gt; 225

&lt;211&gt; 1686

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1663)

&lt;223&gt; RXN01498

&lt;400&gt; 225

cagtggacaa ctacttggcg ggtctttaa atg cagctgtgaa ggattctgca taagctgggc 60

accacacgag	catcagaacg	cgaaacgaag	gtaaaagccc	atg	atc	aaa	cgt	ctt	115
				Met	Ile	Lys	Arg	Leu	
				1				5	

cct	tta	ggt	ccg	ctg	cct	aaa	gaa	ctt	cat	cag	act	ctg	ctt	gat	ctg	163
Pro	Leu	Gly	Pro	Leu	Pro	Lys	Glu	Leu	His	Gln	Thr	Leu	Leu	Asp	Leu	
			10						15					20		

acc	gca	aat	gcc	caa	gat	gcg	gcg	aaa	gtg	gag	gtt	ata	gcg	cca	ttt	211
Thr	Ala	Asn	Ala	Gln	Asp	Ala	Ala	Lys	Val	Glu	Val	Ile	Ala	Pro	Phe	
			25					30					35			

act	ggc	gag	acc	ctc	gga	ttt	ggt	ttt	gat	ggt	gat	gag	caa	gac	gtc	259
Thr	Gly	Glu	Thr	Leu	Gly	Phe	Gly	Phe	Asp	Gly	Asp	Glu	Gln	Asp	Val	
		40					45					50				

gag	cat	gct	ttt	gca	ctt	tca	agg	gca	gcc	cag	aaa	aag	tgg	gtg	cac	307
Glu	His	Ala	Phe	Ala	Leu	Ser	Arg	Ala	Ala	Gln	Lys	Lys	Trp	Val	His	
	55					60					65					

acc	acg	gca	gtg	gaa	cgg	aag	aag	atc	ttc	ctg	aag	gtt	cat	gat	ctg	355
Thr	Thr	Ala	Val	Glu	Arg	Lys	Lys	Ile	Phe	Leu	Lys	Val	His	Asp	Leu	
	70				75					80					85	

gta	ttg	aaa	aac	cgt	gag	ctg	ctc	atg	gac	atc	gtg	cag	ttg	gaa	aca	403
Val	Leu	Lys	Asn	Arg	Glu	Leu	Leu	Met	Asp	Ile	Val	Gln	Leu	Glu	Thr	
			90						95					100		

ggc	aaa	aat	cga	gca	tcg	gct	gcc	gat	gag	gtg	ttg	gac	gtt	gcg	atc	451
Gly	Lys	Asn	Arg	Ala	Ser	Ala	Ala	Asp	Glu	Val	Leu	Asp	Val	Ala	Ile	
			105					110					115			

acc	acc	cgc	ttc	tac	gca	aac	aat	gca	gga	aag	ttt	tta	aat	gac	aag	499
Thr	Thr	Arg	Phe	Tyr	Ala	Asn	Asn	Ala	Gly	Lys	Phe	Leu	Asn	Asp	Lys	
		120					125					130				

aaa	cgc	ccc	ggc	gcg	ctt	ccg	atc	atc	acg	aaa	aac	aca	caa	cag	tat	547
Lys	Arg	Pro	Gly	Ala	Leu	Pro	Ile	Ile	Thr	Lys	Asn	Thr	Gln	Gln	Tyr	
	135					140					145					

gtg	ccc	aag	gga	gtg	gtc	ggg	cag	atc	acg	ccg	tgg	aat	tac	cct	tta	595
Val	Pro	Lys	Gly	Val	Val	Gly	Gln	Ile	Thr	Pro	Trp	Asn	Tyr	Pro	Leu	
	150					155				160					165	

act	ttg	gga	gta	tct	gat	gct	gtt	ccg	gcg	ctg	ctg	gca	gga	aac	gca	643
Thr	Leu	Gly	Val	Ser	Asp	Ala	Val	Pro	Ala	Leu	Leu	Ala	Gly	Asn	Ala	
			170					175						180		

gtg	gtg	gct	aaa	cct	gac	ctc	gcg	aca	cct	ttc	tcc	tgc	ttg	atc	atg	691
Val	Val	Ala	Lys	Pro	Asp	Leu	Ala	Thr	Pro	Phe	Ser	Cys	Leu	Ile	Met	
			185					190							195	

gtg cac ctg ctc att gaa gcc ggt ctg ccg cgt gat ttg atg cag gtt	739
Val His Leu Leu Ile Glu Ala Gly Leu Pro Arg Asp Leu Met Gln Val	
200 205 210	
gtc acc ggc cct ggc gat att gtt ggc ggt gcg att gca gct cag tgt	787
Val Thr Gly Pro Gly Asp Ile Val Gly Gly Ala Ile Ala Ala Gln Cys	
215 220 225	
gat ttc ctc atg ttc act gga tcc acg gcc acg ggc cgg atc ttg ggt	835
Asp Phe Leu Met Phe Thr Gly Ser Thr Ala Thr Gly Arg Ile Leu Gly	
230 235 240 245	
cgg aca atg ggt gag cgt ttg gtg ggt ttc tct gcg gaa tta ggc gga	883
Arg Thr Met Gly Glu Arg Leu Val Gly Phe Ser Ala Glu Leu Gly Gly	
250 255 260	
aag aac cct ctt att gtg gcc aag gat gca gat ctg gac aag gtg gaa	931
Lys Asn Pro Leu Ile Val Ala Lys Asp Ala Asp Leu Asp Lys Val Glu	
265 270 275	
gct gag ctt ccg cag gcg tgt ttt tcc aac tcg ggg caa ttg tgt gtc	979
Ala Glu Leu Pro Gln Ala Cys Phe Ser Asn Ser Gly Gln Leu Cys Val	
280 285 290	
tcc act gaa cgt att tat gtg gag gaa gac gtg tac gag gag gtg att	1027
Ser Thr Glu Arg Ile Tyr Val Glu Glu Asp Val Tyr Glu Glu Val Ile	
295 300 305	
gca cgg ttt agc aag gcg gcg aaa gcc atg tcc att ggt gcc gga ttt	1075
Ala Arg Phe Ser Lys Ala Ala Lys Ala Met Ser Ile Gly Ala Gly Phe	
310 315 320 325	
gag tgg aaa tat gag atg ggt tcg ttg atc aat cac gcg cag ctg gat	1123
Glu Trp Lys Tyr Glu Met Gly Ser Leu Ile Asn His Ala Gln Leu Asp	
330 335 340	
cgg gtg agc acc ttt gtt gat cag gct aaa gct gcg ggc gcc acg gtg	1171
Arg Val Ser Thr Phe Val Asp Gln Ala Lys Ala Ala Gly Ala Thr Val	
345 350 355	
ctg tgc ggt ggc aag tca cgc cct gat att ggt ccc ttc ttc tat gag	1219
Leu Cys Gly Gly Lys Ser Arg Pro Asp Ile Gly Pro Phe Phe Tyr Glu	
360 365 370	
ccc acg gta ttg gcg gat gtc cca gag ggc acc cca ctg ctc acg gag	1267
Pro Thr Val Leu Ala Asp Val Pro Glu Gly Thr Pro Leu Leu Thr Glu	
375 380 385	
gaa gtc ttc ggg ccg gtg gtg ttc atc gaa aag gta gcc aca ctg gaa	1315
Glu Val Phe Gly Pro Val Val Phe Ile Glu Lys Val Ala Thr Leu Glu	
390 395 400 405	
gaa gcc gtc gat aag gca aat ggc acg ccc tac ggc ctg aat gcg tcc	1363
Glu Ala Val Asp Lys Ala Asn Gly Thr Pro Tyr Gly Leu Asn Ala Ser	
410 415 420	
gtc ttt ggg tcg tcg gaa acc ggc aat ctt gtt gca ggc cag ctg gaa	1411
Val Phe Gly Ser Ser Glu Thr Gly Asn Leu Val Ala Gly Gln Leu Glu	
425 430 435	



gct ggc ggt atc ggt att aat gat ggc tac gcc gcg acg tgg gcg agc 1459  
 Ala Gly Gly Ile Gly Ile Asn Asp Gly Tyr Ala Ala Thr Trp Ala Ser  
           440                                  445                                  450

gtg tcc acg cct ctg ggt ggc atg aag cag tcg ggg ctg ggg cac cgc 1507  
 Val Ser Thr Pro Leu Gly Gly Met Lys Gln Ser Gly Leu Gly His Arg  
           455                                  460                                  465

cat ggt gcg gag gga att aca aaa tat gcg gag atc cga aac atc gcg 1555  
 His Gly Ala Glu Gly Ile Thr Lys Tyr Ala Glu Ile Arg Asn Ile Ala  
           470                                  475                                  480                                  485

gag cag cgc tgg atg tct atg cgt ggg ccg gcc aaa atg ccg cga aag 1603  
 Glu Gln Arg Trp Met Ser Met Arg Gly Pro Ala Lys Met Pro Arg Lys  
                                   490                                  495                                  500

gtg tac tca gac acc gtg gcc aca gcg cta aag ctg ggc aaa atc ttt 1651  
 Val Tyr Ser Asp Thr Val Ala Thr Ala Leu Lys Leu Gly Lys Ile Phe  
                                   505                                  510                                  515

aaa gtt ttg ccg tagcaaaaag ccggaccctt gct 1686  
 Lys Val Leu Pro  
                                   520

&lt;210&gt; 226

&lt;211&gt; 521

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 226

Met Ile Lys Arg Leu Pro Leu Gly Pro Leu Pro Lys Glu Leu His Gln  
   1                                  5                                  10                                  15

Thr Leu Leu Asp Leu Thr Ala Asn Ala Gln Asp Ala Ala Lys Val Glu  
                                   20                                  25                                  30

Val Ile Ala Pro Phe Thr Gly Glu Thr Leu Gly Phe Gly Phe Asp Gly  
                                   35                                  40                                  45

Asp Glu Gln Asp Val Glu His Ala Phe Ala Leu Ser Arg Ala Ala Gln  
                                   50                                  55                                  60

Lys Lys Trp Val His Thr Thr Ala Val Glu Arg Lys Lys Ile Phe Leu  
                                   65                                  70                                  75                                  80

Lys Val His Asp Leu Val Leu Lys Asn Arg Glu Leu Leu Met Asp Ile  
                                   85                                  90                                  95

Val Gln Leu Glu Thr Gly Lys Asn Arg Ala Ser Ala Ala Asp Glu Val  
                                   100                                  105                                  110

Leu Asp Val Ala Ile Thr Thr Arg Phe Tyr Ala Asn Asn Ala Gly Lys  
                                   115                                  120                                  125

Phe Leu Asn Asp Lys Lys Arg Pro Gly Ala Leu Pro Ile Ile Thr Lys  
                                   130                                  135                                  140

Asn Thr Gln Gln Tyr Val Pro Lys Gly Val Val Gly Gln Ile Thr Pro  
                                   145                                  150                                  155                                  160

Trp Asn Tyr Pro Leu Thr Leu Gly Val Ser Asp Ala Val Pro Ala Leu  
 165 170 175  
 Leu Ala Gly Asn Ala Val Val Ala Lys Pro Asp Leu Ala Thr Pro Phe  
 180 185 190  
 Ser Cys Leu Ile Met Val His Leu Leu Ile Glu Ala Gly Leu Pro Arg  
 195 200 205  
 Asp Leu Met Gln Val Val Thr Gly Pro Gly Asp Ile Val Gly Gly Ala  
 210 215 220  
 Ile Ala Ala Gln Cys Asp Phe Leu Met Phe Thr Gly Ser Thr Ala Thr  
 225 230 235 240  
 Gly Arg Ile Leu Gly Arg Thr Met Gly Glu Arg Leu Val Gly Phe Ser  
 245 250 255  
 Ala Glu Leu Gly Gly Lys Asn Pro Leu Ile Val Ala Lys Asp Ala Asp  
 260 265 270  
 Leu Asp Lys Val Glu Ala Glu Leu Pro Gln Ala Cys Phe Ser Asn Ser  
 275 280 285  
 Gly Gln Leu Cys Val Ser Thr Glu Arg Ile Tyr Val Glu Glu Asp Val  
 290 295 300  
 Tyr Glu Glu Val Ile Ala Arg Phe Ser Lys Ala Ala Lys Ala Met Ser  
 305 310 315 320  
 Ile Gly Ala Gly Phe Glu Trp Lys Tyr Glu Met Gly Ser Leu Ile Asn  
 325 330 335  
 His Ala Gln Leu Asp Arg Val Ser Thr Phe Val Asp Gln Ala Lys Ala  
 340 345 350  
 Ala Gly Ala Thr Val Leu Cys Gly Gly Lys Ser Arg Pro Asp Ile Gly  
 355 360 365  
 Pro Phe Phe Tyr Glu Pro Thr Val Leu Ala Asp Val Pro Glu Gly Thr  
 370 375 380  
 Pro Leu Leu Thr Glu Glu Val Phe Gly Pro Val Val Phe Ile Glu Lys  
 385 390 395 400  
 Val Ala Thr Leu Glu Glu Ala Val Asp Lys Ala Asn Gly Thr Pro Tyr  
 405 410 415  
 Gly Leu Asn Ala Ser Val Phe Gly Ser Ser Glu Thr Gly Asn Leu Val  
 420 425 430  
 Ala Gly Gln Leu Glu Ala Gly Gly Ile Gly Ile Asn Asp Gly Tyr Ala  
 435 440 445  
 Ala Thr Trp Ala Ser Val Ser Thr Pro Leu Gly Gly Met Lys Gln Ser  
 450 455 460  
 Gly Leu Gly His Arg His Gly Ala Glu Gly Ile Thr Lys Tyr Ala Glu  
 465 470 475 480  
 Ile Arg Asn Ile Ala Glu Gln Arg Trp Met Ser Met Arg Gly Pro Ala

485 490 495

Lys Met Pro Arg Lys Val Tyr Ser Asp Thr Val Ala Thr Ala Leu Lys  
500 505 510

Leu Gly Lys Ile Phe Lys Val Leu Pro  
515 520

<210> 227  
<211> 1575  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1552)  
<223> RXN02674

<400> 227  
atcgacctct agggcagcag tgattgattt cataaaaaatc acaagtttgt aactaaaggt 60  
acagttggtg aagtatccac aatcaacttt aggagacctt gtg act gca aca ttt 115  
Val Thr Ala Thr Phe  
1 5  
gct gga atc gac gcc acc aaa cac ctc atc gga ggt cag tgg gtg gag 163  
Ala Gly Ile Asp Ala Thr Lys His Leu Ile Gly Gly Gln Trp Val Glu  
10 15 20  
gga aac tcg gat cga att tcc acc aat atc aat cct tac gac gat tcc 211  
Gly Asn Ser Asp Arg Ile Ser Thr Asn Ile Asn Pro Tyr Asp Asp Ser  
25 30 35  
gta atc gcc gaa agc aaa caa gct tcc att gct gat gtt gat gcc gcg 259  
Val Ile Ala Glu Ser Lys Gln Ala Ser Ile Ala Asp Val Asp Ala Ala  
40 45 50  
tat gaa gcc gcg aag aag gcc cag gct gag tgg gca gct acg ccc gct 307  
Tyr Glu Ala Ala Lys Lys Ala Gln Ala Glu Trp Ala Ala Thr Pro Ala  
55 60 65  
gcg gaa cga tct gcc atc atc tac cgt gcg gct gaa ctt ctt gaa gag 355  
Ala Glu Arg Ser Ala Ile Ile Tyr Arg Ala Ala Glu Leu Leu Glu Glu  
70 75 80 85  
cac cgg gag gaa atc gtg gaa tgg ctg atc aag gaa tcc ggc tcg acg 403  
His Arg Glu Glu Ile Val Glu Trp Leu Ile Lys Glu Ser Gly Ser Thr  
90 95 100  
cgt tcc aag gct aat ttg gaa atc act ttg gca gga aac atc act aaa 451  
Arg Ser Lys Ala Asn Leu Glu Ile Thr Leu Ala Gly Asn Ile Thr Lys  
105 110 115  
gaa tcg gct tca ttc cct ggt cgt gtg cat ggt cga att tct cct tcg 499  
Glu Ser Ala Ser Phe Pro Gly Arg Val His Gly Arg Ile Ser Pro Ser  
120 125 130  
aat act ccg ggc aaa gaa aac cgt gtg tac cgc gta gcc aag ggc gtt 547  
Asn Thr Pro Gly Lys Glu Asn Arg Val Tyr Arg Val Ala Lys Gly Val  
135 140 145

gtc gga gtg att agt cca tgg aat ttc cca ctg aac ctc tcg atc cgc	595
Val Gly Val Ile Ser Pro Trp Asn Phe Pro Leu Asn Leu Ser Ile Arg	
150 155 160 165	
tcg gtt gct ccg gca cta gcc gtg ggc aac gcc gta gtg att aag cct	643
Ser Val Ala Pro Ala Leu Ala Val Gly Asn Ala Val Val Ile Lys Pro	
170 175 180	
gcg agt gat acc cca gtt act ggt ggt gta att cct gca cga atc ttt	691
Ala Ser Asp Thr Pro Val Thr Gly Gly Val Ile Pro Ala Arg Ile Phe	
185 190 195	
gag gag gcc gga gtt cct gca ggc gtg atc agc acg gtt gcg ggc gca	739
Glu Glu Ala Gly Val Pro Ala Gly Val Ile Ser Thr Val Ala Gly Ala	
200 205 210	
gga tct gaa atc ggt gat cac ttt gtc acc cac gcc gtg cca aag ctg	787
Gly Ser Glu Ile Gly Asp His Phe Val Thr His Ala Val Pro Lys Leu	
215 220 225	
att tct ttc acc ggt tca acc cca gtc ggt cgt cgt gtc ggt gag ctg	835
Ile Ser Phe Thr Gly Ser Thr Pro Val Gly Arg Arg Val Gly Glu Leu	
230 235 240 245	
gca att aat ggt gga cca atg aaa act gtt gca cta gag ctc ggt ggc	883
Ala Ile Asn Gly Gly Pro Met Lys Thr Val Ala Leu Glu Leu Gly Gly	
250 255 260	
aac gcg ccg ttc gtt gtg ctt gcc gac gcc gac atc gac gcc gct gcc	931
Asn Ala Pro Phe Val Val Leu Ala Asp Ala Asp Ile Asp Ala Ala Ala	
265 270 275	
cag gct gcc gca gtt ggc gct ttc cta cac cag gga cag att tgt atg	979
Gln Ala Ala Val Gly Ala Phe Leu His Gln Gly Gln Ile Cys Met	
280 285 290	
tca atc aac cga gtc att gtt gat gct gca gtt cat gat gaa ttc cta	1027
Ser Ile Asn Arg Val Ile Val Asp Ala Ala Val His Asp Glu Phe Leu	
295 300 305	
gag aag ttc gtt gaa gca gtg aag aac att cca acc ggc gat cca agc	1075
Glu Lys Phe Val Glu Ala Val Lys Asn Ile Pro Thr Gly Asp Pro Ser	
310 315 320 325	
gca gaa gga acc ctt gtt gga cct gtc att aat gac agt cag ctc agt	1123
Ala Glu Gly Thr Leu Val Gly Pro Val Ile Asn Asp Ser Gln Leu Ser	
330 335 340	
ggt ttg aag gaa aag atc gag ttg gcc aaa aag gaa ggc gca acc gtc	1171
Gly Leu Lys Glu Lys Ile Glu Leu Ala Lys Lys Glu Gly Ala Thr Val	
345 350 355	
cag gtt gaa ggg cca att gaa ggc cga ctg gtt cat ccg cat gtg ttc	1219
Gln Val Glu Gly Pro Ile Glu Gly Arg Leu Val His Pro His Val Phe	
360 365 370	
tct gat gtc acc tct gac atg gaa atc gct cgt gag gaa atc ttc gga	1267
Ser Asp Val Thr Ser Asp Met Glu Ile Ala Arg Glu Glu Ile Phe Gly	
375 380 385	

cct ctc atc agc gtg ctg aag gcc gat gat gag gca cac gca gca gag 1315  
 Pro Leu Ile Ser Val Leu Lys Ala Asp Asp Glu Ala His Ala Ala Glu  
 390 395 400 405  
  
 ctg gcc aat gct tcc gac ttt ggt ttg agc gcg gca gtg tgg tcg aag 1363  
 Leu Ala Asn Ala Ser Asp Phe Gly Leu Ser Ala Ala Val Trp Ser Lys  
 410 415 420  
  
 gat att gat cgt gca gcc cag ttt gct ctg cag att gat tcc ggc atg 1411  
 Asp Ile Asp Arg Ala Ala Gln Phe Ala Leu Gln Ile Asp Ser Gly Met  
 425 430 435  
  
 gtt cac atc aat gac ctc acc gtc aac gat gaa cca cac gtg atg ttc 1459  
 Val His Ile Asn Asp Leu Thr Val Asn Asp Glu Pro His Val Met Phe  
 440 445 450  
  
 ggt ggt tca aag aac tct ggc ctc ggc cgc ttc aac ggc gat tgg gcg 1507  
 Gly Gly Ser Lys Asn Ser Gly Leu Gly Arg Phe Asn Gly Asp Trp Ala  
 455 460 465  
  
 atc gag gag ttc acc aca gat cga tgg atc ggc atc aag cgc agc 1552  
 Ile Glu Glu Phe Thr Thr Asp Arg Trp Ile Gly Ile Lys Arg Ser  
 470 475 480  
  
 taattgtttt tcgacgtaac ccc 1575

&lt;210&gt; 228

&lt;211&gt; 484

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 228

Val Thr Ala Thr Phe Ala Gly Ile Asp Ala Thr Lys His Leu Ile Gly  
 1 5 10 15  
  
 Gly Gln Trp Val Glu Gly Asn Ser Asp Arg Ile Ser Thr Asn Ile Asn  
 20 25 30  
  
 Pro Tyr Asp Asp Ser Val Ile Ala Glu Ser Lys Gln Ala Ser Ile Ala  
 35 40 45  
  
 Asp Val Asp Ala Ala Tyr Glu Ala Ala Lys Lys Ala Gln Ala Glu Trp  
 50 55 60  
  
 Ala Ala Thr Pro Ala Ala Glu Arg Ser Ala Ile Ile Tyr Arg Ala Ala  
 65 70 75 80  
  
 Glu Leu Leu Glu Glu His Arg Glu Glu Ile Val Glu Trp Leu Ile Lys  
 85 90 95  
  
 Glu Ser Gly Ser Thr Arg Ser Lys Ala Asn Leu Glu Ile Thr Leu Ala  
 100 105 110  
  
 Gly Asn Ile Thr Lys Glu Ser Ala Ser Phe Pro Gly Arg Val His Gly  
 115 120 125  
  
 Arg Ile Ser Pro Ser Asn Thr Pro Gly Lys Glu Asn Arg Val Tyr Arg  
 130 135 140  
  
 Val Ala Lys Gly Val Val Gly Val Ile Ser Pro Trp Asn Phe Pro Leu

145	150	155	160
Asn Leu Ser Ile Arg Ser Val Ala Pro Ala Leu Ala Val Gly Asn Ala	165	170	175
Val Val Ile Lys Pro Ala Ser Asp Thr Pro Val Thr Gly Gly Val Ile	180	185	190
Pro Ala Arg Ile Phe Glu Glu Ala Gly Val Pro Ala Gly Val Ile Ser	195	200	205
Thr Val Ala Gly Ala Gly Ser Glu Ile Gly Asp His Phe Val Thr His	210	215	220
Ala Val Pro Lys Leu Ile Ser Phe Thr Gly Ser Thr Pro Val Gly Arg	225	230	240
Arg Val Gly Glu Leu Ala Ile Asn Gly Gly Pro Met Lys Thr Val Ala	245	250	255
Leu Glu Leu Gly Gly Asn Ala Pro Phe Val Val Leu Ala Asp Ala Asp	260	265	270
Ile Asp Ala Ala Ala Gln Ala Ala Ala Val Gly Ala Phe Leu His Gln	275	280	285
Gly Gln Ile Cys Met Ser Ile Asn Arg Val Ile Val Asp Ala Ala Val	290	295	300
His Asp Glu Phe Leu Glu Lys Phe Val Glu Ala Val Lys Asn Ile Pro	305	310	315
Thr Gly Asp Pro Ser Ala Glu Gly Thr Leu Val Gly Pro Val Ile Asn	325	330	335
Asp Ser Gln Leu Ser Gly Leu Lys Glu Lys Ile Glu Leu Ala Lys Lys	340	345	350
Glu Gly Ala Thr Val Gln Val Glu Gly Pro Ile Glu Gly Arg Leu Val	355	360	365
His Pro His Val Phe Ser Asp Val Thr Ser Asp Met Glu Ile Ala Arg	370	375	380
Glu Glu Ile Phe Gly Pro Leu Ile Ser Val Leu Lys Ala Asp Asp Glu	385	390	395
Ala His Ala Ala Glu Leu Ala Asn Ala Ser Asp Phe Gly Leu Ser Ala	405	410	415
Ala Val Trp Ser Lys Asp Ile Asp Arg Ala Ala Gln Phe Ala Leu Gln	420	425	430
Ile Asp Ser Gly Met Val His Ile Asn Asp Leu Thr Val Asn Asp Glu	435	440	445
Pro His Val Met Phe Gly Gly Ser Lys Asn Ser Gly Leu Gly Arg Phe	450	455	460
Asn Gly Asp Trp Ala Ile Glu Glu Phe Thr Thr Asp Arg Trp Ile Gly	465	470	480

<400> 229																		
cgatgaccca	gcgcacgcct	gggttcgaga	tacatggacc	gggcaagcat	ttgatgatcg	60												
cttgccatat	gagaacgcaa	acaaggaggg	ataaaatttc	atg	gct	gaa	acg	aag	115									
				Met	Ala	Glu	Thr	Lys										
				1														
aga	atg	aca	gtt	agc	cag	gca	ctg	gtt	gaa	ttc	ctt	ggc	cac	cag	tgg	163		
Arg	Met	Thr	Val	Ser	Gln	Ala	Leu	Val	Glu	Phe	Leu	Gly	His	Gln	Trp			
				10					15							20		
act	gtc	gac	ggc	gat	atc	cgc	gag	cgc	acc	att	cca	ggc	atg	ttc	gga	211		
Thr	Val	Asp	Gly	Asp	Ile	Arg	Glu	Arg	Thr	Ile	Pro	Gly	Met	Phe	Gly			
				25					30							35		
att	ttc	gga	cac	gga	aac	gtt	gct	ggc	att	ggc	cag	gca	ctc	aag	cag	259		
Ile	Phe	Gly	His	Gly	Asn	Val	Ala	Gly	Ile	Gly	Gln	Ala	Leu	Lys	Gln			
				40					45							50		
tac	aac	gtt	gaa	caa	cct	gag	ctc	atg	ccg	tac	tac	cag	gct	cgt	aat	307		
Tyr	Asn	Val	Glu	Gln	Pro	Glu	Leu	Met	Pro	Tyr	Tyr	Gln	Ala	Arg	Asn			
				55					60							65		
gag	cag	gcg	atg	gtg	cac	cag	tct	gtt	gga	tat	gca	cgc	atg	cac	cgc	355		
Glu	Gln	Ala	Met	Val	His	Gln	Ser	Val	Gly	Tyr	Ala	Arg	Met	His	Arg			
70					75					80							85	
cgt	cgt	ggc	aca	tac	gca	tct	gcc	gca	tct	gtt	gga	ccc	ggc	gcg	acc	403		
Arg	Arg	Gly	Thr	Tyr	Ala	Ser	Ala	Ala	Ser	Val	Gly	Pro	Gly	Ala	Thr			
				90					95							100		
aac	ctg	tta	acc	ggc	gcg	gct	ctt	gct	acc	acc	aac	cgt	ttg	cca	gcg	451		
Asn	Leu	Leu	Thr	Gly	Ala	Ala	Leu	Ala	Thr	Thr	Asn	Arg	Leu	Pro	Ala			
				105					110							115		
ttg	ctg	ctg	cct	agt	gat	act	ttt	gcc	acc	cgc	gtg	gcg	gat	cca	gtg	499		
Leu	Leu	Leu	Pro	Ser	Asp	Thr	Phe	Ala	Thr	Arg	Val	Ala	Asp	Pro	Val			
				120					125							130		
ttg	cag	cag	ttg	gag	cag	cca	tgg	gat	atc	ggg	ctg	acg	gtt	aat	gat	547		
Leu	Gln	Gln	Leu	Glu	Gln	Pro	Trp	Asp	Ile	Gly	Leu	Thr	Val	Asn	Asp			
				135					140							145		
gct	ttc	cgc	cct	gtg	tct	aag	ttc	ttt	gat	cgg	gtg	cag	cgc	ccg	gag	595		
Ala	Phe	Arg	Pro	Val	Ser	Lys	Phe	Phe	Asp	Arg	Val	Gln	Arg	Pro	Glu			
150					155					160							165	

cag ttg ttc tct att gcg ttg gct gcg atg cgt gtg ttg act gat ccc	643
Gln Leu Phe Ser Ile Ala Leu Ala Ala Met Arg Val Leu Thr Asp Pro	
170 175 180	
gca gaa acc ggt gcg gtc acc att gcg ctt cca gaa gat gtg cag gct	691
Ala Glu Thr Gly Ala Val Thr Ile Ala Leu Pro Glu Asp Val Gln Ala	
185 190 195	
gaa atg ctc gat gtg ccg gtg gag ttc ttg cag gat cgt gag tgg cac	739
Glu Met Leu Asp Val Pro Val Glu Phe Leu Gln Asp Arg Glu Trp His	
200 205 210	
att agg cgc cca cgt cca gag cgt gct gcg ttg gct cgt gcg att gaa	787
Ile Arg Arg Pro Arg Pro Glu Arg Ala Ala Leu Ala Arg Ala Ile Glu	
215 220 225	
gtc atc aaa aac gct aag aat ccg atg atc att gct ggt ggc gga gtg	835
Val Ile Lys Asn Ala Lys Asn Pro Met Ile Ile Ala Gly Gly Gly Val	
230 235 240 245	
ttg tac tcc gat gcg gaa acg cag ctg cag gca ctt gtg gag cag act	883
Leu Tyr Ser Asp Ala Glu Thr Gln Leu Gln Ala Leu Val Glu Gln Thr	
250 255 260	
ggc att cca gtg ggt acc tcc caa gct ggt ggt ggc gtg ttg gcg tgg	931
Gly Ile Pro Val Gly Thr Ser Gln Ala Gly Gly Gly Val Leu Ala Trp	
265 270 275	
gat cat gca caa aac tta ggt ggt gtg ggt gcc acc gga acg ttg gct	979
Asp His Ala Gln Asn Leu Gly Gly Val Gly Ala Thr Gly Thr Leu Ala	
280 285 290	
gcc aac cgc att gcg ggt gat gct gat gtg atc atc ggt atc ggt act	1027
Ala Asn Arg Ile Ala Gly Asp Ala Asp Val Ile Ile Gly Ile Gly Thr	
295 300 305	
cgt tac agc gat ttc acc acc gca tct cgc act gcg ttc caa aac cct	1075
Arg Tyr Ser Asp Phe Thr Thr Ala Ser Arg Thr Ala Phe Gln Asn Pro	
310 315 320 325	
gat gtc acc ttc atc aac atc aat gtt gct tcc ttc gat gct tac aag	1123
Asp Val Thr Phe Ile Asn Ile Asn Val Ala Ser Phe Asp Ala Tyr Lys	
330 335 340	
cat ggc act cag ttg cct gtg att gca gat gca cgc gag gca att gtg	1171
His Gly Thr Gln Leu Pro Val Ile Ala Asp Ala Arg Glu Ala Ile Val	
345 350 355	
gag ctt gct gaa gcc ctg cag gga ttc acc gtg gca gag gat tac gcg	1219
Glu Leu Ala Glu Ala Leu Gln Gly Phe Thr Val Ala Glu Asp Tyr Ala	
360 365 370	
cag cgc atc gcg aag gaa aag gct gcg tgg gac gca gaa gta gat aag	1267
Gln Arg Ile Ala Lys Glu Lys Ala Ala Trp Asp Ala Glu Val Asp Lys	
375 380 385	
tct ttt gcc ccc tcc ggt ctt gcg ctg cct gga cag ccg gag atc atc	1315
Ser Phe Ala Pro Ser Gly Leu Ala Leu Pro Gly Gln Pro Glu Ile Ile	
390 395 400 405	



ggc gcg gtg cag gcg tcg aca agc gaa aaa gac gtc att gtg cag gcc	1363
Gly Ala Val Gln Ala Ser Thr Ser Glu Lys Asp Val Ile Val Gln Ala	
410 415 420	
gct gga tcc ttg cct ggt gac ctg cac aag ctg tgg cgt gtg cgc gat	1411
Ala Gly Ser Leu Pro Gly Asp Leu His Lys Leu Trp Arg Val Arg Asp	
425 430 435	
gcg ctg ggc tac cac gtg gaa tat gcg ttc tcg tgc atg ggc tat gaa	1459
Ala Leu Gly Tyr His Val Glu Tyr Ala Phe Ser Cys Met Gly Tyr Glu	
440 445 450	
atc gcg ggc ggt atc ggc gcg aag cgt gga ctt gat gcc gca ggc gat	1507
Ile Ala Gly Gly Ile Gly Ala Lys Arg Gly Leu Asp Ala Ala Gly Asp	
455 460 465	
gac cgc gac gtg gtg atc atg gtt ggt gat ggg tcc tac ctc atg ctc	1555
Asp Arg Asp Val Val Ile Met Val Gly Asp Gly Ser Tyr Leu Met Leu	
470 475 480 485	
aac act gag ctg gtc acg gcc gtg gca gaa ggt atc aag gtg att gtg	1603
Asn Thr Glu Leu Val Thr Ala Val Ala Glu Gly Ile Lys Val Ile Val	
490 495 500	
gtg ctc atc caa aac cac ggt tat gcc tcc atc ggc cac ctg tct gaa	1651
Val Leu Ile Gln Asn His Gly Tyr Ala Ser Ile Gly His Leu Ser Glu	
505 510 515	
act gtc ggt tcg cag cgt ttt ggt act tgg tac cgc gaa tat gac gct	1699
Thr Val Gly Ser Gln Arg Phe Gly Thr Trp Tyr Arg Glu Tyr Asp Ala	
520 525 530	
gag gcg aaa aac ttc cag ggc gag cag att ctg cct gtt gac ctg gcg	1747
Glu Ala Lys Asn Phe Gln Gly Glu Gln Ile Leu Pro Val Asp Leu Ala	
535 540 545	
atg aat gca cgc agc tac ggc atg gat gtc att gaa gtg gaa cca agc	1795
Met Asn Ala Arg Ser Tyr Gly Met Asp Val Ile Glu Val Glu Pro Ser	
550 555 560 565	
gcg aat gcg atc gag gat ctc aaa gca gcg atg gca acc gcg aag gct	1843
Ala Asn Ala Ile Glu Asp Leu Lys Ala Ala Met Ala Thr Ala Lys Ala	
570 575 580	
tcg gag aaa tcc acc ttc atc cac atc aac agc gat ccg ttg atc tac	1891
Ser Glu Lys Ser Thr Phe Ile His Ile Asn Ser Asp Pro Leu Ile Tyr	
585 590 595	
gca cca gac ggt gct ggt tgg tgg gac gtg ccg gtg tcg gag acg tcc	1939
Ala Pro Asp Gly Ala Gly Trp Trp Asp Val Pro Val Ser Glu Thr Ser	
600 605 610	
act ctg gat agc acc aac gcg gct cgt gaa gat tac ctg aaa aac caa	1987
Thr Leu Asp Ser Thr Asn Ala Ala Arg Glu Asp Tyr Leu Lys Asn Gln	
615 620 625	
gcc ctc cag cgt ccg ctg ctc ggc taaaccagtt ggctaaacca aaa	2034
Ala Leu Gln Arg Pro Leu Leu Gly	
630 635	

<210> 230  
 <211> 637  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 230

```

Met Ala Glu Thr Lys Arg Met Thr Val Ser Gln Ala Leu Val Glu Phe
  1           5           10           15

Leu Gly His Gln Trp Thr Val Asp Gly Asp Ile Arg Glu Arg Thr Ile
          20           25           30

Pro Gly Met Phe Gly Ile Phe Gly His Gly Asn Val Ala Gly Ile Gly
  35           40           45

Gln Ala Leu Lys Gln Tyr Asn Val Glu Gln Pro Glu Leu Met Pro Tyr
  50           55           60

Tyr Gln Ala Arg Asn Glu Gln Ala Met Val His Gln Ser Val Gly Tyr
  65           70           75           80

Ala Arg Met His Arg Arg Arg Gly Thr Tyr Ala Ser Ala Ala Ser Val
          85           90           95

Gly Pro Gly Ala Thr Asn Leu Leu Thr Gly Ala Ala Leu Ala Thr Thr
          100           105           110

Asn Arg Leu Pro Ala Leu Leu Leu Pro Ser Asp Thr Phe Ala Thr Arg
          115           120           125

Val Ala Asp Pro Val Leu Gln Gln Leu Glu Gln Pro Trp Asp Ile Gly
          130           135           140

Leu Thr Val Asn Asp Ala Phe Arg Pro Val Ser Lys Phe Phe Asp Arg
          145           150           155           160

Val Gln Arg Pro Glu Gln Leu Phe Ser Ile Ala Leu Ala Ala Met Arg
          165           170           175

Val Leu Thr Asp Pro Ala Glu Thr Gly Ala Val Thr Ile Ala Leu Pro
          180           185           190

Glu Asp Val Gln Ala Glu Met Leu Asp Val Pro Val Glu Phe Leu Gln
          195           200           205

Asp Arg Glu Trp His Ile Arg Arg Pro Arg Pro Glu Arg Ala Ala Leu
          210           215           220

Ala Arg Ala Ile Glu Val Ile Lys Asn Ala Lys Asn Pro Met Ile Ile
          225           230           235           240

Ala Gly Gly Gly Val Leu Tyr Ser Asp Ala Glu Thr Gln Leu Gln Ala
          245           250           255

Leu Val Glu Gln Thr Gly Ile Pro Val Gly Thr Ser Gln Ala Gly Gly
          260           265           270

Gly Val Leu Ala Trp Asp His Ala Gln Asn Leu Gly Gly Val Gly Ala
          275           280           285

Thr Gly Thr Leu Ala Ala Asn Arg Ile Ala Gly Asp Ala Asp Val Ile

```

290					295					300				
Ile Gly Ile Gly Thr	Arg Tyr Ser Asp Phe Thr Thr Ala Ser Arg Thr													
305	310				315							320		
Ala Phe Gln Asn Pro Asp Val Thr Phe Ile Asn Ile Asn Val Ala Ser														
	325				330							335		
Phe Asp Ala Tyr Lys His Gly Thr Gln Leu Pro Val Ile Ala Asp Ala														
	340				345							350		
Arg Glu Ala Ile Val Glu Leu Ala Glu Ala Leu Gln Gly Phe Thr Val														
	355				360							365		
Ala Glu Asp Tyr Ala Gln Arg Ile Ala Lys Glu Lys Ala Ala Trp Asp														
	370				375							380		
Ala Glu Val Asp Lys Ser Phe Ala Pro Ser Gly Leu Ala Leu Pro Gly														
	385				390							395	400	
Gln Pro Glu Ile Ile Gly Ala Val Gln Ala Ser Thr Ser Glu Lys Asp														
				405									415	
Val Ile Val Gln Ala Ala Gly Ser Leu Pro Gly Asp Leu His Lys Leu														
				420									430	
Trp Arg Val Arg Asp Ala Leu Gly Tyr His Val Glu Tyr Ala Phe Ser														
				435									445	
Cys Met Gly Tyr Glu Ile Ala Gly Gly Ile Gly Ala Lys Arg Gly Leu														
				450									460	
Asp Ala Ala Gly Asp Asp Arg Asp Val Val Ile Met Val Gly Asp Gly														
				465									480	
Ser Tyr Leu Met Leu Asn Thr Glu Leu Val Thr Ala Val Ala Glu Gly														
				485									495	
Ile Lys Val Ile Val Val Leu Ile Gln Asn His Gly Tyr Ala Ser Ile														
				500									510	
Gly His Leu Ser Glu Thr Val Gly Ser Gln Arg Phe Gly Thr Trp Tyr														
				515									525	
Arg Glu Tyr Asp Ala Glu Ala Lys Asn Phe Gln Gly Glu Gln Ile Leu														
				530									540	
Pro Val Asp Leu Ala Met Asn Ala Arg Ser Tyr Gly Met Asp Val Ile														
				545									560	
Glu Val Glu Pro Ser Ala Asn Ala Ile Glu Asp Leu Lys Ala Ala Met														
				565									575	
Ala Thr Ala Lys Ala Ser Glu Lys Ser Thr Phe Ile His Ile Asn Ser														
				580									590	
Asp Pro Leu Ile Tyr Ala Pro Asp Gly Ala Gly Trp Trp Asp Val Pro														
				595									605	
Val Ser Glu Thr Ser Thr Leu Asp Ser Thr Asn Ala Ala Arg Glu Asp														
				610									620	

Tyr Leu Lys Asn Gln Ala Leu Gln Arg Pro Leu Leu Gly  
 625 630 635

<210> 231  
 <211> 1142  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1119)  
 <223> RXN01143

<400> 231  
 atc cca gtt gtc acc acc ttg atg gct ttg ggt act ttc cca gag tct 48  
 Ile Pro Val Val Thr Thr Leu Met Ala Leu Gly Thr Phe Pro Glu Ser  
 1 5 10 15  
 cac gag ctg cac atg ggt atg cca ggc atg cat ggc act gtg tcc gct 96  
 His Glu Leu His Met Gly Met Pro Gly Met His Gly Thr Val Ser Ala  
 20 25 30  
 gtt ggt gca ctg cag cgc agc gac ctg ctg att gct atc ggc tcc cgc 144  
 Val Gly Ala Leu Gln Arg Ser Asp Leu Leu Ile Ala Ile Gly Ser Arg  
 35 40 45  
 ttt gat gac cgc gtc acc ggt gac gtt gac acc ttc gcg cct gac gcc 192  
 Phe Asp Asp Arg Val Thr Gly Asp Val Asp Thr Phe Ala Pro Asp Ala  
 50 55 60  
 aag atc att cac gcc gac att gat cct gcc gaa atc ggc aag atc aag 240  
 Lys Ile Ile His Ala Asp Ile Asp Pro Ala Glu Ile Gly Lys Ile Lys  
 65 70 75 80  
 cag gtt gag gtt cca atc gtg ggc gat gcc cgc gaa gtt ctt gct cgt 288  
 Gln Val Glu Val Pro Ile Val Gly Asp Ala Arg Glu Val Leu Ala Arg  
 85 90 95  
 ctg ctg gaa acc acc aag gca agc aag gca gag acc gag gac atc tcc 336  
 Leu Leu Glu Thr Thr Lys Ala Ser Lys Ala Glu Thr Glu Asp Ile Ser  
 100 105 110  
 gag tgg gtt gac tac ctc aag ggc ctc aag gca cgt ttc ccg cgt ggc 384  
 Glu Trp Val Asp Tyr Leu Lys Gly Leu Lys Ala Arg Phe Pro Arg Gly  
 115 120 125  
 tac gac gag cag cca ggc gat ctg ctg gca cca cag ttt gtc att gaa 432  
 Tyr Asp Glu Gln Pro Gly Asp Leu Leu Ala Pro Gln Phe Val Ile Glu  
 130 135 140  
 acc ctg tcc aag gaa gtt ggc ccc gac gca att tac tgc gcc ggc gtt 480  
 Thr Leu Ser Lys Glu Val Gly Pro Asp Ala Ile Tyr Cys Ala Gly Val  
 145 150 155 160  
 ggc cag cac caa atg tgg gca gct cag ttc gtt gac ttt gaa aag cca 528  
 Gly Gln His Gln Met Trp Ala Ala Gln Phe Val Asp Phe Glu Lys Pro  
 165 170 175  
 cgc acc tgg ctc aac tcc ggt gga ctg ggc acc atg ggc tac gca gtt 576

```

Arg Thr Trp Leu Asn Ser Gly Gly Leu Gly Thr Met Gly Tyr Ala Val
      180                      185                      190

cct gcg gcc ctt gga gca aag gct ggc gca cct gac aag gaa gtc tgg 624
Pro Ala Ala Leu Gly Ala Lys Ala Gly Ala Pro Asp Lys Glu Val Trp
      195                      200                      205

gct atc gac ggc gac ggc tgt ttc cag atg acc aac cag gaa ctc acc 672
Ala Ile Asp Gly Asp Gly Cys Phe Gln Met Thr Asn Gln Glu Leu Thr
      210                      215                      220

acc gcc gca gtt gaa ggt ttc ccc att aag atc gca cta atc aac aac 720
Thr Ala Ala Val Glu Gly Phe Pro Ile Lys Ile Ala Leu Ile Asn Asn
      225                      230                      235                      240

gga aaa cct ggg gca tgg gtt cgc caa tgg cag acc cta ttc tat gaa 768
Gly Lys Pro Gly Ala Trp Val Arg Gln Trp Gln Thr Leu Phe Tyr Glu
      245                      250                      255

gga cgg tac tca aat act aaa ctt cgt aac cag ggc gag tac atg ccc 816
Gly Arg Tyr Ser Asn Thr Lys Leu Arg Asn Gln Gly Glu Tyr Met Pro
      260                      265                      270

gac ttt gtt acc ctt tct gag gga ctt ggc tgt gtt gcc atc cgc gtc 864
Asp Phe Val Thr Leu Ser Glu Gly Leu Gly Cys Val Ala Ile Arg Val
      275                      280                      285

acc aaa gcg gag gaa gta ctg cca gcc atc caa aag gct cga gag atc 912
Thr Lys Ala Glu Glu Val Leu Pro Ala Ile Gln Lys Ala Arg Glu Ile
      290                      295                      300

aac gac cgc cca gta gtc atc gac ttc atc gtc ggt gaa gac gca cag 960
Asn Asp Arg Pro Val Val Ile Asp Phe Ile Val Gly Glu Asp Ala Gln
      305                      310                      315                      320

gta tgg cca atg gtg tct gct gga tca tcc aac tcc gat atc cag tac 1008
Val Trp Pro Met Val Ser Ala Gly Ser Ser Asn Ser Asp Ile Gln Tyr
      325                      330                      335

gca ctc gga ttg cgc cca ttc ttt gat ggt gat gaa tct gca gca gaa 1056
Ala Leu Gly Leu Arg Pro Phe Phe Asp Gly Asp Glu Ser Ala Ala Glu
      340                      345                      350

gat cct gcc gac att cac gaa gcc gtc agc gac att gat gcc gcc gtt 1104
Asp Pro Ala Asp Ile His Glu Ala Val Ser Asp Ile Asp Ala Ala Val
      355                      360                      365

gaa tcg acc gag gca taaggagaga cccaagatgg cta 1142
Glu Ser Thr Glu Ala
      370

```

&lt;210&gt; 232

&lt;211&gt; 373

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 232

```

Ile Pro Val Val Thr Thr Leu Met Ala Leu Gly Thr Phe Pro Glu Ser
  1                      5                      10                      15

```

His Glu Leu His Met Gly Met Pro Gly Met His Gly Thr Val Ser Ala  
                   20                                  25                                  30  
 Val Gly Ala Leu Gln Arg Ser Asp Leu Leu Ile Ala Ile Gly Ser Arg  
                   35                                  40                                  45  
 Phe Asp Asp Arg Val Thr Gly Asp Val Asp Thr Phe Ala Pro Asp Ala  
                   50                                  55                                  60  
 Lys Ile Ile His Ala Asp Ile Asp Pro Ala Glu Ile Gly Lys Ile Lys  
                   65                                  70                                  75                                  80  
 Gln Val Glu Val Pro Ile Val Gly Asp Ala Arg Glu Val Leu Ala Arg  
                                   85                                  90                                  95  
 Leu Leu Glu Thr Thr Lys Ala Ser Lys Ala Glu Thr Glu Asp Ile Ser  
                                   100                                  105                                  110  
 Glu Trp Val Asp Tyr Leu Lys Gly Leu Lys Ala Arg Phe Pro Arg Gly  
                   115                                  120                                  125  
 Tyr Asp Glu Gln Pro Gly Asp Leu Leu Ala Pro Gln Phe Val Ile Glu  
                   130                                  135                                  140  
 Thr Leu Ser Lys Glu Val Gly Pro Asp Ala Ile Tyr Cys Ala Gly Val  
                   145                                  150                                  155                                  160  
 Gly Gln His Gln Met Trp Ala Ala Gln Phe Val Asp Phe Glu Lys Pro  
                                   165                                  170                                  175  
 Arg Thr Trp Leu Asn Ser Gly Gly Leu Gly Thr Met Gly Tyr Ala Val  
                                   180                                  185                                  190  
 Pro Ala Ala Leu Gly Ala Lys Ala Gly Ala Pro Asp Lys Glu Val Trp  
                   195                                  200                                  205  
 Ala Ile Asp Gly Asp Gly Cys Phe Gln Met Thr Asn Gln Glu Leu Thr  
                   210                                  215                                  220  
 Thr Ala Ala Val Glu Gly Phe Pro Ile Lys Ile Ala Leu Ile Asn Asn  
                   225                                  230                                  235                                  240  
 Gly Lys Pro Gly Ala Trp Val Arg Gln Trp Gln Thr Leu Phe Tyr Glu  
                                   245                                  250                                  255  
 Gly Arg Tyr Ser Asn Thr Lys Leu Arg Asn Gln Gly Glu Tyr Met Pro  
                                   260                                  265                                  270  
 Asp Phe Val Thr Leu Ser Glu Gly Leu Gly Cys Val Ala Ile Arg Val  
                   275                                  280                                  285  
 Thr Lys Ala Glu Glu Val Leu Pro Ala Ile Gln Lys Ala Arg Glu Ile  
                   290                                  295                                  300  
 Asn Asp Arg Pro Val Val Ile Asp Phe Ile Val Gly Glu Asp Ala Gln  
                   305                                  310                                  315                                  320  
 Val Trp Pro Met Val Ser Ala Gly Ser Ser Asn Ser Asp Ile Gln Tyr  
                                   325                                  330                                  335  
 Ala Leu Gly Leu Arg Pro Phe Phe Asp Gly Asp Glu Ser Ala Ala Glu

```

340          345          350
Asp Pro Ala Asp Ile His Glu Ala Val Ser Asp Ile Asp Ala Ala Val
355          360          365

Glu Ser Thr Glu Ala
370

<210> 233
<211> 793
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(793)
<223> RXN01146

<400> 233
tatttagtaa aggagccaga aagtcgtgaa tgtggcagct tctcaacagc ccactcccgc 60

cacggttgca agccgtggtc gatccgccgc ccctgagcgg atg aca ggt gca aag 115
Met Thr Gly Ala Lys
1 5

gca att gtt cga tcg ctc gag gag ctt aac gcc gac atc gtg ttc ggt 163
Ala Ile Val Arg Ser Leu Glu Glu Leu Asn Ala Asp Ile Val Phe Gly
10 15 20

att cct ggt ggt gcg gtg cta ccg gtg tat gac ccg ctc tat tcc tcc 211
Ile Pro Gly Gly Ala Val Leu Pro Val Tyr Asp Pro Leu Tyr Ser Ser
25 30 35

aca aag gtg cgc cac gtc ttg gtg cgc cac gag cag ggc gca ggc cac 259
Thr Lys Val Arg His Val Leu Val Arg His Glu Gln Gly Ala Gly His
40 45 50

gca gca acc ggc tac gcg cag gtt act gga cgc gtt ggc gtc tgc att 307
Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Arg Val Gly Val Cys Ile
55 60 65

gca acc tct ggc cca gga gca acc aac ttg gtt acc cca atc gct gat 355
Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val Thr Pro Ile Ala Asp
70 75 80 85

gca aac ttg gac tcc gtt ccc atg gtt gcc atc acc ggc cag gtc gga 403
Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile Thr Gly Gln Val Gly
90 95 100

agt ggc ctg ctg ggt acc gac gct ttc cag gaa gcc gat atc cgc ggc 451
Ser Gly Leu Leu Gly Thr Asp Ala Phe Gln Glu Ala Asp Ile Arg Gly
105 110 115

atc acc atg cca gtg acc aag cac aac ttc atg gtc acc aac cct aac 499
Ile Thr Met Pro Val Thr Lys His Asn Phe Met Val Thr Asn Pro Asn
120 125 130

gac att cca cag gca ttg gct gag gca ttc cac ctc gcg att act ggt 547
Asp Ile Pro Gln Ala Leu Ala Glu Ala Phe His Leu Ala Ile Thr Gly
135 140 145

```

cgc cct ggc cct gtt ctg gtg gat att cct aag gat gtc cag aac gct 595  
 Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys Asp Val Gln Asn Ala  
 150 155 160 165  
  
 gaa ttg gat ttc gtc tgg cca cca aag atc gac ctg cca ggc tac cgc 643  
 Glu Leu Asp Phe Val Trp Pro Pro Lys Ile Asp Leu Pro Gly Tyr Arg  
 170 175 180  
  
 cca gtt tca aca cca cat gct cgc cag atc gag cag gca gtc aag ctg 691  
 Pro Val Ser Thr Pro His Ala Arg Gln Ile Glu Gln Ala Val Lys Leu  
 185 190 195  
  
 atc ggt gag gcc aag aag ccc gtc ctt tac gtt ggt ggt ggc gta atc 739  
 Ile Gly Glu Ala Lys Lys Pro Val Leu Tyr Val Gly Gly Gly Val Ile  
 200 205 210  
  
 aag gct gac gca cac gaa gag ctt cgt gcg ttc gct gag tac acc ggc 787  
 Lys Ala Asp Ala His Glu Glu Leu Arg Ala Phe Ala Glu Tyr Thr Gly  
 215 220 225  
  
 atc cca 793  
 Ile Pro  
 230

<210> 234  
 <211> 231  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 234  
 Met Thr Gly Ala Lys Ala Ile Val Arg Ser Leu Glu Glu Leu Asn Ala  
 1 5 10 15  
  
 Asp Ile Val Phe Gly Ile Pro Gly Gly Ala Val Leu Pro Val Tyr Asp  
 20 25 30  
  
 Pro Leu Tyr Ser Ser Thr Lys Val Arg His Val Leu Val Arg His Glu  
 35 40 45  
  
 Gln Gly Ala Gly His Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Arg  
 50 55 60  
  
 Val Gly Val Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val  
 65 70 75 80  
  
 Thr Pro Ile Ala Asp Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile  
 85 90 95  
  
 Thr Gly Gln Val Gly Ser Gly Leu Leu Gly Thr Asp Ala Phe Gln Glu  
 100 105 110  
  
 Ala Asp Ile Arg Gly Ile Thr Met Pro Val Thr Lys His Asn Phe Met  
 115 120 125  
  
 Val Thr Asn Pro Asn Asp Ile Pro Gln Ala Leu Ala Glu Ala Phe His  
 130 135 140  
  
 Leu Ala Ile Thr Gly Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys  
 145 150 155 160



Asp Val Gln Asn Ala Glu Leu Asp Phe Val Trp Pro Pro Lys Ile Asp  
                   165                  170                  175  
 Leu Pro Gly Tyr Arg Pro Val Ser Thr Pro His Ala Arg Gln Ile Glu  
                   180                  185                  190  
 Gln Ala Val Lys Leu Ile Gly Glu Ala Lys Lys Pro Val Leu Tyr Val  
                   195                  200                  205  
 Gly Gly Gly Val Ile Lys Ala Asp Ala His Glu Glu Leu Arg Ala Phe  
           210                  215                  220  
 Ala Glu Tyr Thr Gly Ile Pro  
 225                  230

<210> 235  
 <211> 639  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(616)  
 <223> RXN01144

<400> 235  
 ggtgatgaat ctgcagcaga agatcctgcc gacattcacg aagccgtcag cgacattgat 60  
 gccgccgttg aatcgaccga ggcataagga gagacccaag atg gct aat tct gac 115  
   Met Ala Asn Ser Asp  
   1                  5  
 gtc acc cgc cac atc ctg tcc gta ctc gtt cag gac gta gac gga atc 163  
 Val Thr Arg His Ile Leu Ser Val Leu Val Gln Asp Val Asp Gly Ile  
                                   10                  15                  20  
 att tcc cgc gta tca ggt atg ttc acc cga cgc gca ttc aac ctc gtg 211  
 Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg Ala Phe Asn Leu Val  
                           25                  30                  35  
 ttc ctc gtg tct gca aag acc gaa aca cac ggc atc aac cgc atc acg 259  
 Phe Leu Val Ser Ala Lys Thr Glu Thr His Gly Ile Asn Arg Ile Thr  
                   40                  45                  50  
 gtt gtt gtc gac gcc gac gag ctc aac att gag cag atc acc aag cag 307  
 Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu Gln Ile Thr Lys Gln  
           55                  60                  65  
 ctc aac aag ctg atc ccc gtg ctc aaa gtc gtg cga ctt gat gaa gag 355  
 Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val Arg Leu Asp Glu Glu  
   70                  75                  80                  85  
 acc act atc gcc cgc gca atc atg ctg gtt aag gtc tct gcg gac agc 403  
 Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys Val Ser Ala Asp Ser  
                   90                  95                  100  
 acc aac cgt ccg cag atc gtc gac gcc gcg aac atc ttc cgc gcc cga 451  
 Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn Ile Phe Arg Ala Arg  
           105                  110                  115

gtc gtc gac gtg gct cca gac tct gtg gtt att gaa tcc aca ggc acc 499  
 Val Val Asp Val Ala Pro Asp Ser Val Val Ile Glu Ser Thr Gly Thr  
           120                          125                          130

cca ggc aag ctc cgc gca ctg ctt gac gtg atg gaa cca ttc gga atc 547  
 Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met Glu Pro Phe Gly Ile  
           135                          140                          145

cgc gaa ctg atc caa tcc gga cag att gca ctc aac cgc ggt ccg aag 595  
 Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu Asn Arg Gly Pro Lys  
           150                          155                          160                          165

acc atg gct ccg gcc aag atc taaacagcaa ttaatctgat tgc 639  
 Thr Met Ala Pro Ala Lys Ile  
                                   170

<210> 236  
 <211> 172  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 236  
 Met Ala Asn Ser Asp Val Thr Arg His Ile Leu Ser Val Leu Val Gln  
   1                          5                          10                          15

Asp Val Asp Gly Ile Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg  
           20                          25                          30

Ala Phe Asn Leu Val Phe Leu Val Ser Ala Lys Thr Glu Thr His Gly  
           35                          40                          45

Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu  
           50                          55                          60

Gln Ile Thr Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val  
           65                          70                          75                          80

Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys  
                           85                          90                          95

Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn  
                           100                          105                          110

Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile  
           115                          120                          125

Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met  
           130                          135                          140

Glu Pro Phe Gly Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu  
           145                          150                          155                          160

Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile  
                           165                          170

<210> 237  
 <211> 897  
 <212> DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(874)

&lt;223&gt; RXA02474

&lt;400&gt; 237

tgctggtcta ttgtggcgac cgagggcctt tgaaggttcg acaaactgta taaggccttg 60

aatcttgaga	atttattttg	aggaagcaag	aggaagtgtc	atg	agc	aaa	ggt	gca	115
				Met	Ser	Lys	Val	Ala	
				1				5	

atg	ggt	acc	ggt	ggt	gca	caa	ggc	atc	ggt	cgt	gga	att	tca	gag	aag	163
Met	Val	Thr	Gly	Gly	Ala	Gln	Gly	Ile	Gly	Arg	Gly	Ile	Ser	Glu	Lys	
			10					15						20		

ctg	gca	gca	gat	ggt	ttc	gat	att	gcc	gta	gcc	gac	ctg	cca	caa	cag	211
Leu	Ala	Ala	Asp	Gly	Phe	Asp	Ile	Ala	Val	Ala	Asp	Leu	Pro	Gln	Gln	
			25					30					35			

gaa	gaa	caa	gct	gca	gag	acc	atc	aag	ttg	att	gaa	gct	gca	ggt	caa	259
Glu	Glu	Gln	Ala	Ala	Glu	Thr	Ile	Lys	Leu	Ile	Glu	Ala	Ala	Gly	Gln	
		40					45				50					

aag	gct	gta	ttc	ggt	gga	tta	gat	gtc	acc	gat	aag	gct	aat	ttc	gac	307
Lys	Ala	Val	Phe	Val	Gly	Leu	Asp	Val	Thr	Asp	Lys	Ala	Asn	Phe	Asp	
	55					60					65					

agt	gca	att	gat	gag	gca	gca	gag	aaa	ctt	ggc	ggc	ttc	gat	gtg	cta	355
Ser	Ala	Ile	Asp	Glu	Ala	Ala	Glu	Lys	Leu	Gly	Gly	Phe	Asp	Val	Leu	
70					75					80					85	

gta	aac	aac	gcc	ggc	atc	gca	caa	att	aag	cca	ctt	ctg	gaa	gtc	acc	403
Val	Asn	Asn	Ala	Gly	Ile	Ala	Gln	Ile	Lys	Pro	Leu	Leu	Glu	Val	Thr	
			90						95					100		

gaa	gaa	gac	cta	aag	cag	atc	tac	tcc	gtg	aac	ggt	ttt	agc	gta	ttt	451
Glu	Glu	Asp	Leu	Lys	Gln	Ile	Tyr	Ser	Val	Asn	Val	Phe	Ser	Val	Phe	
		105						110					115			

ttt	ggt	att	caa	gca	gca	tcc	cga	aag	ttc	gat	gag	ctt	ggc	gta	aaa	499
Phe	Gly	Ile	Gln	Ala	Ala	Ser	Arg	Lys	Phe	Asp	Glu	Leu	Gly	Val	Lys	
		120					125					130				

ggc	aag	atc	atc	aac	gct	gca	tca	atc	gct	gct	atc	caa	ggt	ttc	cca	547
Gly	Lys	Ile	Ile	Asn	Ala	Ala	Ser	Ile	Ala	Ala	Ile	Gln	Gly	Phe	Pro	
	135				140						145					

atc	ttg	agc	gcc	tac	tcc	acc	acc	aaa	ttc	gcg	ggt	cgt	ggc	ctc	acc	595
Ile	Leu	Ser	Ala	Tyr	Ser	Thr	Thr	Lys	Phe	Ala	Val	Arg	Gly	Leu	Thr	
150					155					160				165		

cag	gct	gct	gcg	caa	gaa	ctc	gca	ccc	aag	ggt	cac	acc	gtg	aat	gcc	643
Gln	Ala	Ala	Ala	Gln	Glu	Leu	Ala	Pro	Lys	Gly	His	Thr	Val	Asn	Ala	
			170						175					180		

tac	gca	cct	ggc	atc	gtg	ggc	acc	gga	atg	tgg	gag	caa	atc	gat	gcc	691
Tyr	Ala	Pro	Gly	Ile	Val	Gly	Thr	Gly	Met	Trp	Glu	Gln	Ile	Asp	Ala	
			185					190					195			

gag ctt tcc aag atc aac ggc aag cca atc ggt gag aac ttc aag gag 739  
 Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly Glu Asn Phe Lys Glu  
           200                          205                          210

tac tcc tcc tca atc gca ttg ggc cga cca tca gta cct gag gat gta 787  
 Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser Val Pro Glu Asp Val  
           215                          220                          225

gcc ggt ctg gtt tcc ttc ctg gct tct gaa aac tcc aac tac atc acc 835  
 Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn Ser Asn Tyr Ile Thr  
           230                          235                          240                          245

gga cag gtc atg ctt gtc gac ggc ggc atg ctc tac aac taggggttgc 884  
 Gly Gln Val Met Leu Val Asp Gly Gly Met Leu Tyr Asn  
                           250                          255

tttcccgcaac tca 897

<210> 238  
 <211> 258  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 238  
 Met Ser Lys Val Ala Met Val Thr Gly Gly Ala Gln Gly Ile Gly Arg  
   1                          5                          10                          15

Gly Ile Ser Glu Lys Leu Ala Ala Asp Gly Phe Asp Ile Ala Val Ala  
           20                          25                          30

Asp Leu Pro Gln Gln Glu Glu Gln Ala Ala Glu Thr Ile Lys Leu Ile  
           35                          40                          45

Glu Ala Ala Gly Gln Lys Ala Val Phe Val Gly Leu Asp Val Thr Asp  
           50                          55                          60

Lys Ala Asn Phe Asp Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly  
           65                          70                          75                          80

Gly Phe Asp Val Leu Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro  
                           85                          90                          95

Leu Leu Glu Val Thr Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn  
           100                          105                          110

Val Phe Ser Val Phe Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp  
           115                          120                          125

Glu Leu Gly Val Lys Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala  
           130                          135                          140

Ile Gln Gly Phe Pro Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala  
           145                          150                          155                          160

Val Arg Gly Leu Thr Gln Ala Ala Ala Gln Glu Leu Ala Pro Lys Gly  
           165                          170                          175

His Thr Val Asn Ala Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp  
           180                          185                          190

Glu Gln Ile Asp Ala Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly  
 195 200 205

Glu Asn Phe Lys Glu Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser  
 210 215 220

Val Pro Glu Asp Val Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn  
 225 230 235 240

Ser Asn Tyr Ile Thr Gly Gln Val Met Leu Val Asp Gly Gly Met Leu  
 245 250 255

Tyr Asn

<210> 239  
 <211> 876  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(853)  
 <223> RXA02453

<400> 239  
 aaccaacaaa ggtcatctca accggcttaa gaaaattctg ccagctttct gctgattgaa 60

tcgtgccagc tcagggcata tctcacctaa agtaaacacc atg aaa tca atc ttc 115  
 Met Lys Ser Ile Phe  
 1 5

att tcc ggt gcg gcg aac gga att ggc aaa gct gtg gcg ttg aaa ttt 163  
 Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala Val Ala Leu Lys Phe  
 10 15 20

ctt cac gaa ggt tgg ctc gtt gga gcc tac gac ctc gcg gaa atc acc 211  
 Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp Leu Ala Glu Ile Thr  
 25 30 35

tac tca cac ccc aat ctt cgc tgg ggc tac ctc aat gtt cga cag tcc 259  
 Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu Asn Val Arg Gln Ser  
 40 45 50

gag tcg tgg gac aaa gcc cta gaa gac ttt gcg acg cac acc gga ggc 307  
 Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala Thr His Thr Gly Gly  
 55 60 65

acc atc gat gtg gtg gac aat aat gcc ggc gta att att gag gga ccg 355  
 Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val Ile Ile Glu Gly Pro  
 70 75 80 85

ctg cag gac gca gag gag ggg agc gtc gac aag ctt ctt gca atc aac 403  
 Leu Gln Asp Ala Glu Gly Ser Val Asp Lys Leu Leu Ala Ile Asn  
 90 95 100

gtc aat ggc gtg act ctt ggt gcc cgc gcc gct cat cct tat ttg gcg 451  
 Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala His Pro Tyr Leu Ala  
 105 110 115

cgc acg ccg ggc gcc cag ttg tta aac atg tcc tcg gcg tcg gcg gtg 499  
 Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser Ser Ala Ser Ala Val  
 120 125 130  
 tac ggg cag ccc cag atc gcg gtg tat tcg gct tcg aag ttt tac gtc 547  
 Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala Ser Lys Phe Tyr Val  
 135 140 145  
 gca ggt ctt act gag gcg ctg aat ttg gag tgg cgg aaa gac gat att 595  
 Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp Arg Lys Asp Asp Ile  
 150 155 160 165  
 cgc gtg gtc gat gtt tgg cct ttg tgg gcg aaa acc gat ttg gtg aac 643  
 Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys Thr Asp Leu Val Asn  
 170 175 180  
 ggc gtg aag gct aag tca ctg aag cgt ttg ggt gtc cgg atc act ccg 691  
 Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly Val Arg Ile Thr Pro  
 185 190 195  
 gaa cag gtg gca cag gcg gta tgg gat gcg gtg cat ccg aaa tct cgg 739  
 Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val His Pro Lys Ser Arg  
 200 205 210  
 tgg gcg aag gga aag gtg cat cac ggg gtg tca aag ttg gat aag gcg 787  
 Trp Ala Lys Gly Lys Val His His Gly Val Ser Lys Leu Asp Lys Ala  
 215 220 225  
 ctg tat ctc atg aaa tct ctg tcg cct gat cgg gta gcg atg tgt ttt 835  
 Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg Val Ala Met Cys Phe  
 230 235 240 245  
 gcg cga cta atc gcc gga taaatgaatt gattatttta ggc 876  
 Ala Arg Leu Ile Ala Gly  
 250

&lt;210&gt; 240

&lt;211&gt; 251

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 240

Met Lys Ser Ile Phe Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala  
 1 5 10 15  
 Val Ala Leu Lys Phe Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp  
 20 25 30  
 Leu Ala Glu Ile Thr Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu  
 35 40 45  
 Asn Val Arg Gln Ser Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala  
 50 55 60  
 Thr His Thr Gly Gly Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val  
 65 70 75 80  
 Ile Ile Glu Gly Pro Leu Gln Asp Ala Glu Glu Gly Ser Val Asp Lys  
 85 90 95

Leu Leu Ala Ile Asn Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala  
 100 105 110  
 His Pro Tyr Leu Ala Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser  
 115 120 125  
 Ser Ala Ser Ala Val Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala  
 130 135 140  
 Ser Lys Phe Tyr Val Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp  
 145 150 155 160  
 Arg Lys Asp Asp Ile Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys  
 165 170 175  
 Thr Asp Leu Val Asn Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly  
 180 185 190  
 Val Arg Ile Thr Pro Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val  
 195 200 205  
 His Pro Lys Ser Arg Trp Ala Lys Gly Lys Val His His Gly Val Ser  
 210 215 220  
 Lys Leu Asp Lys Ala Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg  
 225 230 235 240  
 Val Ala Met Cys Phe Ala Arg Leu Ile Ala Gly  
 245 250

&lt;210&gt; 241

&lt;211&gt; 1140

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1117)

&lt;223&gt; RXS01758

&lt;400&gt; 241

cccccttatt cagagtgatg gtctaccgga gaagtaccca gaccaatagc atcgaccaac 60

gatagcgcgc tcagaagttc tttagtga aa gcagaaccaa atg ccc aaa tac att 115  
 Met Pro Lys Tyr Ile  
 1 5

gcc atg cag gta tcc gaa tcc ggt gca ccg tta gcc gcg aat ctc gtg 163  
 Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu Ala Ala Asn Leu Val  
 10 15 20

caa cct gct ccg ttg aaa tcg agg gaa gtc cgc gtg gaa atc gct gct 211  
 Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg Val Glu Ile Ala Ala  
 25 30 35

agt ggt gtg tgc cat gca gat att ggc acg gca gca gca tcg ggg aag 259  
 Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala Ala Ala Ser Gly Lys  
 40 45 50

cac act gtt ttt cct gtt acc cct ggt cat gag att gca gga acc atc	307
His Thr Val Phe Pro Val Thr Pro Gly His Glu Ile Ala Gly Thr Ile	
55 60 65	
gcg gaa att ggt gaa aac gta tct cgg tgg acg gtt ggt gat cgc gtt	355
Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr Val Gly Asp Arg Val	
70 75 80 85	
gca atc ggt tgg ttt ggt ggc aat tgc ggt gac tgc gct ttt tgt cgt	403
Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp Cys Ala Phe Cys Arg	
90 95 100	
gca ggt gat cct gtg cat tgc aga gag cgg aag att cct ggc gtt tct	451
Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys Ile Pro Gly Val Ser	
105 110 115	
tat gcg ggt ggt tgg gca cag aat att gtt gtt cca gcg gag gct ctt	499
Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val Pro Ala Glu Ala Leu	
120 125 130	
gct gcg att cca gat ggc atg gac ttt tac gag ccc gcc ccg atg ggc	547
Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu Pro Ala Pro Met Gly	
135 140 145	
tgc gca ggt gtg aca aca ttc aat gcg ttg cga aac ctg aag ctg gat	595
Cys Ala Gly Val Thr Phe Asn Ala Leu Arg Asn Leu Lys Leu Asp	
150 155 160 165	
ccc ggt gcg gct gtc gcg gtc ttt gga atc ggc ggt tta gtg cgc cta	643
Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly Gly Leu Val Arg Leu	
170 175 180	
gct att cag ttt gct gcg aaa atg ggt tat cga acc atc acc atc gcc	691
Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg Thr Ile Thr Ile Ala	
185 190 195	
cgc ggt tta gag cgt gag gag cta gct agg caa ctt ggc gcc aac cac	739
Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln Leu Gly Ala Asn His	
200 205 210	
tac atc gat agc aat gat ctg cac cct ggc cag gcg tta ttt gaa ctt	787
Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln Ala Leu Phe Glu Leu	
215 220 225	
ggc ggg gct gac ttg atc ttg tct act gcg tcc acc acg gag cct ctt	835
Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser Thr Thr Glu Pro Leu	
230 235 240 245	
tcg gag ttg tct acc ggt ctt tct att ggc ggg cag cta acc att atc	883
Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly Gln Leu Thr Ile Ile	
250 255 260	
gga gtt gat ggg gga gat atc acc gtt tcg gca gcc caa ttg atg atg	931
Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala Ala Gln Leu Met Met	
265 270 275	
aac cgt cag atc atc aca ggt cac ctc act gga agt gcg aat gac acg	979
Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly Ser Ala Asn Asp Thr	
280 285 290	
gaa cag act atg aaa ttt gct cat ctc cat ggc gtg aaa ccg ctt att	1027



Glu Gln Thr Met Lys Phe Ala His Leu His Gly Val Lys Pro Leu Ile  
 295 300 305

gaa cgg atg cct ctc gat caa gcc aac gag gct att gca cgt att tca 1075  
 Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala Ile Ala Arg Ile Ser  
 310 315 320 325

gct ggt aaa cca cgt ttc cgt att gtc ttg gag ccg aat tca 1117  
 Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu Pro Asn Ser  
 330 335

taatgccaac agcaagccca att 1140

<210> 242  
 <211> 339  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 242  
 Met Pro Lys Tyr Ile Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu  
 1 5 10 15

Ala Ala Asn Leu Val Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg  
 20 25 30

Val Glu Ile Ala Ala Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala  
 35 40 45

Ala Ala Ser Gly Lys His Thr Val Phe Pro Val Thr Pro Gly His Glu  
 50 55 60

Ile Ala Gly Thr Ile Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr  
 65 70 75 80

Val Gly Asp Arg Val Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp  
 85 90 95

Cys Ala Phe Cys Arg Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys  
 100 105 110

Ile Pro Gly Val Ser Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val  
 115 120 125

Pro Ala Glu Ala Leu Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu  
 130 135 140

Pro Ala Pro Met Gly Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg  
 145 150 155 160

Asn Leu Lys Leu Asp Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly  
 165 170 175

Gly Leu Val Arg Leu Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg  
 180 185 190

Thr Ile Thr Ile Ala Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln  
 195 200 205

Leu Gly Ala Asn His Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln  
 210 215 220

Ala Leu Phe Glu Leu Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser  
 225 230 235 240

Thr Thr Glu Pro Leu Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly  
 245 250 255

Gln Leu Thr Ile Ile Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala  
 260 265 270

Ala Gln Leu Met Met Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly  
 275 280 285

Ser Ala Asn Asp Thr Glu Gln Thr Met Lys Phe Ala His Leu His Gly  
 290 295 300

Val Lys Pro Leu Ile Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala  
 305 310 315 320

Ile Ala Arg Ile Ser Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu  
 325 330 335

Pro Asn Ser

<210> 243  
 <211> 1665  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1642)  
 <223> RXA02737

<400> 243  
 agcagcgtgc atcagtaacg gcgacatgaa atcgaattag ttcgatctta tgtggccgtt 60

acacatcttt cattaaagaa aggatcgtga cactaccatc gtg agc aca aac acg 115  
 Val Ser Thr Asn Thr  
 1 5

acc ccc tcc agc tgg aca aac cca ctg cgc gac ccg cag gat aaa cga 163  
 Thr Pro Ser Ser Trp Thr Asn Pro Leu Arg Asp Pro Gln Asp Lys Arg  
 10 15 20

ctc ccc cgc atc gct ggc cct tcc ggc atg gtg atc ttc ggt gtc act 211  
 Leu Pro Arg Ile Ala Gly Pro Ser Gly Met Val Ile Phe Gly Val Thr  
 25 30 35

ggc gac ttg gct cga aag aag ctg ctc ccc gcc att tat gat cta gca 259  
 Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro Ala Ile Tyr Asp Leu Ala  
 40 45 50

aac cgc gga ttg ctg ccc cca gga ttc tcg ttg gta ggt tac ggc cgc 307  
 Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu Val Gly Tyr Gly Arg  
 55 60 65

cgc gaa tgg tcc aaa gaa gac ttt gaa aaa tac gta cgc gat gcc gca 355  
 Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr Val Arg Asp Ala Ala

70	75	80	85	
agt gct ggt gct cgt acg gaa ttc cgt gaa aat gtt tgg gag cgc ctc				403
Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn Val Trp Glu Arg Leu	90	95	100	
gcc gag ggt atg gaa ttt gtt cgc ggc aac ttt gat gat gat gca gct				451
Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe Asp Asp Ala Ala	105	110	115	
ttc gac aac ctc gct gca aca ctc aag cgc atc gac aaa acc cgc ggc				499
Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile Asp Lys Thr Arg Gly	120	125	130	
acc gcc ggc aac tgg gct tac tac ctg tcc att cca cca gat tcc ttc				547
Thr Ala Gly Asn Trp Ala Tyr Leu Ser Ile Pro Pro Asp Ser Phe	135	140	145	
aca gcg gtc tgc cac cag ctg gag cgt tcc ggc atg gct gaa tcc acc				595
Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly Met Ala Glu Ser Thr	150	155	160	165
gaa gaa gca tgg cgc cgc gtg atc atc gag aag cct ttc ggc cac aac				643
Glu Glu Ala Trp Arg Val Ile Ile Glu Lys Pro Phe Gly His Asn	170	175	180	
ctc gaa tcc gca cac gag ctc aac cag ctg gtc aac gca gtc ttc cca				691
Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val Asn Ala Val Phe Pro	185	190	195	
gaa tct tct gtg ttc cgc atc gac cac tat ttg ggc aag gaa aca gtt				739
Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu Gly Lys Glu Thr Val	200	205	210	
caa aac atc ctg gct ctg cgt ttt gct aac cag ctg ttt gag cca ctg				787
Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln Leu Phe Glu Pro Leu	215	220	225	
tgg aac tcc aac tac gtt gac cac gtc cag atc acc atg gct gaa gat				835
Trp Asn Ser Asn Tyr Val Asp His Val Gln Ile Thr Met Ala Glu Asp	230	235	240	245
att ggc ttg ggt gga cgt gct ggt tac tac gac ggc atc ggc gca gcc				883
Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp Gly Ile Gly Ala Ala	250	255	260	
cgc gac gtc atc cag aac cac ctg atc cag ctc ttg gct ctg gtt gcc				931
Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu Leu Ala Leu Val Ala	265	270	275	
atg gaa gaa cca att tct ttc gtg cca gcg cag ctg cag gca gaa aag				979
Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln Leu Gln Ala Glu Lys	280	285	290	
atc aag gtg ctc tct gcg aca aag ccg tgc tac cca ttg gat aaa acc				1027
Ile Lys Val Leu Ser Ala Thr Lys Pro Cys Tyr Pro Leu Asp Lys Thr	295	300	305	
tcc gct cgt ggt cag tac gct gcc ggt tgg cag ggc tct gag tta gtc				1075
Ser Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln Gly Ser Glu Leu Val	310	315	320	325

aag gga ctt cgc gaa gaa gat ggc ttc aac cct gag tcc acc act gag 1123  
Lys Gly Leu Arg Glu Glu Asp Gly Phe Asn Pro Glu Ser Thr Thr Glu  
330 335 340

act ttt gcg gct tgt acc tta gag atc acg tct cgt cgc tgg gct ggt 1171  
Thr Phe Ala Ala Cys Thr Leu Glu Ile Thr Ser Arg Arg Trp Ala Gly  
345 350 355

gtg ccg ttc tac ctg cgc acc ggt aag cgt ctt ggt cgc cgt gtt act 1219  
Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu Gly Arg Arg Val Thr  
360 365 370

gag att gcc gtg gtg ttt aaa gac gca cca cac cag cct ttc gac ggc 1267  
Glu Ile Ala Val Val Phe Lys Asp Ala Pro His Gln Pro Phe Asp Gly  
375 380 385

gac atg act gta tcc ctt ggc caa aac gcc atc gtg att cgc gtg cag 1315  
Asp Met Thr Val Ser Leu Gly Gln Asn Ala Ile Val Ile Arg Val Gln  
390 395 400 405

cct gat gaa ggt gtg ctc atc cgc ttc ggt tcc aag gtt cca ggt tct 1363  
Pro Asp Glu Gly Val Leu Ile Arg Phe Gly Ser Lys Val Pro Gly Ser  
410 415 420

gcc atg gaa gtc cgt gac gtc aac atg gac ttc tcc tac tca gaa tcc 1411  
Ala Met Glu Val Arg Asp Val Asn Met Asp Phe Ser Tyr Ser Glu Ser  
425 430 435

ttc act gaa gaa tca cct gaa gca tac gag cgc ctc att ttg gat gcg 1459  
Phe Thr Glu Glu Ser Pro Glu Ala Tyr Glu Arg Leu Ile Leu Asp Ala  
440 445 450

ctg tta gat gaa tcc agc ctc ttc cct acc aac gag gaa gtg gaa ctg 1507  
Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn Glu Glu Val Glu Leu  
455 460 465

agc tgg aag att ctg gat cca att ctt gaa gca tgg gat gcc gat gga 1555  
Ser Trp Lys Ile Leu Asp Pro Ile Leu Glu Ala Trp Asp Ala Asp Gly  
470 475 480 485

gaa cca gag gat tac cca gcg ggt acg tgg ggt cca aag agc gct gat 1603  
Glu Pro Glu Asp Tyr Pro Ala Gly Thr Trp Gly Pro Lys Ser Ala Asp  
490 495 500

gaa atg ctt tcc cgc aac ggt cac acc tgg cgc agg cca taatttaggg 1652  
Glu Met Leu Ser Arg Asn Gly His Thr Trp Arg Arg Pro  
505 510

gcaaaaaatg atc 1665

&lt;210&gt; 244

&lt;211&gt; 514

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 244

Val Ser Thr Asn Thr Thr Pro Ser Ser Trp Thr Asn Pro Leu Arg Asp  
1 5 10 15

Pro Gln Asp Lys Arg Leu Pro Arg Ile Ala Gly Pro Ser Gly Met Val  
                   20                  25                  30  
 Ile Phe Gly Val Thr Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro Ala  
                   35                  40                  45  
 Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu  
                   50                  55                  60  
 Val Gly Tyr Gly Arg Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr  
                   65                  70                  75                  80  
 Val Arg Asp Ala Ala Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn  
                   85                  90                  95  
 Val Trp Glu Arg Leu Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe  
                   100                  105                  110  
 Asp Asp Asp Ala Ala Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile  
                   115                  120                  125  
 Asp Lys Thr Arg Gly Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile  
                   130                  135                  140  
 Pro Pro Asp Ser Phe Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly  
                   145                  150                  155                  160  
 Met Ala Glu Ser Thr Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys  
                   165                  170                  175  
 Pro Phe Gly His Asn Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val  
                   180                  185                  190  
 Asn Ala Val Phe Pro Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu  
                   195                  200                  205  
 Gly Lys Glu Thr Val Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln  
                   210                  215                  220  
 Leu Phe Glu Pro Leu Trp Asn Ser Asn Tyr Val Asp His Val Gln Ile  
                   225                  230                  235                  240  
 Thr Met Ala Glu Asp Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp  
                   245                  250                  255  
 Gly Ile Gly Ala Ala Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu  
                   260                  265                  270  
 Leu Ala Leu Val Ala Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln  
                   275                  280                  285  
 Leu Gln Ala Glu Lys Ile Lys Val Leu Ser Ala Thr Lys Pro Cys Tyr  
                   290                  295                  300  
 Pro Leu Asp Lys Thr Ser Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln  
                   305                  310                  315                  320  
 Gly Ser Glu Leu Val Lys Gly Leu Arg Glu Glu Asp Gly Phe Asn Pro  
                   325                  330                  335  
 Glu Ser Thr Thr Glu Thr Phe Ala Ala Cys Thr Leu Glu Ile Thr Ser

340 345 350  
 Arg Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu  
 355 360 365  
 Gly Arg Arg Val Thr Glu Ile Ala Val Val Phe Lys Asp Ala Pro His  
 370 375 380  
 Gln Pro Phe Asp Gly Asp Met Thr Val Ser Leu Gly Gln Asn Ala Ile  
 385 390 395 400  
 Val Ile Arg Val Gln Pro Asp Glu Gly Val Leu Ile Arg Phe Gly Ser  
 405 410 415  
 Lys Val Pro Gly Ser Ala Met Glu Val Arg Asp Val Asn Met Asp Phe  
 420 425 430  
 Ser Tyr Ser Glu Ser Phe Thr Glu Glu Ser Pro Glu Ala Tyr Glu Arg  
 435 440 445  
 Leu Ile Leu Asp Ala Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn  
 450 455 460  
 Glu Glu Val Glu Leu Ser Trp Lys Ile Leu Asp Pro Ile Leu Glu Ala  
 465 470 475 480  
 Trp Asp Ala Asp Gly Glu Pro Glu Asp Tyr Pro Ala Gly Thr Trp Gly  
 485 490 495  
 Pro Lys Ser Ala Asp Glu Met Leu Ser Arg Asn Gly His Thr Trp Arg  
 500 505 510

Arg Pro

<210> 245  
 <211> 1203  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1180)  
 <223> RXA02738

<400> 245  
 ttgttgtaa tcggtacaaa gggctttaag cacatccctt acttgccctgc tctccttgag 60  
 cacagttcaa gaacaattct ttaaggaaa atttagtttc atg tct cac att gat 115  
 Met Ser His Ile Asp  
 1 5  
 gat ctt gca cag ctg ggc act tcc act tgg ctg gac gac ctg tcc cgc 163  
 Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu Asp Asp Leu Ser Arg  
 10 15 20  
 gag cgc att act tcc ggc aat ctg agc cag gtt att gag gaa aag tct 211  
 Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val Ile Glu Glu Lys Ser  
 25 30 35

gta gtc ggt gtc acc acc aac cca gct att ttc gca gca gca atg tcc	259
Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe Ala Ala Ala Met Ser	
40 45 50	
aag ggc gat tcc tac gac gct cag atc gca gag ctc aag gcc gct ggc	307
Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu Leu Lys Ala Ala Gly	
55 60 65	
gca tct gtt gac cag gct gtt tac gcc atg agc atc gac gac gtt cgc	355
Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser Ile Asp Asp Val Arg	
70 75 80 85	
aat gct tgt gat ctg ttc acc ggc atc ttc gag tcc tcc aac ggc tac	403
Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu Ser Ser Asn Gly Tyr	
90 95 100	
gac ggc cgc gtg tcc atc gag gtt gac cca cgt atc tct gct gac cgc	451
Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg Ile Ser Ala Asp Arg	
105 110 115	
gac gca acc ctg gct cag gcc aag gag ctg tgg gca aag gtt gat cgt	499
Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp Ala Lys Val Asp Arg	
120 125 130	
cca aac gtc atg atc aag atc cct gca acc cca ggt tct ttg cca gca	547
Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro Gly Ser Leu Pro Ala	
135 140 145	
atc acc gac gct ttg gct gag ggc atc agc gtt aac gtc acc ttg atc	595
Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val Asn Val Thr Leu Ile	
150 155 160 165	
ttc tcc gtt gct cgc tac cgc gag gtc atc gct gcg ttc atc gag ggc	643
Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala Ala Phe Ile Glu Gly	
170 175 180	
atc aag cag gct gct gca aac ggc cac gac gtc tcc aag atc cac tct	691
Ile Lys Gln Ala Ala Asn Gly His Asp Val Ser Lys Ile His Ser	
185 190 195	
gtg gct tcc ttc ttc gtc tcc cgc gtc gac gtt gag atc gac aag cgc	739
Val Ala Ser Phe Phe Val Ser Arg Val Asp Val Glu Ile Asp Lys Arg	
200 205 210	
ctc gag gca atc gga tcc gat gag gct ttg gct ctg cgc ggc aag gca	787
Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala Leu Arg Gly Lys Ala	
215 220 225	
ggc gtt gcc aac gct cag cgc gct tac gct gtg tac aag gag ctt ttc	835
Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val Tyr Lys Glu Leu Phe	
230 235 240 245	
gac gcc gcc gag ctg cct gaa ggt gcc aac act cag cgc cca ctg tgg	883
Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr Gln Arg Pro Leu Trp	
250 255 260	
gca tcc acc ggc gtg aag aac cct gcg tac gct gca act ctt tac gtt	931
Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala Ala Thr Leu Tyr Val	
265 270 275	
tcc gag ctg gct ggt cca aac acc gtc aac acc atg cca gaa ggc acc	979

Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr Met Pro Glu Gly Thr  
 280 285 290

atc gac gcg gtt ctg gag cag ggc aac ctg cac ggt gac acc ctg tcc 1027  
 Ile Asp Ala Val Leu Glu Gln Gly Asn Leu His Gly Asp Thr Leu Ser  
 295 300 305

aac tcc gcg gca gaa gct gac gct gtg ttc tcc cag ctt gag gct ctg 1075  
 Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser Gln Leu Glu Ala Leu  
 310 315 320 325

ggc gtt gac ttg gca gat gtc ttc cag gtc ctg gag acc gag ggt gtg 1123  
 Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu Glu Thr Glu Gly Val  
 330 335 340

gac aag ttc gtt gct tct tgg agc gaa ctg ctt gag tcc atg gaa gct 1171  
 Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu Glu Ser Met Glu Ala  
 345 350 355

cgc ctg aag tagaatcagc acgctgcac agt 1203  
 Arg Leu Lys  
 360

<210> 246  
 <211> 360  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 246  
 Met Ser His Ile Asp Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu  
 1 5 10 15

Asp Asp Leu Ser Arg Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val  
 20 25 30

Ile Glu Glu Lys Ser Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe  
 35 40 45

Ala Ala Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu  
 50 55 60

Leu Lys Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser  
 65 70 75 80

Ile Asp Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu  
 85 90 95

Ser Ser Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg  
 100 105 110

Ile Ser Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp  
 115 120 125

Ala Lys Val Asp Arg Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro  
 130 135 140

Gly Ser Leu Pro Ala Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val  
 145 150 155 160

Asn Val Thr Leu Ile Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala



```
<210> 247
<211> 2223
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(2200)  
<223> RXA02739
```

<400> 247  
cctttgccaa atttgaacca attaacctaa gtcgtagatc tgatcatcgg atctaacgaa 60

aacgaaccaa aactttggtc ccggtttaac ccaggaagga ttg acc acc ttg acg 115  
Leu Thr Thr Leu Thr  
1 5

ctg tca cct gaa ctt cag gcg ctc act gta cgc aat tac ccc tct gat 163  
Leu Ser Pro Glu Leu Gln Ala Leu Thr Val Arg Asn Tyr Pro Ser Asp  
10 15 20

tgg tcc gat gtg gac acc aag gct gta gac act gtt cgt gtc ctc gct 211

Trp	Ser	Asp	Val	Asp	Thr	Lys	Ala	Val	Asp	Thr	Val	Arg	Val	Leu	Ala	
			25					30					35			
gca	gac	gct	gta	gaa	aac	tgt	ggc	tcc	ggc	cac	cca	ggc	acc	gca	atg	259
Ala	Asp	Ala	Val	Glu	Asn	Cys	Gly	Ser	Gly	His	Pro	Gly	Thr	Ala	Met	
		40					45					50				
agc	ctg	gct	ccc	ctt	gca	tac	acc	ttg	tac	cag	cgg	gtt	atg	aac	gta	307
Ser	Leu	Ala	Pro	Leu	Ala	Tyr	Thr	Leu	Tyr	Gln	Arg	Val	Met	Asn	Val	
	55					60					65					
gat	cca	cag	gac	acc	aac	tgg	gca	ggc	cgt	gac	cgc	ttc	gtt	ctt	tct	355
Asp	Pro	Gln	Asp	Thr	Asn	Trp	Ala	Gly	Arg	Asp	Arg	Phe	Val	Leu	Ser	
70					75					80					85	
tgt	ggc	cac	tcc	tct	ttg	acc	cag	tac	atc	cag	ctt	tac	ttg	ggt	gga	403
Cys	Gly	His	Ser	Ser	Leu	Thr	Gln	Tyr	Ile	Gln	Leu	Tyr	Leu	Gly	Gly	
				90					95					100		
ttc	ggc	ctt	gag	atg	gat	gac	ctg	aag	gct	ctg	cgc	acc	tgg	gat	tcc	451
Phe	Gly	Leu	Glu	Met	Asp	Asp	Leu	Lys	Ala	Leu	Arg	Thr	Trp	Asp	Ser	
			105					110					115			
ttg	acc	cca	gga	cac	cct	gag	tac	cgc	cac	acc	aag	ggc	gtt	gag	atc	499
Leu	Thr	Pro	Gly	His	Pro	Glu	Tyr	Arg	His	Thr	Lys	Gly	Val	Glu	Ile	
		120					125					130				
acc	act	ggc	cct	ctt	ggc	cag	ggt	ctt	gca	tct	gca	gtt	ggt	atg	gcc	547
Thr	Thr	Gly	Pro	Leu	Gly	Gln	Gly	Leu	Ala	Ser	Ala	Val	Gly	Met	Ala	
		135				140					145					
atg	gct	gct	cgt	cgt	gag	cgt	ggc	cta	ttc	gac	cca	acc	gct	gct	gag	595
Met	Ala	Ala	Arg	Arg	Glu	Arg	Gly	Leu	Phe	Asp	Pro	Thr	Ala	Ala	Glu	
150					155					160					165	
ggc	gaa	tcc	cca	ttc	gac	cac	cac	atc	tac	gtc	att	gct	tct	gat	ggt	643
Gly	Glu	Ser	Pro	Phe	Asp	His	His	Ile	Tyr	Val	Ile	Ala	Ser	Asp	Gly	
				170					175					180		
gac	ctg	cag	gaa	ggt	gtc	acc	tct	gag	gca	tcc	tcc	atc	gct	ggc	acc	691
Asp	Leu	Gln	Glu	Gly	Val	Thr	Ser	Glu	Ala	Ser	Ser	Ile	Ala	Gly	Thr	
			185					190					195			
cag	cag	ctg	ggc	aac	ctc	atc	gtg	ttc	tgg	gat	gac	aac	cgc	atc	tcc	739
Gln	Gln	Leu	Gly	Asn	Leu	Ile	Val	Phe	Trp	Asp	Asp	Asn	Arg	Ile	Ser	
		200					205					210				
atc	gaa	gac	aac	act	gag	atc	gct	ttc	aac	gag	gac	gtt	gtt	gct	cgt	787
Ile	Glu	Asp	Asn	Thr	Glu	Ile	Ala	Phe	Asn	Glu	Asp	Val	Val	Ala	Arg	
	215					220					225					
tac	aag	gct	tac	ggc	tgg	cag	acc	att	gag	gtt	gag	gct	ggc	gag	gac	835
Tyr	Lys	Ala	Tyr	Gly	Trp	Gln	Thr	Ile	Glu	Val	Glu	Ala	Gly	Glu	Asp	
230					235					240				245		
gtt	gca	gca	atc	gaa	gct	gca	gtg	gct	gag	gct	aag	aag	gac	acc	aag	883
Val	Ala	Ala	Ile	Glu	Ala	Ala	Val	Ala	Glu	Ala	Lys	Lys	Asp	Thr	Lys	
				250					255					260		
cga	cct	acc	ttc	atc	cgc	gtt	cgc	acc	atc	atc	ggc	ttc	cca	gct	cca	931
Arg	Pro	Thr	Phe	Ile	Arg	Val	Arg	Thr	Ile	Ile	Gly	Phe	Pro	Ala	Pro	

265										270					275					
act	atg	atg	aac	acc	ggt	gct	gtg	cac	ggt	gct	gct	ctt	ggc	gca	gct	979				
Thr	Met	Met	Asn	Thr	Gly	Ala	Val	His	Gly	Ala	Ala	Leu	Gly	Ala	Ala					
280					285					290										
gag	gtt	gca	gca	acc	aag	act	gag	ctt	gga	ttc	gat	cct	gag	gct	cac	1027				
Glu	Val	Ala	Ala	Thr	Lys	Thr	Glu	Leu	Gly	Phe	Asp	Pro	Glu	Ala	His					
295					300					305										
ttc	gcg	atc	gac	gat	gag	gtt	atc	gct	cac	acc	cgc	tcc	ctc	gca	gag	1075				
Phe	Ala	Ile	Asp	Asp	Glu	Val	Ile	Ala	His	Thr	Arg	Ser	Leu	Ala	Glu					
310					315					320					325					
cgc	gct	gca	cag	aag	aag	gct	gca	tgg	cag	gtc	aag	ttc	gat	gag	tgg	1123				
Arg	Ala	Ala	Gln	Lys	Lys	Ala	Ala	Trp	Gln	Val	Lys	Phe	Asp	Glu	Trp					
330					335					340										
gca	gct	gcc	aac	cct	gag	aac	aag	gct	ctg	ttc	gat	cgc	ctg	aac	tcc	1171				
Ala	Ala	Ala	Asn	Pro	Glu	Asn	Lys	Ala	Leu	Phe	Asp	Arg	Leu	Asn	Ser					
345					350					355										
cgt	gag	ctt	cca	gcg	ggc	tac	gct	gac	gag	ctc	cca	aca	tgg	gat	gca	1219				
Arg	Glu	Leu	Pro	Ala	Gly	Tyr	Ala	Asp	Glu	Leu	Pro	Thr	Trp	Asp	Ala					
360					365					370										
gat	gag	aag	ggc	gtc	gca	act	cgt	aag	gct	tcc	gag	gct	gca	ctt	cag	1267				
Asp	Glu	Lys	Gly	Val	Ala	Thr	Arg	Lys	Ala	Ser	Glu	Ala	Ala	Leu	Gln					
375					380					385										
gca	ctg	ggc	aag	acc	ctt	cct	gag	ctg	tgg	ggc	ggt	tcc	gct	gac	ctc	1315				
Ala	Leu	Gly	Lys	Thr	Leu	Pro	Glu	Leu	Trp	Gly	Gly	Ser	Ala	Asp	Leu					
390					395					400					405					
gca	ggt	tcc	aac	aac	acc	gtg	atc	aag	ggc	tcc	cct	tcc	ttc	ggc	cct	1363				
Ala	Gly	Ser	Asn	Asn	Thr	Val	Ile	Lys	Gly	Ser	Pro	Ser	Phe	Gly	Pro					
410					415					420										
gag	tcc	atc	tcc	acc	gag	acc	tgg	tct	gct	gag	cct	tac	ggc	cgt	aac	1411				
Glu	Ser	Ile	Ser	Thr	Glu	Thr	Trp	Ser	Ala	Glu	Pro	Tyr	Gly	Arg	Asn					
425					430					435										
ctg	cac	ttc	ggt	atc	cgt	gag	cac	gct	atg	gga	tcc	atc	ctc	aac	ggc	1459				
Leu	His	Phe	Gly	Ile	Arg	Glu	His	Ala	Met	Gly	Ser	Ile	Leu	Asn	Gly					
440					445					450										
att	tcc	ctc	cac	ggt	ggc	acc	cgc	cca	tac	ggc	gga	acc	ttc	ctc	atc	1507				
Ile	Ser	Leu	His	Gly	Gly	Thr	Arg	Pro	Tyr	Gly	Gly	Thr	Phe	Leu	Ile					
455					460					465										
ttc	tcc	gac	tac	atg	cgt	cct	gca	gtt	cgt	ctt	gca	gct	ctc	atg	gag	1555				
Phe	Ser	Asp	Tyr	Met	Arg	Pro	Ala	Val	Arg	Leu	Ala	Ala	Leu	Met	Glu					
470					475					480					485					
acc	gac	gct	tac	tac	gtc	tgg	acc	cac	gac	tcc	atc	ggt	ctg	ggc	gaa	1603				
Thr	Asp	Ala	Tyr	Tyr	Val	Trp	Thr	His	Asp	Ser	Ile	Gly	Leu	Gly	Glu					
490					495					500										
gat	ggc	cca	acc	cac	cag	cct	gtt	gaa	acc	ttg	gct	gca	ctg	cgc	gcc	1651				
Asp	Gly	Pro	Thr	His	Gln	Pro	Val	Glu	Thr	Leu	Ala	Ala	Leu	Arg	Ala					
505					510					515										

atc cca ggt ctg tcc gtc ctg cgt cct gca gat gcg aac gag acc gcc 1699  
 Ile Pro Gly Leu Ser Val Leu Arg Pro Ala Asp Ala Asn Glu Thr Ala  
 520 525 530

cag gct tgg gct gca gca ctt gag tac aag gaa ggc cct aag ggt ctt 1747  
 Gln Ala Trp Ala Ala Ala Leu Glu Tyr Lys Glu Gly Pro Lys Gly Leu  
 535 540 545

gca ctg acc cgc cag aac gtt cct gtt ctg gaa ggc acc aag gag aag 1795  
 Ala Leu Thr Arg Gln Asn Val Pro Val Leu Glu Gly Thr Lys Glu Lys  
 550 555 560 565

gct gct gaa ggc gtt cgc cgc ggt ggc tac gtc ctg gtt gag ggt tcc 1843  
 Ala Ala Glu Gly Val Arg Arg Gly Gly Tyr Val Leu Val Glu Gly Ser  
 570 575 580

aag gaa acc cca gat gtg atc ctc atg ggc tcc ggc tcc gag gtt cag 1891  
 Lys Glu Thr Pro Asp Val Ile Leu Met Gly Ser Gly Ser Glu Val Gln  
 585 590 595

ctt gca gtt aac gct gcg aag gct ctg gaa gct gag ggc gtt gca gct 1939  
 Leu Ala Val Asn Ala Ala Lys Ala Leu Glu Ala Glu Gly Val Ala Ala  
 600 605 610

cgc gtt gtt tcc gtt cct tgc atg gat tgg ttc cag gag cag gac gca 1987  
 Arg Val Val Ser Val Pro Cys Met Asp Trp Phe Gln Glu Gln Asp Ala  
 615 620 625

gag tac atc gag tcc gtt ctg cct gca gct gtg acc gct cgt gtg tct 2035  
 Glu Tyr Ile Glu Ser Val Leu Pro Ala Ala Val Thr Ala Arg Val Ser  
 630 635 640 645

gtt gaa gct ggc atc gca atg cct tgg tac cgc ttc ttg ggc acc cag 2083  
 Val Glu Ala Gly Ile Ala Met Pro Trp Tyr Arg Phe Leu Gly Thr Gln  
 650 655 660

ggc cgt gct gtc tcc ctt gag cac ttc ggt gct tct gcg gat tac cag 2131  
 Gly Arg Ala Val Ser Leu Glu His Phe Gly Ala Ser Ala Asp Tyr Gln  
 665 670 675

acc ctg ttt gag aag ttc ggc atc acc acc gat gca gtc gtg gca gcg 2179  
 Thr Leu Phe Glu Lys Phe Gly Ile Thr Thr Asp Ala Val Val Ala Ala  
 680 685 690

gcc aag gac tcc att aac ggt taattgccct gctgttttta gct 2223  
 Ala Lys Asp Ser Ile Asn Gly  
 695 700

&lt;210&gt; 248

&lt;211&gt; 700

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 248

Leu Thr Thr Leu Thr Leu Ser Pro Glu Leu Gln Ala Leu Thr Val Arg  
 1 5 10 15

Asn Tyr Pro Ser Asp Trp Ser Asp Val Asp Thr Lys Ala Val Asp Thr  
 20 25 30

Val Arg Val Leu Ala Ala Asp Ala Val Glu Asn Cys Gly Ser Gly His  
 35 40 45  
 Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr Leu Tyr Gln  
 50 55 60  
 Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala Gly Arg Asp  
 65 70 75 80  
 Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln Tyr Ile Gln  
 85 90 95  
 Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu Lys Ala Leu  
 100 105 110  
 Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr Arg His Thr  
 115 120 125  
 Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly Leu Ala Ser  
 130 135 140  
 Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly Leu Phe Asp  
 145 150 155 160  
 Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His Ile Tyr Val  
 165 170 175  
 Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser Glu Ala Ser  
 180 185 190  
 Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val Phe Trp Asp  
 195 200 205  
 Asp Asn Arg Ile Ser Ile Glu Asp Asn Thr Glu Ile Ala Phe Asn Glu  
 210 215 220  
 Asp Val Val Ala Arg Tyr Lys Ala Tyr Gly Trp Gln Thr Ile Glu Val  
 225 230 235 240  
 Glu Ala Gly Glu Asp Val Ala Ala Ile Glu Ala Ala Val Ala Glu Ala  
 245 250 255  
 Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg Thr Ile Ile  
 260 265 270  
 Gly Phe Pro Ala Pro Thr Met Met Asn Thr Gly Ala Val His Gly Ala  
 275 280 285  
 Ala Leu Gly Ala Ala Glu Val Ala Ala Thr Lys Thr Glu Leu Gly Phe  
 290 295 300  
 Asp Pro Glu Ala His Phe Ala Ile Asp Asp Glu Val Ile Ala His Thr  
 305 310 315 320  
 Arg Ser Leu Ala Glu Arg Ala Ala Gln Lys Lys Ala Ala Trp Gln Val  
 325 330 335  
 Lys Phe Asp Glu Trp Ala Ala Ala Asn Pro Glu Asn Lys Ala Leu Phe  
 340 345 350

Asp Arg Leu Asn Ser Arg Glu Leu Pro Ala Gly Tyr Ala Asp Glu Leu  
 355 360 365  
 Pro Thr Trp Asp Ala Asp Glu Lys Gly Val Ala Thr Arg Lys Ala Ser  
 370 375 380  
 Glu Ala Ala Leu Gln Ala Leu Gly Lys Thr Leu Pro Glu Leu Trp Gly  
 385 390 395 400  
 Gly Ser Ala Asp Leu Ala Gly Ser Asn Asn Thr Val Ile Lys Gly Ser  
 405 410 415  
 Pro Ser Phe Gly Pro Glu Ser Ile Ser Thr Glu Thr Trp Ser Ala Glu  
 420 425 430  
 Pro Tyr Gly Arg Asn Leu His Phe Gly Ile Arg Glu His Ala Met Gly  
 435 440 445  
 Ser Ile Leu Asn Gly Ile Ser Leu His Gly Gly Thr Arg Pro Tyr Gly  
 450 455 460  
 Gly Thr Phe Leu Ile Phe Ser Asp Tyr Met Arg Pro Ala Val Arg Leu  
 465 470 475 480  
 Ala Ala Leu Met Glu Thr Asp Ala Tyr Tyr Val Trp Thr His Asp Ser  
 485 490 495  
 Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Thr Leu  
 500 505 510  
 Ala Ala Leu Arg Ala Ile Pro Gly Leu Ser Val Leu Arg Pro Ala Asp  
 515 520 525  
 Ala Asn Glu Thr Ala Gln Ala Trp Ala Ala Ala Leu Glu Tyr Lys Glu  
 530 535 540  
 Gly Pro Lys Gly Leu Ala Leu Thr Arg Gln Asn Val Pro Val Leu Glu  
 545 550 555 560  
 Gly Thr Lys Glu Lys Ala Ala Glu Gly Val Arg Arg Gly Gly Tyr Val  
 565 570 575  
 Leu Val Glu Gly Ser Lys Glu Thr Pro Asp Val Ile Leu Met Gly Ser  
 580 585 590  
 Gly Ser Glu Val Gln Leu Ala Val Asn Ala Ala Lys Ala Leu Glu Ala  
 595 600 605  
 Glu Gly Val Ala Ala Arg Val Val Ser Val Pro Cys Met Asp Trp Phe  
 610 615 620  
 Gln Glu Gln Asp Ala Glu Tyr Ile Glu Ser Val Leu Pro Ala Ala Val  
 625 630 635 640  
 Thr Ala Arg Val Ser Val Glu Ala Gly Ile Ala Met Pro Trp Tyr Arg  
 645 650 655  
 Phe Leu Gly Thr Gln Gly Arg Ala Val Ser Leu Glu His Phe Gly Ala  
 660 665 670  
 Ser Ala Asp Tyr Gln Thr Leu Phe Glu Lys Phe Gly Ile Thr Thr Asp

675	680	685
Ala Val Val Ala Ala Ala Lys Asp Ser Ile Asn Gly		
690	695	700
<p>&lt;210&gt; 249            &lt;211&gt; 793            &lt;212&gt; DNA            &lt;213&gt; Corynebacterium glutamicum</p> <p>&lt;220&gt;            &lt;221&gt; CDS            &lt;222&gt; (48)..(770)            &lt;223&gt; RXA00965</p> <p>&lt;400&gt; 249</p>		
agattgcggg cctcggcttc attgaaaaca agacggtgtt tgaataaatg aca act		56
	Met Thr Thr	
	1	
ttc cac gat ctt ccg ctg gag gag cgg ctg aca ctg gcc agg ttg ggc		104
Phe His Asp Leu Pro Leu Glu Glu Arg Leu Thr Leu Ala Arg Leu Gly		
5 10 15		
aca tcc cac tac tcc cgt cag ctc tcc ctc gtg gac aac gct gag ttc		152
Thr Ser His Tyr Ser Arg Gln Leu Ser Leu Val Asp Asn Ala Glu Phe		
20 25 30 35		
ggc gag cat tcc ctg cta gaa ggg tgg act cgt tcc cac ctc att gcc		200
Gly Glu His Ser Leu Leu Glu Gly Trp Thr Arg Ser His Leu Ile Ala		
40 45 50		
cac gtg gca tac aac gcc atc gca ctg tgc aac ctc atg cac tgg gca		248
His Val Ala Tyr Asn Ala Ile Ala Leu Cys Asn Leu Met His Trp Ala		
55 60 65		
aat act ggt gag gaa acc cca atg tac gtg tgc cca gaa gcg cgc aac		296
Asn Thr Gly Glu Glu Thr Pro Met Tyr Val Ser Pro Glu Ala Arg Asn		
70 75 80		
gag gaa att gcc tac ggt tcc acg ctc aat ccc gat gcg ttg cgt aac		344
Glu Glu Ile Ala Tyr Gly Ser Thr Leu Asn Pro Asp Ala Leu Arg Asn		
85 90 95		
ctg cat gaa cac tcc gtc gca cgc ctg gac gtg gct tgg cgt gaa acg		392
Leu His Glu His Ser Val Ala Arg Leu Asp Val Ala Trp Arg Glu Thr		
100 105 110 115		
tct gaa gat gct tgg tca cac gag gtt ctg aca gct cag gga cgc act		440
Ser Glu Asp Ala Trp Ser His Glu Val Leu Thr Ala Gln Gly Arg Thr		
120 125 130		
gtc cca gct agt gaa aca ttg tgg atg cgt tcc cgc gaa gtc tgg atc		488
Val Pro Ala Ser Glu Thr Leu Trp Met Arg Ser Arg Glu Val Trp Ile		
135 140 145		
cac gca gtt gac ctc ggt gca gtg gca acc ttt ggc gac atc cca gag		536
His Ala Val Asp Leu Gly Ala Val Ala Thr Phe Gly Asp Ile Pro Glu		
150 155 160		

gtc atc ctg cgc acc tta gct gca gaa atc aca caa aag tgg aca agc 584  
 Val Ile Leu Arg Thr Leu Ala Ala Glu Ile Thr Gln Lys Trp Thr Ser  
 165 170 175  
  
 caa gga gcc ggc gag gga ctt gtg ctt ctc gac gag ccc tcc agc act 632  
 Gln Gly Ala Gly Glu Gly Leu Val Leu Leu Asp Glu Pro Ser Ser Thr  
 180 185 190 195  
  
 cgc tac ccc gcc gcc cca ggg cag gac gag gta gta gtg tcc ggt agc 680  
 Arg Tyr Pro Ala Ala Pro Gly Gln Asp Glu Val Val Val Ser Gly Ser  
 200 205 210  
  
 ctt gca ggc att gtt cgc tac gcc gct ggc cgc ggt tcc gat gga gtc 728  
 Leu Ala Gly Ile Val Arg Tyr Ala Ala Gly Arg Gly Ser Asp Gly Val  
 215 220 225  
  
 act tct tcc act gga gag gtt cca gag cca ccg cgc tgg ctg 770  
 Thr Ser Ser Thr Gly Glu Val Pro Glu Pro Pro Arg Trp Leu  
 230 235 240  
  
 tagtttccac acattcttaa atg 793

&lt;210&gt; 250

&lt;211&gt; 241

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 250

Met Thr Thr Phe His Asp Leu Pro Leu Glu Glu Arg Leu Thr Leu Ala  
 1 5 10 15  
  
 Arg Leu Gly Thr Ser His Tyr Ser Arg Gln Leu Ser Leu Val Asp Asn  
 20 25 30  
  
 Ala Glu Phe Gly Glu His Ser Leu Leu Glu Gly Trp Thr Arg Ser His  
 35 40 45  
  
 Leu Ile Ala His Val Ala Tyr Asn Ala Ile Ala Leu Cys Asn Leu Met  
 50 55 60  
  
 His Trp Ala Asn Thr Gly Glu Glu Thr Pro Met Tyr Val Ser Pro Glu  
 65 70 75 80  
  
 Ala Arg Asn Glu Glu Ile Ala Tyr Gly Ser Thr Leu Asn Pro Asp Ala  
 85 90 95  
  
 Leu Arg Asn Leu His Glu His Ser Val Ala Arg Leu Asp Val Ala Trp  
 100 105 110  
  
 Arg Glu Thr Ser Glu Asp Ala Trp Ser His Glu Val Leu Thr Ala Gln  
 115 120 125  
  
 Gly Arg Thr Val Pro Ala Ser Glu Thr Leu Trp Met Arg Ser Arg Glu  
 130 135 140  
  
 Val Trp Ile His Ala Val Asp Leu Gly Ala Val Ala Thr Phe Gly Asp  
 145 150 155 160  
  
 Ile Pro Glu Val Ile Leu Arg Thr Leu Ala Ala Glu Ile Thr Gln Lys  
 165 170 175



Trp Thr Ser Gln Gly Ala Gly Glu Gly Leu Val Leu Leu Asp Glu Pro  
 180 185 190  
 Ser Ser Thr Arg Tyr Pro Ala Ala Pro Gly Gln Asp Glu Val Val Val  
 195 200 205  
 Ser Gly Ser Leu Ala Gly Ile Val Arg Tyr Ala Ala Gly Arg Gly Ser  
 210 215 220  
 Asp Gly Val Thr Ser Ser Thr Gly Glu Val Pro Glu Pro Pro Arg Trp  
 225 230 235 240  
 Leu

<210> 251  
 <211> 1575  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1552)  
 <223> RXN00999

<400> 251  
 cctcctgtga cctggtaaaa tcgccactac ccccaaatgg tcacaccttt taggccgatt 60  
 ttgctgacac cgggctatgc cgtcaagtac gatcaataac atg act aat gga gat 115  
 Met Thr Asn Gly Asp  
 1 5  
 aat ctc gca cag atc ggc gtt gta ggc cta gca gta atg ggc tca aac 163  
 Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala Val Met Gly Ser Asn  
 10 15 20  
 ctc gcc cgc aac ttc gcc cgc aac ggc aac act gtc gct gtc tac aac 211  
 Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr Val Ala Val Tyr Asn  
 25 30 35  
 cgc agc act gac aaa acc gac aag ctc atc gcc gat cac ggc tcc gaa 259  
 Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala Asp His Gly Ser Glu  
 40 45 50  
 ggc aac ttc atc cct tct gca acc gtc gaa gag ttc gta gca tcc ctg 307  
 Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu Phe Val Ala Ser Leu  
 55 60 65  
 gaa aag cca cgc cgc gcc atc atc atg gtt cag gct ggt aac gcc acc 355  
 Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln Ala Gly Asn Ala Thr  
 70 75 80 85  
 gac gca gtc atc aac cag ctg gca gat gcc atg gac gaa ggc gac atc 403  
 Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met Asp Glu Gly Asp Ile  
 90 95 100  
 atc atc gac ggc ggc aac gcc ctc tac acc gac acc att cgt cgc gag 451  
 Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp Thr Ile Arg Arg Glu  
 105 110 115

aag gaa atc tcc gca cgc ggt ctc cac ttc gtc ggt gct ggt atc tcc	499
Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val Gly Ala Gly Ile Ser	
120 125 130	
ggc ggc gaa gaa ggc gca ctc aac ggc cca tcc atc atg cct ggt ggc	547
Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser Ile Met Pro Gly Gly	
135 140 145	
cca gca aag tcc tac gag tcc ctc gga cca ctg ctt gag tcc atc gct	595
Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu Leu Glu Ser Ile Ala	
150 155 160 165	
gcc aac gtt gac ggc acc cca tgt gtc acc cac atc ggc cca gac ggc	643
Ala Asn Val Asp Thr Pro Cys Val Thr His Ile Gly Pro Asp Gly	
170 175 180	
gcc ggc cac ttc gtc aag atg gtc cac aac ggc atc gag tac gcc gac	691
Ala Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp	
185 190 195	
atg cag gtc atc ggc gag gca tac cac ctt ctc cgc tac gca gca ggc	739
Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu Arg Tyr Ala Ala Gly	
200 205 210	
atg cag cca gct gaa atc gct gag gtt ttc aag gaa tgg aac gca ggc	787
Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys Glu Trp Asn Ala Gly	
215 220 225	
gac ctg gat tcc tac ctc atc gaa atc acc gca gag gtt ctc tcc cag	835
Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Glu Val Leu Ser Gln	
230 235 240 245	
gtg gat gct gaa acc ggc aag cca cta atc gac gtc atc gtt gac gct	883
Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp Val Ile Val Asp Ala	
250 255 260	
gca ggt cag aag ggc acc gga cgt tgg acc gtc aag gct gct ctt gat	931
Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val Lys Ala Ala Leu Asp	
265 270 275	
ctg ggt att gct acc acc ggc atc ggc gaa gct gtt ttc gca cgt gca	979
Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala Val Phe Ala Arg Ala	
280 285 290	
ctc tcc ggc gca acc agc cag cgc gct gca gca cag ggc aac cta cct	1027
Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala Gln Gly Asn Leu Pro	
295 300 305	
gca ggt gtc ctc acc gat ctg gaa gca ctt ggc gtg gac aag gca cag	1075
Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly Val Asp Lys Ala Gln	
310 315 320 325	
ttc gtc gaa gac gtt cgc cgt gca ctg tac gca tcc aag ctt gtt gct	1123
Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala Ser Lys Leu Val Ala	
330 335 340	
tac gca cag ggc ttc gac gag atc aag gct ggc tcc gac gag aac aac	1171
Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly Ser Asp Glu Asn Asn	
345 350 355	

tgg gac gtt gac cct cgc gac ctc gct acc atc tgg cgc ggc ggc tgc 1219  
 Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile Trp Arg Gly Gly Cys  
 360 365 370  
  
 atc att cgc gct aag ttc ctc aac cgc atc gtc gaa gca tac gat gca 1267  
 Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val Glu Ala Tyr Asp Ala  
 375 380 385  
  
 aac gct gaa ctt gag tcc ctg ctg ctc gat cct tac ttc aag agc gag 1315  
 Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro Tyr Phe Lys Ser Glu  
 390 395 400 405  
  
 ctc ggc gac ctc atc gat tca tgg cgt cgc gtg att gtc acc gcc acc 1363  
 Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val Ile Val Thr Ala Thr  
 410 415 420  
  
 cag ctt ggc ctg cca atc cca gtg ttc gct tcc tcc ctg tcc tac tac 1411  
 Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser Ser Leu Ser Tyr Tyr  
 425 430 435  
  
 gac agc ctg cgt gca gag cgt ctg cca gca gcc ctg atc caa gga cag 1459  
 Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala Leu Ile Gln Gly Gln  
 440 445 450  
  
 cgc gac ttc ttc ggt gcg cac acc tac aag cgc atc gac aag gat ggc 1507  
 Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg Ile Asp Lys Asp Gly  
 455 460 465  
  
 tcc ttc cac acc gag tgg tcc ggc gac cgc tcc gag gtt gaa gct 1552  
 Ser Phe His Thr Glu Trp Ser Gly Asp Arg Ser Glu Val Glu Ala  
 470 475 480  
  
 taaaggctct ccttttaaca caa 1575

&lt;210&gt; 252

&lt;211&gt; 484

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 252

Met Thr Asn Gly Asp Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala  
 1 5 10 15

Val Met Gly Ser Asn Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr  
 20 25 30

Val Ala Val Tyr Asn Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala  
 35 40 45

Asp His Gly Ser Glu Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu  
 50 55 60

Phe Val Ala Ser Leu Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln  
 65 70 75 80

Ala Gly Asn Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met  
 85 90 95

Asp Glu Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp  
 100 105 110

Thr Ile Arg Arg Glu Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val  
 115 120 125  
 Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser  
 130 135 140  
 Ile Met Pro Gly Gly Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu  
 145 150 155 160  
 Leu Glu Ser Ile Ala Ala Asn Val Asp Gly Thr Pro Cys Val Thr His  
 165 170 175  
 Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly  
 180 185 190  
 Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu  
 195 200 205  
 Arg Tyr Ala Ala Gly Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys  
 210 215 220  
 Glu Trp Asn Ala Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala  
 225 230 235 240  
 Glu Val Leu Ser Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp  
 245 250 255  
 Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val  
 260 265 270  
 Lys Ala Ala Leu Asp Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala  
 275 280 285  
 Val Phe Ala Arg Ala Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala  
 290 295 300  
 Gln Gly Asn Leu Pro Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly  
 305 310 315 320  
 Val Asp Lys Ala Gln Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala  
 325 330 335  
 Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly  
 340 345 350  
 Ser Asp Glu Asn Asn Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile  
 355 360 365  
 Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val  
 370 375 380  
 Glu Ala Tyr Asp Ala Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro  
 385 390 395 400  
 Tyr Phe Lys Ser Glu Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val  
 405 410 415  
 Ile Val Thr Ala Thr Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser  
 420 425 430

Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala  
 435 440 445

Leu Ile Gln Gly Gln Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg  
 450 455 460

Ile Asp Lys Asp Gly Ser Phe His Thr Glu Trp Ser Gly Asp Arg Ser  
 465 470 475 480

Glu Val Glu Ala

<210> 253  
 <211> 1537  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1537)  
 <223> FRXA00999

<400> 253  
 cctcctgtga cctggtaaaa tcgccactac ccccaaattgg tcacaccttt taggccgatt 60

ttgctgacac cgggctatgc cgtcaagtac gatcaataac atg act aat gga gat 115  
 Met Thr Asn Gly Asp  
 1 5

aat ctc gca cag atc ggc gtt gta ggc cta gca gta atg ggc tca aac 163  
 Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala Val Met Gly Ser Asn  
 10 15 20

ctc gcc cgc aac ttc gcc cgc aac ggc aac act gtc gct gtc tac aac 211  
 Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr Val Ala Val Tyr Asn  
 25 30 35

cgc agc act gac aaa acc gac aag ctc atc gcc gat cac ggc tcc gaa 259  
 Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala Asp His Gly Ser Glu  
 40 45 50

ggc aac ttc atc cct tct gca acc gtc gaa gag ttc gta gca tcc ctg 307  
 Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu Phe Val Ala Ser Leu  
 55 60 65

gaa aag cca cgc cgc gcc atc atc atg gtt cag gct ggt aac gcc acc 355  
 Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln Ala Gly Asn Ala Thr  
 70 75 80 85

gac gca gtc atc aac cag ctg gca gat gcc atg gac gaa ggc gac atc 403  
 Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met Asp Glu Gly Asp Ile  
 90 95 100

atc atc gac ggc ggc aac gcc ctc tac acc gac acc att cgt cgc gag 451  
 Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp Thr Ile Arg Arg Glu  
 105 110 115

aag gaa atc tcc gca cgc ggt ctc cac ttc gtc ggt gct ggt atc tcc 499  
 Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val Gly Ala Gly Ile Ser  
 120 125 130

ggc ggc gaa gaa ggc gca ctc aac ggc cca tcc atc atg cct ggt ggc Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser Ile Met Pro Gly Gly 135 140 145	547
cca gca aag tcc tac gag tcc ctc gga cca ctg ctt gag tcc atc gct Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu Leu Glu Ser Ile Ala 150 155 160 165	595
gcc aac gtt gac ggc acc cca tgt gtc acc cac atc ggc cca gac ggc Ala Asn Val Asp Gly Thr Pro Cys Val Thr His Ile Gly Pro Asp Gly 170 175 180	643
gcc ggc cac ttc gtc aag atg gtc cac aac ggc atc gag tac gcc gac Ala Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp 185 190 195	691
atg cag gtc atc ggc gag gca tac cac ctt ctc cgc tac gca gca ggc Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu Arg Tyr Ala Ala Gly 200 205 210	739
atg cag cca gct gaa atc gct gag gtt ttc aag gaa tgg aac gca ggc Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys Glu Trp Asn Ala Gly 215 220 225	787
gac ctg gat tcc tac ctc atc gaa atc acc gca gag gtt ctc tcc cag Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Glu Val Leu Ser Gln 230 235 240 245	835
gtg gat gct gaa acc ggc aag cca cta atc gac gtc atc gtt gac gct Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp Val Ile Val Asp Ala 250 255 260	883
gca ggt cag aag ggc acc gga cgt tgg acc gtc aag gct gct ctt gat Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val Lys Ala Ala Leu Asp 265 270 275	931
ctg ggt att gct acc acc ggc atc ggc gaa gct gtt ttc gca cgt gca Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala Val Phe Ala Arg Ala 280 285 290	979
ctc tcc ggc gca acc agc cag cgc gct gca gca cag ggc aac cta cct Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala Gln Gly Asn Leu Pro 295 300 305	1027
gca ggt gtc ctc acc gat ctg gaa gca ctt ggc gtg gac aag gca cag Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly Val Asp Lys Ala Gln 310 315 320 325	1075
ttc gtc gaa gac gtt cgc cgt gca ctg tac gca tcc aag ctt gtt gct Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala Ser Lys Leu Val Ala 330 335 340	1123
tac gca cag ggc ttc gac gag atc aag gct ggc tcc gac gag aac aac Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly Ser Asp Glu Asn Asn 345 350 355	1171
tgg gac gtt gac cct cgc gac ctc gct acc atc tgg cgc ggc ggc tgc Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile Trp Arg Gly Gly Cys 360 365 370	1219

atc att cgc gct aag ttc ctc aac cgc atc gtc gaa gca tac gat gca 1267  
 Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val Glu Ala Tyr Asp Ala  
 375 380 385  
  
 aac gct gaa ctt gag tcc ctg ctg ctc gat cct tac ttc aag agc gag 1315  
 Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro Tyr Phe Lys Ser Glu  
 390 395 400 405  
  
 ctc ggc gac ctc atc gat tca tgg cgt cgc gtg att gtc acc gcc acc 1363  
 Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val Ile Val Thr Ala Thr  
 410 415 420  
  
 cag ctt ggc ctg cca atc cca gtg ttc gct tcc tcc ctg tcc tac tac 1411  
 Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser Ser Leu Ser Tyr Tyr  
 425 430 435  
  
 gac agc ctg cgt gca gag cgt ctg cca gca gcc ctg atc caa gga cag 1459  
 Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala Leu Ile Gln Gly Gln  
 440 445 450  
  
 cgc gac ttc ttc ggt gcg cac acc tac aag cgc atc gac aag gat ggc 1507  
 Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg Ile Asp Lys Asp Gly  
 455 460 465  
  
 tcc ttc cac acc gag tgg tcc ggc gac cgc 1537  
 Ser Phe His Thr Glu Trp Ser Gly Asp Arg  
 470 475

&lt;210&gt; 254

&lt;211&gt; 479

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 254

Met Thr Asn Gly Asp Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala  
 1 5 10 15  
  
 Val Met Gly Ser Asn Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr  
 20 25 30  
  
 Val Ala Val Tyr Asn Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala  
 35 40 45  
  
 Asp His Gly Ser Glu Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu  
 50 55 60  
  
 Phe Val Ala Ser Leu Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln  
 65 70 75 80  
  
 Ala Gly Asn Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met  
 85 90 95  
  
 Asp Glu Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp  
 100 105 110  
  
 Thr Ile Arg Arg Glu Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val  
 115 120 125  
  
 Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser  
 130 135 140

Ile Met Pro Gly Gly Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu  
 145 150 155 160  
 Leu Glu Ser Ile Ala Ala Asn Val Asp Gly Thr Pro Cys Val Thr His  
 165 170 175  
 Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly  
 180 185 190  
 Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu  
 195 200 205  
 Arg Tyr Ala Ala Gly Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys  
 210 215 220  
 Glu Trp Asn Ala Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala  
 225 230 235 240  
 Glu Val Leu Ser Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp  
 245 250 255  
 Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val  
 260 265 270  
 Lys Ala Ala Leu Asp Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala  
 275 280 285  
 Val Phe Ala Arg Ala Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala  
 290 295 300  
 Gln Gly Asn Leu Pro Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly  
 305 310 315 320  
 Val Asp Lys Ala Gln Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala  
 325 330 335  
 Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly  
 340 345 350  
 Ser Asp Glu Asn Asn Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile  
 355 360 365  
 Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val  
 370 375 380  
 Glu Ala Tyr Asp Ala Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro  
 385 390 395 400  
 Tyr Phe Lys Ser Glu Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val  
 405 410 415  
 Ile Val Thr Ala Thr Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser  
 420 425 430  
 Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala  
 435 440 445  
 Leu Ile Gln Gly Gln Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg  
 450 455 460



Ile Asp Lys Asp Gly Ser Phe His Thr Glu Trp Ser Gly Asp Arg  
 465 470 475

<210> 255  
 <211> 1326  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1303)  
 <223> RXN02596

<400> 255  
 aaggatatctg ggtgtggata tgccctgcta actggagaaa cttggcccga tcgggtgtct 60  
 gaaatttcgg caacgccgaa tgtaagttag tgtcgaatgc atg acg gaa tcg aaa 115  
 Met Thr Glu Ser Lys  
 1 5  
 aat tac gac tta atc gtt gta ggc tcc ggc ctc ttc ggg ctc acc gtg 163  
 Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu Phe Gly Leu Thr Val  
 10 15 20  
 gct gag cgt gca gct agc cag ctg ggt aag aaa gtc ctc atc gtt gaa 211  
 Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys Val Leu Ile Val Glu  
 25 30 35  
 cgc cgc tcg cac ctc ggt ggc aat gct tac tct gaa gca gaa cca gag 259  
 Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser Glu Ala Glu Pro Glu  
 40 45 50  
 acc ggc att gaa atc cac aaa tac ggc gcg cac ctc ttc cac acc tcc 307  
 Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His Leu Phe His Thr Ser  
 55 60 65  
 aac aca cgc gtg tgg gaa tac gtc aac cag ttc acc agt ttc acc ggc 355  
 Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe Thr Ser Phe Thr Gly  
 70 75 80 85  
 tac cag cac cgc gtc ttc gca atg cac aac ggc acc gcc tac caa ttc 403  
 Tyr Gln His Arg Val Phe Ala Met His Asn Gly Thr Ala Tyr Gln Phe  
 90 95 100  
 ccc atg gga ctg ggc ctg att aac cag ttc ttc ggc aag tac tac agc 451  
 Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe Gly Lys Tyr Tyr Ser  
 105 110 115  
 cca gat gaa gcc cgt gag ctc atc aag gaa cag tct gca gaa atc gat 499  
 Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln Ser Ala Glu Ile Asp  
 120 125 130  
 tcc tcc gac gcc acc aac ctc gaa gaa aag gcc att tcc ctc att ggt 547  
 Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala Ile Ser Leu Ile Gly  
 135 140 145  
 cgc cca ctt tac gag gca ttc atc cgc gac tac acc gca aag cag tgg 595  
 Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr Thr Ala Lys Gln Trp  
 150 155 160 165

cag act gat cca aag aac ctc cca gcc ggc aac atc acc cgc ctg cca Gln Thr Asp Pro Lys Asn Leu Pro Ala Gly Asn Ile Thr Arg Leu Pro 170 175 180	643
gtt cgc tac aac ttc aac aac cgc tat ttc aac gac acc tac gaa ggc Val Arg Tyr Asn Phe Asn Asn Arg Tyr Phe Asn Asp Thr Tyr Glu Gly 185 190 195	691
ctt ccc aca gac ggc tac gcg gca tgg ttg gaa aag atg gca gag cat Leu Pro Thr Asp Gly Tyr Ala Trp Leu Glu Lys Met Ala Glu His 200 205 210	739
gag ctt atc gac gtc cgc ctc gac acc gac tgg ttc gac gtt cgc gat Glu Leu Ile Asp Val Arg Leu Asp Thr Asp Trp Phe Asp Val Arg Asp 215 220 225	787
gac ctc cgc gca agc aac ccc gac gca cct gtg gtc tac acc ggc cca Asp Leu Arg Ala Ser Asn Pro Asp Ala Pro Val Val Tyr Thr Gly Pro 230 235 240 245	835
ctc gac ctc tac ttc aac tac gca gag ggc aag ctg gga tgg cgc acc Leu Asp Leu Tyr Phe Asn Tyr Ala Glu Gly Lys Leu Gly Trp Arg Thr 250 255 260	883
ctc gac ttt gaa acc gaa gta gta gaa acc ggt gac ttc caa gga acc Leu Asp Phe Glu Thr Glu Val Val Glu Thr Gly Asp Phe Gln Gly Thr 265 270 275	931
cca gtg atg aac tac aac gat gcg gac gta cct ttc acc cgc atc cac Pro Val Met Asn Tyr Asn Asp Ala Asp Val Pro Phe Thr Arg Ile His 280 285 290	979
gag ttc cgt cac ttc cac cca gag cgt gat gac agt tac ccc aag gat Glu Phe Arg His Phe His Pro Glu Arg Asp Asp Ser Tyr Pro Lys Asp 295 300 305	1027
aag acc gtc atc atg cgc gag ttc tcc cgt ttc gca gat aac gag gat Lys Thr Val Ile Met Arg Glu Phe Ser Arg Phe Ala Asp Asn Glu Asp 310 315 320 325	1075
gag cct tat tac cca atc aac act cca gac gac cga gac atg ctg aag Glu Pro Tyr Tyr Pro Ile Asn Thr Pro Asp Asp Arg Asp Met Leu Lys 330 335 340	1123
cag tac cgc ctt ctg gct gct gaa gag gct gct aat aat aag gtg ctg Gln Tyr Arg Leu Leu Ala Ala Glu Glu Ala Ala Asn Asn Lys Val Leu 345 350 355	1171
ttc ggc ggt cga ctg ggc acg tac cag tac ctc gac atg cac atg gct Phe Gly Gly Arg Leu Gly Thr Tyr Gln Tyr Leu Asp Met His Met Ala 360 365 370	1219
atc ggt tct gcg ctg agc atg ttt gac aac aag ctg gtg ccg ttc ttt Ile Gly Ser Ala Leu Ser Met Phe Asp Asn Lys Leu Val Pro Phe Phe 375 380 385	1267
gaa gaa ggc aca ccg cta gag cag gaa cgc gga cac taaaaggaag Glu Glu Gly Thr Pro Leu Glu Gln Glu Arg Gly His 390 395 400	1313
ggcatctccc aca	1326

&lt;210&gt; 256

&lt;211&gt; 401

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 256

Met Thr Glu Ser Lys Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu  
 1 5 10 15

Phe Gly Leu Thr Val Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys  
 20 25 30

Val Leu Ile Val Glu Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser  
 35 40 45

Glu Ala Glu Pro Glu Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His  
 50 55 60

Leu Phe His Thr Ser Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe  
 65 70 75 80

Thr Ser Phe Thr Gly Tyr Gln His Arg Val Phe Ala Met His Asn Gly  
 85 90 95

Thr Ala Tyr Gln Phe Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe  
 100 105 110

Gly Lys Tyr Tyr Ser Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln  
 115 120 125

Ser Ala Glu Ile Asp Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala  
 130 135 140

Ile Ser Leu Ile Gly Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr  
 145 150 155 160

Thr Ala Lys Gln Trp Gln Thr Asp Pro Lys Asn Leu Pro Ala Gly Asn  
 165 170 175

Ile Thr Arg Leu Pro Val Arg Tyr Asn Phe Asn Asn Arg Tyr Phe Asn  
 180 185 190

Asp Thr Tyr Glu Gly Leu Pro Thr Asp Gly Tyr Ala Ala Trp Leu Glu  
 195 200 205

Lys Met Ala Glu His Glu Leu Ile Asp Val Arg Leu Asp Thr Asp Trp  
 210 215 220

Phe Asp Val Arg Asp Asp Leu Arg Ala Ser Asn Pro Asp Ala Pro Val  
 225 230 235 240

Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu Gly Lys  
 245 250 255

Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu Thr Gly  
 260 265 270

Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp Val Pro  
 275 280 285

Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg Asp Asp  
 290 295 300  
 Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser Arg Phe  
 305 310 315 320  
 Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro Asp Asp  
 325 330 335  
 Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu Ala Ala  
 340 345 350  
 Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln Tyr Leu  
 355 360 365  
 Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp Asn Lys  
 370 375 380  
 Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu Arg Gly  
 385 390 395 400  
 His

<210> 257  
 <211> 512  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(489)  
 <223> FRXA02596

<400> 257  
 cct gtg gtc tac acc ggc cca ctc gac ctc tac ttc aac tac gca gag 48  
 Pro Val Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu  
 1 5 10 15  
 ggc aag ctg gga tgg cgc acc ctc gac ttt gaa acc gaa gta gta gaa 96  
 Gly Lys Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu  
 20 25 30  
 acc ggt gac ttc caa gga acc cca gtg atg aac tac aac gat gcg gac 144  
 Thr Gly Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp  
 35 40 45  
 gta cct ttc acc cgc atc cac gag ttc cgt cac ttc cac cca gag cgt 192  
 Val Pro Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg  
 50 55 60  
 gat gac agt tac ccc aag gat aag acc gtc atc atg cgc gag ttc tcc 240  
 Asp Asp Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser  
 65 70 75 80  
 cgt ttc gca gat aac gag gat gag cct tat tac cca atc aac act cca 288  
 Arg Phe Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro  
 85 90 95

gac gac cga gac atg ctg aag cag tac cgc ctt ctg gct gct gaa gag 336  
 Asp Asp Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu  
                   100                  105                  110

gct gct aat aat aag gtg ctg ttc ggc ggt cga ctg ggc acg tac cag 384  
 Ala Ala Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln  
                   115                  120                  125

tac ctc gac atg cac atg gct atc ggt tct gcg ctg agc atg ttt gac 432  
 Tyr Leu Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp  
                   130                  135                  140

aac aag ctg gtg ccg ttc ttt gaa gaa ggc aca ccg cta gag cag gaa 480  
 Asn Lys Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu  
                   145                  150                  155                  160

cgc gga cac taaaaggaag ggcattctccc aca 512  
 Arg Gly His

<210> 258  
 <211> 163  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 258  
 Pro Val Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu  
   1                  5                  10                  15

Gly Lys Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu  
                   20                  25                  30

Thr Gly Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp  
                   35                  40                  45

Val Pro Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg  
                   50                  55                  60

Asp Asp Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser  
   65                  70                  75                  80

Arg Phe Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro  
                   85                  90                  95

Asp Asp Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu  
                   100                  105                  110

Ala Ala Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln  
                   115                  120                  125

Tyr Leu Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp  
   130                  135                  140

Asn Lys Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu  
   145                  150                  155                  160

Arg Gly His

<400> 259																	
aaggtatctg ggtgtggata tgccctgcta actggagaaaa cttggcccga tcgggtgtct																	60
gaaatttcgg caacgccgaa tgtaagttag tgtcgaatgc atg acg gaa tcg aaa																	115
Met Thr Glu Ser Lys																	
1 5																	
aat tac gac tta atc gtt gta ggc tcc ggc ctc ttc ggg ctc acc gtg																	163
Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu Phe Gly Leu Thr Val																	
10 15 20																	
gct gag cgt gca gct agc cag ctg ggt aag aaa gtc ctc atc gtt gaa																	211
Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys Val Leu Ile Val Glu																	
25 30 35																	
cgc cgc tcg cac ctc ggt ggc aat gct tac tct gaa gca gaa cca gag																	259
Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser Glu Ala Glu Pro Glu																	
40 45 50																	
acc ggc att gaa atc cac aaa tac ggc gcg cac ctc ttc cac acc tcc																	307
Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His Leu Phe His Thr Ser																	
55 60 65																	
aac aca cgc gtg tgg gaa tac gtc aac cag ttc acc agt ttc acc ggc																	355
Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe Thr Ser Phe Thr Gly																	
70 75 80 85																	
tac cag cac cgc gtc ttc gca atg cac aac ggc acc gcc tac caa ttc																	403
Tyr Gln His Arg Val Phe Ala Met His Asn Gly Thr Ala Tyr Gln Phe																	
90 95 100																	
ccc atg gga ctg ggc ctg att aac cag ttc ttc ggc aag tac tac agc																	451
Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe Gly Lys Tyr Tyr Ser																	
105 110 115																	
cca gat gaa gcc cgt gag ctc atc aag gaa cag tct gca gaa atc gat																	499
Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln Ser Ala Glu Ile Asp																	
120 125 130																	
tcc tcc gac gcc acc aac ctc gaa gaa aag gcc att tcc ctc att ggt																	547
Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala Ile Ser Leu Ile Gly																	
135 140 145																	
cgc cca ctt tac gag gca ttc atc cgc gac tac acc gca aag cag tgg																	595
Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr Thr Ala Lys Gln Trp																	
150 155 160 165																	
cag																	598
Gln																	

<210> 260  
 <211> 166  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 260  
 Met Thr Glu Ser Lys Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu  
   1                  5                  10                  15  
 Phe Gly Leu Thr Val Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys  
                   20                  25                  30  
 Val Leu Ile Val Glu Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser  
           35                  40                  45  
 Glu Ala Glu Pro Glu Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His  
       50                  55                  60  
 Leu Phe His Thr Ser Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe  
   65                  70                  75                  80  
 Thr Ser Phe Thr Gly Tyr Gln His Arg Val Phe Ala Met His Asn Gly  
                   85                  90                  95  
 Thr Ala Tyr Gln Phe Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe  
                   100                  105                  110  
 Gly Lys Tyr Tyr Ser Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln  
       115                  120                  125  
 Ser Ala Glu Ile Asp Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala  
   130                  135                  140  
 Ile Ser Leu Ile Gly Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr  
  145                  150                  155                  160  
 Thr Ala Lys Gln Trp Gln  
                   165

<210> 261  
 <211> 668  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(645)  
 <223> RXA02572

<400> 261  
 gcg gtc gct gag att tgc gag ccg acc ggc gcc gat gcg gtt gcg ctt 48  
 Ala Val Ala Glu Ile Cys Glu Pro Thr Gly Ala Asp Ala Val Ala Leu  
   1                  5                  10                  15  
 gtg gat gcc atc ggt cac gac gat cgt atc ggc cga aag ttc tta ggc 96  
 Val Asp Ala Ile Gly His Asp Asp Arg Ile Gly Arg Lys Phe Leu Gly  
           20                  25                  30  
 gcg ggc ctg gga ttc ggt ggc ggt tgt ttg cct aaa gac atc cgc gct 144

Ala Gly Leu Gly Phe Gly Gly Gly Cys Leu Pro Lys Asp Ile Arg Ala  
 35 40 45

ttc atg gca cgc gcg ggc gaa ttg ggt gct gac cag gca tta acg ttc 192  
 Phe Met Ala Arg Ala Gly Glu Leu Gly Ala Asp Gln Ala Leu Thr Phe  
 50 55 60

ttg cgt gag gtc gat tcc atc aat atg cgt cgt cgc gac cgt gtg gtg 240  
 Leu Arg Glu Val Asp Ser Ile Asn Met Arg Arg Asp Arg Val Val  
 65 70 75 80

cag ctg gcc aaa gag atg tgt ggc ggt tcg ctg ctg ggc aag cgg gtt 288  
 Gln Leu Ala Lys Glu Met Cys Gly Gly Ser Leu Leu Gly Lys Arg Val  
 85 90 95

aca gtg ctc ggc gcc gca ttc aaa ccc aac tcg gac gat gtc cgc gat 336  
 Thr Val Leu Gly Ala Ala Phe Lys Pro Asn Ser Asp Asp Val Arg Asp  
 100 105 110

tct ccg gcg ctg tcg gtc gcg ggt tcg ctg tcg ctc cag ggt gcg gcg 384  
 Ser Pro Ala Leu Ser Val Ala Gly Ser Leu Ser Leu Gln Gly Ala Ala  
 115 120 125

gtc tcg gtc tac gac ccg gaa gct atg gac aac gct cga cgc gtc ttc 432  
 Val Ser Val Tyr Asp Pro Glu Ala Met Asp Asn Ala Arg Arg Val Phe  
 130 135 140

ccg acg ctc agc tat gcg tcc agc act aaa gag gcg ctt atc gac gcc 480  
 Pro Thr Leu Ser Tyr Ala Ser Ser Thr Lys Glu Ala Leu Ile Asp Ala  
 145 150 155 160

cac ctc gtc gtt ctt gcc act gaa tgg caa gaa ttc cgc gac ctt gac 528  
 His Leu Val Val Leu Ala Thr Glu Trp Gln Glu Phe Arg Asp Leu Asp  
 165 170 175

ccc gaa gtg gcg gga ggg gtc gtc gag aag cgc gct att att gat ggc 576  
 Pro Glu Val Ala Gly Gly Val Val Glu Lys Arg Ala Ile Ile Asp Gly  
 180 185 190

cga aac gtc ctc gat gtt gcc aaa tgg aag gcc gcc ggt tgg gaa atg 624  
 Arg Asn Val Leu Asp Val Ala Lys Trp Lys Ala Ala Gly Trp Glu Met  
 195 200 205

gaa gcg ctc ggc cgc aac ctt tagtgcggtg gatcaggcgg ggc 668  
 Glu Ala Leu Gly Arg Asn Leu  
 210 215

&lt;210&gt; 262

&lt;211&gt; 215

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 262

Ala Val Ala Glu Ile Cys Glu Pro Thr Gly Ala Asp Ala Val Ala Leu  
 1 5 10 15

Val Asp Ala Ile Gly His Asp Asp Arg Ile Gly Arg Lys Phe Leu Gly  
 20 25 30

Ala Gly Leu Gly Phe Gly Gly Gly Cys Leu Pro Lys Asp Ile Arg Ala



376

gcc gta cgt tgc cag acc acg gag gcg ctg gtc agc gcc ata aaa ttg	259
Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val Ser Ala Ile Lys Leu	
40 45 50	
ctt gac gac gcc tcc ctc ccc ctc ctc att gtc ggc ggc ggg tcc aat	307
Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val Gly Gly Gly Ser Asn	
55 60 65	
ctc gtc gtg gcc gac ggc gat ctg gat gtt att gcc gtc atc atc gaa	355
Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile Ala Val Ile Ile Glu	
70 75 80 85	
acc gac gac gtc tcc atc aac ctc acc gac ggt ctc ctc acc gcc gat	403
Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly Leu Leu Thr Ala Asp	
90 95 100	
gca ggc gct gtt tgg gac gat gtt gtc cac ctt tcg gtg gat gcc ggc	451
Ala Gly Ala Val Trp Asp Asp Val Val His Leu Ser Val Asp Ala Gly	
105 110 115	
ctc ggt gga att gaa tgc ctc tcc gga atc ccc ggc tcc gcc ggc gcc	499
Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro Gly Ser Ala Gly Ala	
120 125 130	
acc cca gtc caa aac gtg ggc gcc tac ggc acg gaa gtt tcc gat gta	547
Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr Glu Val Ser Asp Val	
135 140 145	
ctc acc cgc gtc cag ctt ctc gac cgc acc acc cac caa gtc tcc tgg	595
Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr His Gln Val Ser Trp	
150 155 160 165	
gtc gac gcc tcc gaa ctc gac ctc tct tac cga tac tcc aat ctc aaa	643
Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg Tyr Ser Asn Leu Lys	
170 175 180	
ttc acc aac cgc gca gtc gtc ttg gcg atc gaa ctc cag ctc ctc acc	691
Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu Leu Gln Leu Leu Thr	
185 190 195	
gac gga ttg tcc gcg ccg cta cgt ttt ggt gaa ttg gga cgt cga tta	739
Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu Leu Gly Arg Arg Leu	
200 205 210	
gcg atc tcc gag gcc gaa ccc cac cca cgt cgc ccc gtc cgc atg gtc	787
Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg Pro Val Arg Met Val	
215 220 225	
cgc gac gcc gtc cta gaa ctc cgc cgc gcc aaa ggc atg gtc gtg gaa	835
Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys Gly Met Val Val Glu	
230 235 240 245	
cac acc gac cac gac acc tgg tcc gcc gga tcc ttc ttc acc aac cca	883
His Thr Asp His Asp Thr Trp Ser Ala Gly Ser Phe Phe Thr Asn Pro	
250 255 260	
atc gtc gac cca gcc ctt gcc gac gca gtc ttt gaa aaa gtc ggc gaa	931
Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe Glu Lys Val Gly Glu	
265 270 275	
ccc acc atg ccc cgc ttc cca gcc ggc gat ggc aaa gaa aaa ctc tcc	979

Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly Lys Glu Lys Leu Ser  
 280 285 290

gca gcc tgg ctc atc gaa cgc gcc ggc ttc aaa aag gga cac ccc ggc 1027  
 Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys Lys Gly His Pro Gly  
 295 300 305

gca ggc gca aaa gcc tcc ctg agc acc aaa cac acc ctc gca ctc acc 1075  
 Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His Thr Leu Ala Leu Thr  
 310 315 320 325

aac cgt ggc gac gcc cgc gcc tcc gac ctc gtc gca tta gcc aaa gaa 1123  
 Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val Ala Leu Ala Lys Glu  
 330 335 340

atc cgc gac gga gtc ctc gaa acc ttc ggc gtc acc ctc gtc cca gaa 1171  
 Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val Thr Leu Val Pro Glu  
 345 350 355

ccc gtc tgg att gga atc agc atc gat gac tgaattttcc gacgtccctg 1221  
 Pro Val Trp Ile Gly Ile Ser Ile Asp Asp  
 360 365

gca 1224

<210> 264  
 <211> 367  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 264  
 Leu Asp Ser Ser Leu Ala Gln Glu Ile Ala Ala Ile Asp Gly Val Glu  
 1 5 10 15

Leu Asp Ser Glu Val Thr Phe Ala Asp Leu Thr Thr Leu Arg Ile Gly  
 20 25 30

Gly Lys Pro Arg Ser Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val  
 35 40 45

Ser Ala Ile Lys Leu Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val  
 50 55 60

Gly Gly Gly Ser Asn Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile  
 65 70 75 80

Ala Val Ile Ile Glu Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly  
 85 90 95

Leu Leu Thr Ala Asp Ala Gly Ala Val Trp Asp Asp Val Val His Leu  
 100 105 110

Ser Val Asp Ala Gly Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro  
 115 120 125

Gly Ser Ala Gly Ala Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr  
 130 135 140

Glu Val Ser Asp Val Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr  
 145 150 155 160

His Gln Val Ser Trp Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg  
 165 170 175  
 Tyr Ser Asn Leu Lys Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu  
 180 185 190  
 Leu Gln Leu Leu Thr Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu  
 195 200 205  
 Leu Gly Arg Arg Leu Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg  
 210 215 220  
 Pro Val Arg Met Val Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys  
 225 230 235 240  
 Gly Met Val Val Glu His Thr Asp His Asp Thr Trp Ser Ala Gly Ser  
 245 250 255  
 Phe Phe Thr Asn Pro Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe  
 260 265 270  
 Glu Lys Val Gly Glu Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly  
 275 280 285  
 Lys Glu Lys Leu Ser Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys  
 290 295 300  
 Lys Gly His Pro Gly Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His  
 305 310 315 320  
 Thr Leu Ala Leu Thr Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val  
 325 330 335  
 Ala Leu Ala Lys Glu Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val  
 340 345 350  
 Thr Leu Val Pro Glu Pro Val Trp Ile Gly Ile Ser Ile Asp Asp  
 355 360 365

<210> 265  
 <211> 1124  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1101)  
 <223> RXA01216

<400> 265  
 acc gac cac act ctg tct gca ctg ctg gat gca cac gtg gaa gtt cca 48  
 Thr Asp His Thr Leu Ser Ala Leu Leu Asp Ala His Val Glu Val Pro  
 1 5 10 15  
 acc gct gtc acc gtg ttg acc atg cgt ctg gat gac ccc acc ggc tac 96  
 Thr Ala Val Thr Val Leu Thr Met Arg Leu Asp Asp Pro Thr Gly Tyr  
 20 25 30  
 ggc cgc atc gtg cgc aac gaa gaa ggc gaa gtc acc gcc atc gtt gag 144

Gly	Arg	Ile	Val	Arg	Asn	Glu	Glu	Gly	Glu	Val	Thr	Ala	Ile	Val	Glu		
		35					40					45					
caa	aaa	gat	gct	tca	gca	gaa	gtc	caa	gcc	atc	gat	gag	gtc	aac	tcc	192	
Gln	Lys	Asp	Ala	Ser	Ala	Glu	Val	Gln	Ala	Ile	Asp	Glu	Val	Asn	Ser		
	50					55					60						
ggt	gtc	ttt	gct	ttc	gac	gcc	gcc	atc	ttg	cgt	tcc	gca	ctg	gct	gaa	240	
Gly	Val	Phe	Ala	Phe	Asp	Ala	Ala	Ile	Leu	Arg	Ser	Ala	Leu	Ala	Glu		
65				70				75						80			
ctg	aag	tcc	gac	aac	gct	cag	ggc	gag	ctg	tac	ctg	acc	gac	gtt	ttg	288	
Leu	Lys	Ser	Asp	Asn	Ala	Gln	Gly	Glu	Leu	Tyr	Leu	Thr	Asp	Val	Leu		
				85				90						95			
ggc	att	gct	cgt	ggc	gag	ggc	cac	cca	gtg	cgc	gcc	cac	acc	gcc	gcc	336	
Gly	Ile	Ala	Arg	Gly	Glu	Gly	His	Pro	Val	Arg	Ala	His	Thr	Ala	Ala		
		100						105					110				
gat	gct	cgt	gaa	ctc	gcc	ggc	gtc	aac	gat	cgt	gtg	cag	ctc	gca	gaa	384	
Asp	Ala	Arg	Glu	Leu	Ala	Gly	Val	Asn	Asp	Arg	Val	Gln	Leu	Ala	Glu		
	115						120					125					
gcc	ggc	gcc	gaa	cta	aac	cgt	cgc	acc	gtc	atc	gcc	gct	atg	cgt	ggt	432	
Ala	Gly	Ala	Glu	Leu	Asn	Arg	Arg	Thr	Val	Ile	Ala	Ala	Met	Arg	Gly		
	130					135					140						
ggc	gca	acc	atc	gtt	gat	cca	gca	acc	acc	tgg	atc	gat	gtg	gag	gtt	480	
Gly	Ala	Thr	Ile	Val	Asp	Pro	Ala	Thr	Thr	Trp	Ile	Asp	Val	Glu	Val		
145					150					155				160			
tct	atc	gga	cgc	gac	gtg	atc	atc	cac	cct	ggc	acc	cag	ctc	aag	ggc	528	
Ser	Ile	Gly	Arg	Asp	Val	Ile	Ile	His	Pro	Gly	Thr	Gln	Leu	Lys	Gly		
				165					170					175			
gaa	act	gtc	atc	gga	gac	cgc	gtt	gaa	gtt	ggt	cca	gac	acc	acc	ttg	576	
Glu	Thr	Val	Ile	Gly	Asp	Arg	Val	Glu	Val	Gly	Pro	Asp	Thr	Thr	Leu		
		180						185					190				
acc	aac	atg	acc	atc	ggc	gac	ggc	gca	tcc	gta	atc	cgc	acc	cac	ggt	624	
Thr	Asn	Met	Thr	Ile	Gly	Asp	Gly	Ala	Ser	Val	Ile	Arg	Thr	His	Gly		
	195						200					205					
ttc	gac	tcc	acc	atc	ggt	gaa	aac	gcc	acc	gtt	ggc	ccc	ttc	acc	tac	672	
Phe	Asp	Ser	Thr	Ile	Gly	Glu	Asn	Ala	Thr	Val	Gly	Pro	Phe	Thr	Tyr		
	210					215					220						
atc	cgc	cca	gga	acc	aca	ctg	gga	cca	gaa	ggc	aag	ctc	ggt	ggc	ttc	720	
Ile	Arg	Pro	Gly	Thr	Thr	Leu	Gly	Pro	Glu	Gly	Lys	Leu	Gly	Gly	Phe		
225					230					235				240			
gta	gaa	acc	aag	aag	gcc	aca	atc	ggc	cgt	ggc	tcc	aag	gtt	cca	cac	768	
Val	Glu	Thr	Lys	Lys	Ala	Thr	Ile	Gly	Arg	Gly	Ser	Lys	Val	Pro	His		
				245				250					255				
ctc	acc	tat	gtc	ggc	gac	gcc	acc	atc	ggc	gag	gaa	tcc	aac	atc	gga	816	
Leu	Thr	Tyr	Val	Gly	Asp	Ala	Thr	Ile	Gly	Glu	Glu	Ser	Asn	Ile	Gly		
			260					265					270				
gcc	tcc	tct	gtc	ttc	gtg	aac	tac	gac	ggt	gaa	aac	aag	cac	cac	acc	864	
Ala	Ser	Ser	Val	Phe	Val	Asn	Tyr	Asp	Gly	Glu	Asn	Lys	His	His	Thr		

275	280	285	
acc atc ggc agc cac gtt cgc act ggt tct gac acc atg ttt atc gct			912
Thr Ile Gly Ser His Val Arg Thr Gly Ser Asp Thr Met Phe Ile Ala			
290	295	300	
cca gtg acc gtg ggt gac gga gcg tat tcc gga gcc ggt aca gta att			960
Pro Val Thr Val Gly Asp Gly Ala Tyr Ser Gly Ala Gly Thr Val Ile			
305	310	315	320
aaa gac gat gtt ccg cca gga gcc ctt gcc gtg tcc ggc gga cgc caa			1008
Lys Asp Asp Val Pro Pro Gly Ala Leu Ala Val Ser Gly Gly Arg Gln			
	325	330	335
cga aac atc gaa ggc tgg gtg caa aag aag cgc cct gga acc gct gca			1056
Arg Asn Ile Glu Gly Trp Val Gln Lys Lys Arg Pro Gly Thr Ala Ala			
	340	345	350
gca caa gcc gca gaa gcc gcc caa aac gtc cac aac cag gaa ggc			1101
Ala Gln Ala Ala Glu Ala Ala Gln Asn Val His Asn Gln Glu Gly			
	355	360	365
taagcaggat cctcatgact gct			1124
<210> 266			
<211> 367			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 266			
Thr Asp His Thr Leu Ser Ala Leu Leu Asp Ala His Val Glu Val Pro			
1	5	10	15
Thr Ala Val Thr Val Leu Thr Met Arg Leu Asp Asp Pro Thr Gly Tyr			
	20	25	30
Gly Arg Ile Val Arg Asn Glu Glu Gly Glu Val Thr Ala Ile Val Glu			
	35	40	45
Gln Lys Asp Ala Ser Ala Glu Val Gln Ala Ile Asp Glu Val Asn Ser			
	50	55	60
Gly Val Phe Ala Phe Asp Ala Ala Ile Leu Arg Ser Ala Leu Ala Glu			
	65	70	75
Leu Lys Ser Asp Asn Ala Gln Gly Glu Leu Tyr Leu Thr Asp Val Leu			
	85	90	95
Gly Ile Ala Arg Gly Glu Gly His Pro Val Arg Ala His Thr Ala Ala			
	100	105	110
Asp Ala Arg Glu Leu Ala Gly Val Asn Asp Arg Val Gln Leu Ala Glu			
	115	120	125
Ala Gly Ala Glu Leu Asn Arg Arg Thr Val Ile Ala Ala Met Arg Gly			
	130	135	140
Gly Ala Thr Ile Val Asp Pro Ala Thr Thr Trp Ile Asp Val Glu Val			
	145	150	155
			160

Ser Ile Gly Arg Asp Val Ile Ile His Pro Gly Thr Gln Leu Lys Gly  
 165 170 175  
 Glu Thr Val Ile Gly Asp Arg Val Glu Val Gly Pro Asp Thr Thr Leu  
 180 185 190  
 Thr Asn Met Thr Ile Gly Asp Gly Ala Ser Val Ile Arg Thr His Gly  
 195 200 205  
 Phe Asp Ser Thr Ile Gly Glu Asn Ala Thr Val Gly Pro Phe Thr Tyr  
 210 215 220  
 Ile Arg Pro Gly Thr Thr Leu Gly Pro Glu Gly Lys Leu Gly Gly Phe  
 225 230 235 240  
 Val Glu Thr Lys Lys Ala Thr Ile Gly Arg Gly Ser Lys Val Pro His  
 245 250 255  
 Leu Thr Tyr Val Gly Asp Ala Thr Ile Gly Glu Glu Ser Asn Ile Gly  
 260 265 270  
 Ala Ser Ser Val Phe Val Asn Tyr Asp Gly Glu Asn Lys His His Thr  
 275 280 285  
 Thr Ile Gly Ser His Val Arg Thr Gly Ser Asp Thr Met Phe Ile Ala  
 290 295 300  
 Pro Val Thr Val Gly Asp Gly Ala Tyr Ser Gly Ala Gly Thr Val Ile  
 305 310 315 320  
 Lys Asp Asp Val Pro Pro Gly Ala Leu Ala Val Ser Gly Gly Arg Gln  
 325 330 335  
 Arg Asn Ile Glu Gly Trp Val Gln Lys Lys Arg Pro Gly Thr Ala Ala  
 340 345 350  
 Ala Gln Ala Ala Glu Ala Ala Gln Asn Val His Asn Gln Glu Gly  
 355 360 365

&lt;210&gt; 267

&lt;211&gt; 981

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(958)

&lt;223&gt; RXA01259

&lt;400&gt; 267

aagagaatta ttctaaaat tcggtatcgt ctaagaaatg agtttgccaa tagctcagca 60

tcaaaatgct gtaaaaactg tcgtggtacc agctgcagga atg gga aca cgg ttc 115  
 Met Gly Thr Arg Phe  
 1 5

ctt cct gca acg aag aca att cca aag gag ctt ctt cct gta gtt gat 163  
 Leu Pro Ala Thr Lys Thr Ile Pro Lys Glu Leu Leu Pro Val Val Asp  
 10 15 20

acc ccg ggt att gaa ctt gtt gcc aaa gag gct gct gat ctt ggt gca	211
Thr Pro Gly Ile Glu Leu Val Ala Lys Glu Ala Ala Asp Leu Gly Ala	
25 30 35	
act cgg tta gca att atc act gct ccg aac aaa gac gga att ctt aaa	259
Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys Asp Gly Ile Leu Lys	
40 45 50	
cac ttc gag gag ttc cct gag ctt gag gca act ctt gag gct cgc ggt	307
His Phe Glu Glu Phe Pro Glu Leu Glu Ala Thr Leu Glu Ala Arg Gly	
55 60 65	
aag act gat caa ctg aat aaa gtt cga gca gct cga gaa ttg att gca	355
Lys Thr Asp Gln Leu Asn Lys Val Arg Ala Ala Arg Glu Leu Ile Ala	
70 75 80 85	
aca gtt cca gtg gtt caa gaa aag cca ttg ggg ctt ggt cac gct gtt	403
Thr Val Pro Val Val Gln Glu Lys Pro Leu Gly Leu Gly His Ala Val	
90 95 100	
ggc ctt gct gag tct gtg ctc gat gat gat gaa gat gtt gtg gct gtc	451
Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu Asp Val Val Ala Val	
105 110 115	
atg ctg cca gac gat ttg gtg ctg cca ttt ggt gtg acc gag aga atg	499
Met Leu Pro Asp Asp Leu Val Leu Pro Phe Gly Val Thr Glu Arg Met	
120 125 130	
gca gaa gtt cgc gct aag ttt ggc gga tct gtt ctt gca gca att gag	547
Ala Glu Val Arg Ala Lys Phe Gly Gly Ser Val Leu Ala Ala Ile Glu	
135 140 145	
gtg gct gaa gat gaa gtc tca aat tac gga gta ttt aag ctc ggt gaa	595
Val Ala Glu Asp Glu Val Ser Asn Tyr Gly Val Phe Lys Leu Gly Glu	
150 155 160 165	
ctc gat gca gag tcc gaa agt gaa ggc att agg cgt gtt gta gga atg	643
Leu Asp Ala Glu Ser Glu Ser Glu Gly Ile Arg Arg Val Val Gly Met	
170 175 180	
gtt gaa aag cct gcg cct gaa gat gca cca tca agg ttt gcc gca acg	691
Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser Arg Phe Ala Ala Thr	
185 190 195	
ggc cgt tat cta ctt gat cga gct att ttt gat gca ctg cgt cga att	739
Gly Arg Tyr Leu Leu Asp Arg Ala Ile Phe Asp Ala Leu Arg Arg Ile	
200 205 210	
gag cct ggt gct ggt gga gaa ctg caa tta aca gat gcc atc gca tta	787
Glu Pro Gly Ala Gly Gly Glu Leu Gln Leu Thr Asp Ala Ile Ala Leu	
215 220 225	
ttg atc gaa gaa ggc cat ccg gta cac att gtg gtt cat gaa gga aag	835
Leu Ile Glu Glu Gly His Pro Val His Ile Val Val His Glu Gly Lys	
230 235 240 245	
cgc cat gac ctt ggt aat cca gct ggg tac att cct gct gtt gtg tac	883
Arg His Asp Leu Gly Asn Pro Ala Gly Tyr Ile Pro Ala Val Val Tyr	
250 255 260	
ttc gga ctt cgt cat gca gag tac ggt tcc aag att cac cgt gcg gtg	931



Phe Gly Leu Arg His Ala Glu Tyr Gly Ser Lys Ile His Arg Ala Val  
                   265                                  270                                  275

aag gaa ata ctc gct gag ttt gaa tct taaaaaggaa accgccttcc 978  
 Lys Glu Ile Leu Ala Glu Phe Glu Ser  
                   280                                  285

aca 981

<210> 268

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

Met Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr Ile Pro Lys Glu Leu  
   1                                  5                                  10                                  15

Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu Val Ala Lys Glu Ala  
                   20                                  25                                  30

Ala Asp Leu Gly Ala Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys  
                   35                                  40                                  45

Asp Gly Ile Leu Lys His Phe Glu Glu Phe Pro Glu Leu Glu Ala Thr  
                   50                                  55                                  60

Leu Glu Ala Arg Gly Lys Thr Asp Gln Leu Asn Lys Val Arg Ala Ala  
   65                                  70                                  75                                  80

Arg Glu Leu Ile Ala Thr Val Pro Val Val Gln Glu Lys Pro Leu Gly  
                   85                                  90                                  95

Leu Gly His Ala Val Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu  
                   100                                  105                                  110

Asp Val Val Ala Val Met Leu Pro Asp Asp Leu Val Leu Pro Phe Gly  
                   115                                  120                                  125

Val Thr Glu Arg Met Ala Glu Val Arg Ala Lys Phe Gly Gly Ser Val  
                   130                                  135                                  140

Leu Ala Ala Ile Glu Val Ala Glu Asp Glu Val Ser Asn Tyr Gly Val  
   145                                  150                                  155                                  160

Phe Lys Leu Gly Glu Leu Asp Ala Glu Ser Glu Ser Glu Gly Ile Arg  
                   165                                  170                                  175

Arg Val Val Gly Met Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser  
                   180                                  185                                  190

Arg Phe Ala Ala Thr Gly Arg Tyr Leu Leu Asp Arg Ala Ile Phe Asp  
                   195                                  200                                  205

Ala Leu Arg Arg Ile Glu Pro Gly Ala Gly Gly Glu Leu Gln Leu Thr  
                   210                                  215                                  220

Asp Ala Ile Ala Leu Leu Ile Glu Glu Gly His Pro Val His Ile Val  
   225                                  230                                  235                                  240

Val His Glu Gly Lys Arg His Asp Leu Gly Asn Pro Ala Gly Tyr Ile  
                   245                  250                  255

Pro Ala Val Val Tyr Phe Gly Leu Arg His Ala Glu Tyr Gly Ser Lys  
                   260                  265                  270

Ile His Arg Ala Val Lys Glu Ile Leu Ala Glu Phe Glu Ser  
                   275                  280                  285

<210> 269

<211> 526

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(526)

<223> RXA02028

<400> 269

tgcgagcagttc ctgcttagtt tggctcataa atctaaggat aaccggttatt ttcggagggg 60

tacgacgatt ggggttgccg gggcaggtac tcttggttcc atg agt ttg cct atc 115  
   Met Ser Leu Pro Ile  
   1                  5

gat gag cac gtg aac gcg gtt aaa acc gtc gta gtg cct gct gca gga 163  
   Asp Glu His Val Asn Ala Val Lys Thr Val Val Val Pro Ala Ala Gly  
                                   10                                  15                                  20

ctg gga acc cga ttc ctt ccg gcc acc aaa acc gta ccc aag gag ttg 211  
   Leu Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr Val Pro Lys Glu Leu  
                                   25                                  30                                  35

ctg ccg gtt gtc gat acc cca ggt att gag ctg att gct gct gag gct 259  
   Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu Ile Ala Ala Glu Ala  
                                   40                                  45                                  50

gcc gaa ctt ggt gcg acc agg ctg gcg atc atc act gcg cca aac aaa 307  
   Ala Glu Leu Gly Ala Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys  
                                   55                                  60                                  65

gct ggg gta ctt gca cac ttt gag cgt tct tct gaa ttg gaa gaa acg 355  
   Ala Gly Val Leu Ala His Phe Glu Arg Ser Ser Glu Leu Glu Glu Thr  
                                   70                                  75                                  80                                  85

ctg atg gag cgt ggc aag act gac cag gtg gag ata atc cgc cgc gcc 403  
   Leu Met Glu Arg Gly Lys Thr Asp Gln Val Glu Ile Ile Arg Arg Ala  
                                   90                                  95                                  100

gcc gat tta atc aag gca gtt cca gta acc cag gac aag ccg ctg ggg 451  
   Ala Asp Leu Ile Lys Ala Val Pro Val Thr Gln Asp Lys Pro Leu Gly  
                                   105                                  110                                  115

cta ggt cat gct gtt ggt ttg gct gag tct gtg ttg gat gat gat gaa 499  
   Leu Gly His Ala Val Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu  
                                   120                                  125                                  130

gat gtc gta gcg gtg atg ttg ccg cac 526  
   Asp Val Val Ala Val Met Leu Pro His

135

140

&lt;210&gt; 270

&lt;211&gt; 142

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 270

Met Ser Leu Pro Ile Asp Glu His Val Asn Ala Val Lys Thr Val Val  
 1 5 10 15

Val Pro Ala Ala Gly Leu Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr  
 20 25 30

Val Pro Lys Glu Leu Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu  
 35 40 45

Ile Ala Ala Glu Ala Ala Glu Leu Gly Ala Thr Arg Leu Ala Ile Ile  
 50 55 60

Thr Ala Pro Asn Lys Ala Gly Val Leu Ala His Phe Glu Arg Ser Ser  
 65 70 75 80

Glu Leu Glu Glu Thr Leu Met Glu Arg Gly Lys Thr Asp Gln Val Glu  
 85 90 95

Ile Ile Arg Arg Ala Ala Asp Leu Ile Lys Ala Val Pro Val Thr Gln  
 100 105 110

Asp Lys Pro Leu Gly Leu Gly His Ala Val Gly Leu Ala Glu Ser Val  
 115 120 125

Leu Asp Asp Asp Glu Asp Val Val Ala Val Met Leu Pro His  
 130 135 140

&lt;210&gt; 271

&lt;211&gt; 1284

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1261)

&lt;223&gt; RXA01262

&lt;400&gt; 271

tatactcgtc aagggccttc gataaaacaa agacaatttt ccccgacgg gacaatctga 60

aaacttgctg tatcaataaa acacgaaaag gaatactttt atg aaa att gcc gtc 115  
 Met Lys Ile Ala Val  
 1 5

gca ggg ctc gga tat gtt ggg ctt tca aat gca gct ctc ctc tct aaa 163  
 Ala Gly Leu Gly Tyr Val Gly Leu Ser Asn Ala Ala Leu Leu Ser Lys  
 10 15 20

aat cat aaa gtt gtt gca gtt gac att gat gaa gaa cga gtg aaa cta 211  
 Asn His Lys Val Val Ala Val Asp Ile Asp Glu Glu Arg Val Lys Leu  
 25 30 35

gtt caa gaa ttt cgt tgc cca att gtc gat agc gat ctc gaa gaa tat	259
Val Gln Glu Phe Arg Ser Pro Ile Val Asp Ser Asp Leu Glu Glu Tyr	
40 45 50	
ctg tcc act aag cct caa aac tta act gcc aca acg gac gcc gaa gcc	307
Leu Ser Thr Lys Pro Gln Asn Leu Thr Ala Thr Thr Asp Ala Glu Ala	
55 60 65	
gct tac aaa ggc gca gat ttt att gtt att gca acg cca act aat tac	355
Ala Tyr Lys Gly Ala Asp Phe Ile Val Ile Ala Thr Pro Thr Asn Tyr	
70 75 80 85	
gac cca gag tca aac ttt ttt gat act tcc agc gtt gag tcc gta att	403
Asp Pro Glu Ser Asn Phe Phe Asp Thr Ser Ser Val Glu Ser Val Ile	
90 95 100	
gag ata gtc ctt aag gtt tct cct gga tcc aca atc gta att aaa tcg	451
Glu Ile Val Leu Lys Val Ser Pro Gly Ser Thr Ile Val Ile Lys Ser	
105 110 115	
act atc cct gtt ggt ttt aca tcg gaa cta cgc att aag cat cca gaa	499
Thr Ile Pro Val Gly Phe Thr Ser Glu Leu Arg Ile Lys His Pro Glu	
120 125 130	
gct tcg att att ttt tca cct gag ttc ctg cgt gaa ggc cga gca ttc	547
Ala Ser Ile Ile Phe Ser Pro Glu Phe Leu Arg Glu Gly Arg Ala Phe	
135 140 145	
tac gac aat ctc tac cca tcc aga gtt gtc gtt ggt gat cgc agt cct	595
Tyr Asp Asn Leu Tyr Pro Ser Arg Val Val Val Gly Asp Arg Ser Pro	
150 155 160 165	
ctg ggg gaa gaa ttt gcg act ctg tta gct gag ggg gca aaa gaa aag	643
Leu Gly Glu Glu Phe Ala Thr Leu Leu Ala Glu Gly Ala Lys Glu Lys	
170 175 180	
cct ccg att cta ctt acg gac tca act gag gca gag gcg att aaa tta	691
Pro Pro Ile Leu Leu Thr Asp Ser Thr Glu Ala Glu Ala Ile Lys Leu	
185 190 195	
ttt tct aat aca tat ctt gca ctg cga gtt gct ttt ttc aac gaa ctg	739
Phe Ser Asn Thr Tyr Leu Ala Leu Arg Val Ala Phe Phe Asn Glu Leu	
200 205 210	
gat act tat gcg tct gtt cga agc ttg gat act aag cag att att gaa	787
Asp Thr Tyr Ala Ser Val Arg Ser Leu Asp Thr Lys Gln Ile Ile Glu	
215 220 225	
ggg gta ggg ctc gat cca cgt att gga tct cat tac aat aat cct tca	835
Gly Val Gly Leu Asp Pro Arg Ile Gly Ser His Tyr Asn Asn Pro Ser	
230 235 240 245	
ttt gga tat ggc gga tat tgt ctt ccg aaa gat acg aaa cag ctt ctc	883
Phe Gly Tyr Gly Tyr Cys Leu Pro Lys Asp Thr Lys Gln Leu Leu	
250 255 260	
gcc aac tat aag gat gtc ccg cag aat cta atc tct gca gta gtc caa	931
Ala Asn Tyr Lys Asp Val Pro Gln Asn Leu Ile Ser Ala Val Val Gln	
265 270 275	

gca aat aag act cgt aag gac ttt att gca gag gat atc ctc agt aaa 979  
 Ala Asn Lys Thr Arg Lys Asp Phe Ile Ala Glu Asp Ile Leu Ser Lys  
 280 285 290  
  
 tca cct act gta gtt gga att tac cgc ctt gta atg aag tct gga tca 1027  
 Ser Pro Thr Val Val Gly Ile Tyr Arg Leu Val Met Lys Ser Gly Ser  
 295 300 305  
  
 gat aac ttt cgt tct tct tct att caa gga gtc atg aaa cga att aag 1075  
 Asp Asn Phe Arg Ser Ser Ser Ile Gln Gly Val Met Lys Arg Ile Lys  
 310 315 320 325  
  
 gcc aag gga atc gaa att gta gta ttt gaa ccg aat ctc gga gaa gaa 1123  
 Ala Lys Gly Ile Glu Ile Val Val Phe Glu Pro Asn Leu Gly Glu Glu  
 330 335 340  
  
 act ttc tac aat tcg aag atc ctt aat gac atc gaa gag ttt aag gat 1171  
 Thr Phe Tyr Asn Ser Lys Ile Leu Asn Asp Ile Glu Glu Phe Lys Asp  
 345 350 355  
  
 tac tgc gac atc att att gca aat cgt cca acc gat gag ctt tct gat 1219  
 Tyr Cys Asp Ile Ile Ile Ala Asn Arg Pro Thr Asp Glu Leu Ser Asp  
 360 365 370  
  
 gta cca gaa aaa gtt tat aca cgt gat att ttc cag cgt gac 1261  
 Val Pro Glu Lys Val Tyr Thr Arg Asp Ile Phe Gln Arg Asp  
 375 380 385  
  
 taagtggaaa gaatcttttg ttg 1284

&lt;210&gt; 272

&lt;211&gt; 387

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 272

Met Lys Ile Ala Val Ala Gly Leu Gly Tyr Val Gly Leu Ser Asn Ala  
 1 5 10 15  
  
 Ala Leu Leu Ser Lys Asn His Lys Val Val Ala Val Asp Ile Asp Glu  
 20 25 30  
  
 Glu Arg Val Lys Leu Val Gln Glu Phe Arg Ser Pro Ile Val Asp Ser  
 35 40 45  
  
 Asp Leu Glu Glu Tyr Leu Ser Thr Lys Pro Gln Asn Leu Thr Ala Thr  
 50 55 60  
  
 Thr Asp Ala Glu Ala Ala Tyr Lys Gly Ala Asp Phe Ile Val Ile Ala  
 65 70 75 80  
  
 Thr Pro Thr Asn Tyr Asp Pro Glu Ser Asn Phe Phe Asp Thr Ser Ser  
 85 90 95  
  
 Val Glu Ser Val Ile Glu Ile Val Leu Lys Val Ser Pro Gly Ser Thr  
 100 105 110  
  
 Ile Val Ile Lys Ser Thr Ile Pro Val Gly Phe Thr Ser Glu Leu Arg  
 115 120 125

Ile Lys His Pro Glu Ala Ser Ile Ile Phe Ser Pro Glu Phe Leu Arg  
 130 135 140  
 Glu Gly Arg Ala Phe Tyr Asp Asn Leu Tyr Pro Ser Arg Val Val Val  
 145 150 155 160  
 Gly Asp Arg Ser Pro Leu Gly Glu Glu Phe Ala Thr Leu Leu Ala Glu  
 165 170 175  
 Gly Ala Lys Glu Lys Pro Pro Ile Leu Leu Thr Asp Ser Thr Glu Ala  
 180 185 190  
 Glu Ala Ile Lys Leu Phe Ser Asn Thr Tyr Leu Ala Leu Arg Val Ala  
 195 200 205  
 Phe Phe Asn Glu Leu Asp Thr Tyr Ala Ser Val Arg Ser Leu Asp Thr  
 210 215 220  
 Lys Gln Ile Ile Glu Gly Val Gly Leu Asp Pro Arg Ile Gly Ser His  
 225 230 235 240  
 Tyr Asn Asn Pro Ser Phe Gly Tyr Gly Gly Tyr Cys Leu Pro Lys Asp  
 245 250 255  
 Thr Lys Gln Leu Leu Ala Asn Tyr Lys Asp Val Pro Gln Asn Leu Ile  
 260 265 270  
 Ser Ala Val Val Gln Ala Asn Lys Thr Arg Lys Asp Phe Ile Ala Glu  
 275 280 285  
 Asp Ile Leu Ser Lys Ser Pro Thr Val Val Gly Ile Tyr Arg Leu Val  
 290 295 300  
 Met Lys Ser Gly Ser Asp Asn Phe Arg Ser Ser Ser Ile Gln Gly Val  
 305 310 315 320  
 Met Lys Arg Ile Lys Ala Lys Gly Ile Glu Ile Val Val Phe Glu Pro  
 325 330 335  
 Asn Leu Gly Glu Glu Thr Phe Tyr Asn Ser Lys Ile Leu Asn Asp Ile  
 340 345 350  
 Glu Glu Phe Lys Asp Tyr Cys Asp Ile Ile Ile Ala Asn Arg Pro Thr  
 355 360 365  
 Asp Glu Leu Ser Asp Val Pro Glu Lys Val Tyr Thr Arg Asp Ile Phe  
 370 375 380  
 Gln Arg Asp  
 385

&lt;210&gt; 273

&lt;211&gt; 1209

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1186)

&lt;223&gt; RXA01377

390

Val Phe Gly His Val Asp Ala Ser Tyr Trp Arg Asp Met Gly Thr Pro  
 215 220 225  
 agc gac ttc gtc cgc ggc tcg gct gac ctg gtc cgc ggc att gcg tac 835  
 Ser Asp Phe Val Arg Gly Ser Ala Asp Leu Val Arg Gly Ile Ala Tyr  
 230 235 240 245  
 tcc cca ttg ctc gaa ggc aaa aca gga gag tcg ctt gtc gac gcc tcc 883  
 Ser Pro Leu Leu 250 Gly Lys Thr Gly Glu Ser Leu Val Asp Ala Ser  
 255 260  
 gcc ggc gtt cgc gac ggc gtc ctg ctg ctc ggc gga acc gta gtc ggc 931  
 Ala Gly Val Arg Asp Gly Val Leu Leu Leu Gly Gly Thr Val Val Gly  
 265 270 275  
 cgc ggc act gag atc ggt gcc ggc tgc cgc gtt gac aac act gtt att 979  
 Arg Gly Thr Glu Ile Gly Ala Gly Cys Arg Val Asp Asn Thr Val Ile  
 280 285 290  
 ttc gac ggc gtc acc att gaa cca ggt gcg gtc att gaa aat tcc atc 1027  
 Phe Asp Gly Val Thr Ile Glu Pro Gly Ala Val Ile Glu Asn Ser Ile  
 295 300 305  
 att tcc tcg gga gca cgc atc ggt gct aat gcg cac atc tcc ggt tgc 1075  
 Ile Ser Ser Gly Ala Arg Ile Gly Ala Asn Ala His Ile Ser Gly Cys  
 310 315 320 325  
 atc att ggc gag ggc gca cag gtt ggt gct cgg tgt gaa ctc aac gca 1123  
 Ile Ile Gly Glu Gly Ala Gln Val Gly Ala Arg Cys Glu Leu Asn Ala  
 330 335 340  
 ggg atg cgc gtc ttc cca ggc gtt gtg atc cca gac agc gga att cgt 1171  
 Gly Met Arg Val Phe Pro Gly Val Val Ile Pro Asp Ser Gly Ile Arg  
 345 350 355  
 ttt tcg tct gat cag taggcatttt tagccctttt gga 1209  
 Phe Ser Ser Asp Gln  
 360

&lt;210&gt; 274

&lt;211&gt; 362

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 274

Met Thr Leu Thr Asp Asn Ser Lys Asn Val Asp Ala Val Ile Leu Val  
 1 5 10 15  
 Gly Gly Lys Gly Thr Arg Leu Arg Pro Leu Thr Val Asn Thr Pro Lys  
 20 25 30  
 Pro Met Leu Pro Thr Ala Gly His Pro Phe Leu Thr His Leu Leu Ala  
 35 40 45  
 Arg Ile Lys Ala Ala Gly Ile Thr His Val Val Leu Gly Thr Ser Phe  
 50 55 60  
 Lys Ala Glu Val Phe Glu Tyr Phe Gly Asp Gly Ser Glu Met Gly  
 65 70 75 80



Leu	Glu	Ile	Glu	Tyr	Val	Val	Glu	Asp	Gln	Pro	Leu	Gly	Thr	Gly	Gly	
				85					90					95		
Gly	Ile	Arg	Asn	Val	Tyr	Asp	Lys	Leu	Arg	His	Asp	Thr	Ala	Ile	Val	
				100					105					110		
Phe	Asn	Gly	Asp	Val	Leu	Ser	Gly	Ala	Asp	Leu	Asn	Ser	Ile	Leu	Asp	
				115					120					125		
Thr	His	Arg	Glu	Lys	Asp	Ala	Asp	Leu	Thr	Met	His	Leu	Val	Arg	Val	
				130					135					140		
Ala	Asn	Pro	Arg	Ala	Phe	Gly	Cys	Val	Pro	Thr	Asp	Glu	Asp	Gly	Arg	
				145					150					155		
Val	Ser	Glu	Phe	Leu	Glu	Lys	Thr	Glu	Asp	Pro	Pro	Thr	Asp	Gln	Ile	
				165					170					175		
Asn	Ala	Gly	Cys	Tyr	Val	Phe	Lys	Lys	Glu	Leu	Ile	Glu	Gln	Ile	Pro	
				180					185					190		
Ala	Gly	Arg	Ala	Val	Ser	Val	Glu	Arg	Glu	Thr	Phe	Pro	Gln	Leu	Leu	
				195					200					205		
Glu	Glu	Gly	Lys	Arg	Val	Phe	Gly	His	Val	Asp	Ala	Ser	Tyr	Trp	Arg	
				210					215					220		
Asp	Met	Gly	Thr	Pro	Ser	Asp	Phe	Val	Arg	Gly	Ser	Ala	Asp	Leu	Val	
				225					230					235		
Arg	Gly	Ile	Ala	Tyr	Ser	Pro	Leu	Leu	Glu	Gly	Lys	Thr	Gly	Glu	Ser	
				245					250					255		
Leu	Val	Asp	Ala	Ser	Ala	Gly	Val	Arg	Asp	Gly	Val	Leu	Leu	Leu	Gly	
				260					265					270		
Gly	Thr	Val	Val	Gly	Arg	Gly	Thr	Glu	Ile	Gly	Ala	Gly	Cys	Arg	Val	
				275					280					285		
Asp	Asn	Thr	Val	Ile	Phe	Asp	Gly	Val	Thr	Ile	Glu	Pro	Gly	Ala	Val	
				290					295					300		
Ile	Glu	Asn	Ser	Ile	Ile	Ser	Ser	Gly	Ala	Arg	Ile	Gly	Ala	Asn	Ala	
				305					310					315		
His	Ile	Ser	Gly	Cys	Ile	Ile	Gly	Glu	Gly	Ala	Gln	Val	Gly	Ala	Arg	
				325					330					335		
Cys	Glu	Leu	Asn	Ala	Gly	Met	Arg	Val	Phe	Pro	Gly	Val	Val	Ile	Pro	
				340					345					350		
Asp	Ser	Gly	Ile	Arg	Phe	Ser	Ser	Asp	Gln							
				355					360							

<210> 275

<211> 1350

<212> DNA

<213> Corynebacterium glutamicum

$\langle 220 \rangle$

&lt;221&gt; CDS

&lt;222&gt; (101)..(1327)

&lt;223&gt; RXA02063

&lt;400&gt; 275

```

accgaaatgg gggcattaaa aggggctatc attcggaccc caaaacgatg tttagacaat 60

ttgttaccca gctttcatgc gggatagtta ttttgccttt atg gtt aag ggt gtg 115
                                         Met Val Lys Gly Val
                                         1 5

aag ggt aga cca aat gtt cta gca atc gtt ctc gca ggt ggc gag ggc 163
Lys Gly Arg Pro Asn Val Leu Ala Ile Val Leu Ala Gly Gly Glu Gly
                        10 15 20

aaa cga ctt ttt ccg ttg acg gag gac cga gct aag cct gcg gtc cca 211
Lys Arg Leu Phe Pro Leu Thr Glu Asp Arg Ala Lys Pro Ala Val Pro
                        25 30 35

ttc ggc gga act tac aga ttg atc gac ttt gtt ttg tcg aac ctg gtg 259
Phe Gly Gly Thr Tyr Arg Leu Ile Asp Phe Val Leu Ser Asn Leu Val
                        40 45 50

aac tcc gga ttc ctc aag atc gcg gta ctg act cag tac aag tcg cat 307
Asn Ser Gly Phe Leu Lys Ile Ala Val Leu Thr Gln Tyr Lys Ser His
                        55 60 65

tca ttg gat agg cat att tca ttg tcg tgg aac gtg tct ggt cca acg 355
Ser Leu Asp Arg His Ile Ser Leu Ser Trp Asn Val Ser Gly Pro Thr
                        70 75 80 85

ggg cag tac att gct tct gtt cct gcg cag cag cgc ctg ggc aag cga 403
Gly Gln Tyr Ile Ala Ser Val Pro Ala Gln Gln Arg Leu Gly Lys Arg
                        90 95 100

tgg ttc act ggt tcc gcg gat gca att ttg cag tct ctg aac ttg atc 451
Trp Phe Thr Gly Ser Ala Asp Ala Ile Leu Gln Ser Leu Asn Leu Ile
                        105 110 115

tct gat gag aaa ccg gat tat gtc atc gtt ttc ggc gcg gac cac gtg 499
Ser Asp Glu Lys Pro Asp Tyr Val Ile Val Phe Gly Ala Asp His Val
                        120 125 130

tat cgc atg gac cca agc cag atg cta gat gag cac att gca tct ggt 547
Tyr Arg Met Asp Pro Ser Gln Met Leu Asp Glu His Ile Ala Ser Gly
                        135 140 145

cgc gcg gtg tct gtg gca ggt att cgc gtt cca cgt gag gaa gca act 595
Arg Ala Val Ser Val Ala Gly Ile Arg Val Pro Arg Glu Glu Ala Thr
                        150 155 160 165

gcg ttt ggt tgc atc cag tcc gat gtc gac ggc aac ata acc gag ttc 643
Ala Phe Gly Cys Ile Gln Ser Asp Val Asp Gly Asn Ile Thr Glu Phe
                        170 175 180

ttg gaa aag cca gct gac cct ccg gga acc cct gat gat cct gac atg 691
Leu Glu Lys Pro Ala Asp Pro Pro Gly Thr Pro Asp Asp Pro Asp Met
                        185 190 195

act tac gcg tcg atg ggt aac tac att ttc acc act gaa gcc ctg atc 739
Thr Tyr Ala Ser Met Gly Asn Tyr Ile Phe Thr Thr Glu Ala Leu Ile

```

200	205	210	
cag gcg ctg aaa gat gat	gaa aat aac gag aac agt gat cat gac atg		787
Gln Ala Leu Lys Asp Asp	Glu Asn Asn Glu Asn Ser Asp His Asp Met		
215	220	225	
ggc gga gac atc att ccg tac ttc gtc tct cgc aat gat gcg cat gtt			835
Gly Gly Asp Ile Ile Pro Tyr Phe Val Ser Arg Asn Asp Ala His Val			
230	235	240	245
tat gat ttc tcc gga aac att gtt cct ggc gca act gag cgt gac aag			883
Tyr Asp Phe Ser Gly Asn Ile Val Pro Gly Ala Thr Glu Arg Asp Lys			
250	255	260	
ggc tac tgg cgc gac gtc ggt acc att gat gcg ttc tac gag tgc cac			931
Gly Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala Phe Tyr Glu Cys His			
265	270	275	
atg gac ctg att tcc gtg cac cca atc ttc aat ctg tat aac tct gag			979
Met Asp Leu Ile Ser Val His Pro Ile Phe Asn Leu Tyr Asn Ser Glu			
280	285	290	
tgg cca atc cac acg acc tct gaa ggt aac ttg cct ccg gct aag ttc			1027
Trp Pro Ile His Thr Thr Ser Glu Gly Asn Leu Pro Pro Ala Lys Phe			
295	300	305	
gtt cgg ggc ggt atc gcg cag tcg tcg atg gtg tct tca ggt tcc atc			1075
Val Arg Gly Gly Ile Ala Gln Ser Ser Met Val Ser Ser Gly Ser Ile			
310	315	320	325
att tct gct ggg act gtt cgc aac tcc gtg ctg tcc aac aac gtt gtc			1123
Ile Ser Ala Gly Thr Val Arg Asn Ser Val Leu Ser Asn Asn Val Val			
330	335	340	
gtc gaa gag ggc gca acg gtg gaa ggt gca gtg ctg atg cca ggc gtg			1171
Val Glu Glu Gly Ala Thr Val Glu Gly Ala Val Leu Met Pro Gly Val			
345	350	355	
cgc atc ggt aag ggt gct gtt gtc cgc cat gcg att ctg gac aag aac			1219
Arg Ile Gly Lys Gly Ala Val Val Arg His Ala Ile Leu Asp Lys Asn			
360	365	370	
gtg gtt gtc cgc gac gga gag ctc atc ggt gtc gac caa gtg cgc gat			1267
Val Val Val Arg Asp Gly Glu Leu Ile Gly Val Asp Gln Val Arg Asp			
375	380	385	
gcg cag cgc ttc aag gtg agc gcc ggc ggc gtc gtg gtt gtc ggt aag			1315
Ala Gln Arg Phe Lys Val Ser Ala Gly Gly Val Val Val Val Gly Lys			
390	395	400	405
aac cag gta gtc taaacgggaa agggacctta aaa			1350
Asn Gln Val Val			

&lt;210&gt; 276

&lt;211&gt; 409

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 276

Met Val Lys Gly Val Lys Gly Arg Pro Asn Val Leu Ala Ile Val Leu  
 1 5 10 15  
 Ala Gly Gly Glu Gly Lys Arg Leu Phe Pro Leu Thr Glu Asp Arg Ala  
 20 25 30  
 Lys Pro Ala Val Pro Phe Gly Gly Thr Tyr Arg Leu Ile Asp Phe Val  
 35 40 45  
 Leu Ser Asn Leu Val Asn Ser Gly Phe Leu Lys Ile Ala Val Leu Thr  
 50 55 60  
 Gln Tyr Lys Ser His Ser Leu Asp Arg His Ile Ser Leu Ser Trp Asn  
 65 70 75 80  
 Val Ser Gly Pro Thr Gly Gln Tyr Ile Ala Ser Val Pro Ala Gln Gln  
 85 90 95  
 Arg Leu Gly Lys Arg Trp Phe Thr Gly Ser Ala Asp Ala Ile Leu Gln  
 100 105 110  
 Ser Leu Asn Leu Ile Ser Asp Glu Lys Pro Asp Tyr Val Ile Val Phe  
 115 120 125  
 Gly Ala Asp His Val Tyr Arg Met Asp Pro Ser Gln Met Leu Asp Glu  
 130 135 140  
 His Ile Ala Ser Gly Arg Ala Val Ser Val Ala Gly Ile Arg Val Pro  
 145 150 155 160  
 Arg Glu Glu Ala Thr Ala Phe Gly Cys Ile Gln Ser Asp Val Asp Gly  
 165 170 175  
 Asn Ile Thr Glu Phe Leu Glu Lys Pro Ala Asp Pro Pro Gly Thr Pro  
 180 185 190  
 Asp Asp Pro Asp Met Thr Tyr Ala Ser Met Gly Asn Tyr Ile Phe Thr  
 195 200 205  
 Thr Glu Ala Leu Ile Gln Ala Leu Lys Asp Asp Glu Asn Asn Glu Asn  
 210 215 220  
 Ser Asp His Asp Met Gly Gly Asp Ile Ile Pro Tyr Phe Val Ser Arg  
 225 230 235 240  
 Asn Asp Ala His Val Tyr Asp Phe Ser Gly Asn Ile Val Pro Gly Ala  
 245 250 255  
 Thr Glu Arg Asp Lys Gly Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala  
 260 265 270  
 Phe Tyr Glu Cys His Met Asp Leu Ile Ser Val His Pro Ile Phe Asn  
 275 280 285  
 Leu Tyr Asn Ser Glu Trp Pro Ile His Thr Thr Ser Glu Gly Asn Leu  
 290 295 300  
 Pro Pro Ala Lys Phe Val Arg Gly Gly Ile Ala Gln Ser Ser Met Val  
 305 310 315 320  
 Ser Ser Gly Ser Ile Ile Ser Ala Gly Thr Val Arg Asn Ser Val Leu

	325		330		335
Ser Asn Asn Val Val Val Glu Glu Gly Ala Thr Val Glu Gly Ala Val	340		345		350
Leu Met Pro Gly Val Arg Ile Gly Lys Gly Ala Val Val Arg His Ala	355		360		365
Ile Leu Asp Lys Asn Val Val Val Arg Asp Gly Glu Leu Ile Gly Val	370		375		380
Asp Gln Val Arg Asp Ala Gln Arg Phe Lys Val Ser Ala Gly Gly Val	385		390		395
Val Val Val Gly Lys Asn Gln Val Val	405				400

&lt;210&gt; 277

&lt;211&gt; 903

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(880)

&lt;223&gt; RXN00014

&lt;400&gt; 277

```

catcaaagtg accgccggcg gcgtcgaaatg gtccgttgca ggaaacgcgg aagcagttag 60
tgagatctcc gaaacttta ggcactaga ctaacaacac atg agc aaa tat gca 115
                                         Met Ser Lys Tyr Ala
                                         1 5
gac gat tta gcc tta gcc ctc gaa ctt gcc gaa ctt gcc gat tcc atc 163
Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu Leu Ala Asp Ser Ile
                        10 15 20
acc ctc gac cgc ttc gaa gcc tct gac ctg gaa gta tcc tcc aag cca 211
Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu Val Ser Ser Lys Pro
                        25 30 35
gac atg act ccc gtc agc gat gcc gac ctg gcg acc gaa gaa gca ctc 259
Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala Thr Glu Glu Ala Leu
                        40 45 50
cgt gag aaa atc gcc acc gcc cgc ccc gcc gac tcc atc ctc ggt gaa 307
Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp Ser Ile Leu Gly Glu
                        55 60 65
gaa ttc ggt ggc gac gta gaa ttc agc ggc cgc cag tgg atc atc gac 355
Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg Gln Trp Ile Ile Asp
                        70 75 80 85
ccc atc gac ggc acc aaa aac tac gtc cgc ggc gtc ccc gta tgg gca 403
Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly Val Pro Val Trp Ala
                        90 95 100
acc ctg atc gcg ctg ctc gac aac ggc aaa ccc gtc gca ggt gtc atc 451
Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro Val Ala Gly Val Ile

```

105	110	115	
tcc gca ccc gca ctg gct agg cgt tgg tgg gca tcc gaa ggg gcc ggc			499
Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala Ser Glu Gly Ala Gly			
120	125	130	
gca tgg cgc acc ttc aac ggc agc tcc cca cgc aaa ctg tcc gtg tcc			547
Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg Lys Leu Ser Val Ser			
135	140	145	
cag gtg tcc aag ctt gac gac gcc tcc ctc tcc ttc tcc tcc ctc tcc			595
Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser Phe Ser Ser Leu Ser			
150	155	160	165
ggc tgg gcc gaa cga gat ttg cgc gat cag ttc gtc tcc cta act gat			643
Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe Val Ser Leu Thr Asp			
	170	175	180
acc acc tgg cga ctc cgc ggc tac ggc gac ttc ttc tcc tac tgc ctc			691
Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe Phe Ser Tyr Cys Leu			
	185	190	195
gtc gcc gaa ggt gcc gtc gat atc gcc gct gaa cca gaa gtc agc ctc			739
Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu Pro Glu Val Ser Leu			
200	205	210	
tgg gat ctt gct ccc ctg tcc atc ctg gtc acc gaa gcc gga gga aag			787
Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr Glu Ala Gly Gly Lys			
215	220	225	
ttc acc tca ctg gct ggc gtc gat gga cca cac ggt ggc gat gca gta			835
Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His Gly Gly Asp Ala Val			
230	235	240	245
gcc acc aac ggc atc ctg cac gat gag acg ctg gat cgt tta aaa			880
Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu Asp Arg Leu Lys			
	250	255	260
tagactcccg gggttttgctt ggt			903
<210> 278			
<211> 260			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 278			
Met Ser Lys Tyr Ala Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu			
1	5	10	15
Leu Ala Asp Ser Ile Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu			
	20	25	30
Val Ser Ser Lys Pro Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala			
	35	40	45
Thr Glu Glu Ala Leu Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp			
	50	55	60
Ser Ile Leu Gly Glu Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg			
65	70	75	80

[illegible]

```
<210> 279
<211> 903
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(880)  
<223> FRXA00014
```

```

<400> 279
catcaaagtg accgccggcg gcgtcgaatg gtccgttgca ggaaacgcgg aagcagttag 60

tgagatctcc gaaacttta ggcactaga ctgcaaacac atg agc aaa tat gca 115
Met Ser Lys Tyr Ala
1 5

gac gat tta gcc tta gcc ctc gaa ctc gcc gaa ctt gcc gat tcc atc 163
Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu Leu Ala Asp Ser Ile
10 15 20

acc ctc gac cgc ttc gaa gcc tct gac ctg gaa gta tcc tcc aag cca 211
Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu Val Ser Ser Lys Pro

```

25	30	35	
gac atg act ccc gtc agc gat gcc gac ctg gcg acc gaa gaa gca ctc Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala Thr Glu Glu Ala Leu 40 45 50			259
cgc gag aaa atc gcc acc gcc cgc ccc gcc gac tcc atc ctc ggt gaa Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp Ser Ile Leu Gly Glu 55 60 65			307
gaa ttc ggt ggc gac gta gaa ttc agc ggc cgc cag tgg atc atc gac Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg Gln Trp Ile Ile Asp 70 75 80 85			355
ccc atc gac ggc acc aaa aac tac gtc cgc ggc gtc ccc gta tgg gca Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly Val Pro Val Trp Ala 90 95 100			403
acc ctg atc gcg ctg ctc gac aac ggc aaa ccc gtc gca ggt gtc atc Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro Val Ala Gly Val Ile 105 110 115			451
tcc gca ccc gca ctg gct agg cgt tgg tgg gca tcc gaa ggg gcc ggc Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala Ser Glu Gly Ala Gly 120 125 130			499
gca tgg cgc acc ttc aac ggc agc tcc cca cgc aaa ctg tcc gtg tcc Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg Lys Leu Ser Val Ser 135 140 145			547
cag gtg tcc aag ctt gac gac gcc tcc ctc tcc ttc tcc tcc ctc tcc Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser Phe Ser Ser Leu Ser 150 155 160 165			595
ggc tgg gcc gaa cga gat ttg cgc gat cag ttc gtc tcc cta act gat Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe Val Ser Leu Thr Asp 170 175 180			643
acc acc tgg cga ctc cgc ggc tac ggc gac ttc ttc tcc tac tgc ctc Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe Phe Ser Tyr Cys Leu 185 190 195			691
gtc gcc gaa ggt gcc gtc gat atc gcc gct gaa cca gaa gtc agc ctc Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu Pro Glu Val Ser Leu 200 205 210			739
tgg gat ctt gct ccc ctg tcc atc ctg gtc acc gaa gcc gga gga aag Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr Glu Ala Gly Gly Lys 215 220 225			787
ttc acc tca ctg gct ggc gtc gat gga cca cac ggt ggc gat gca gta Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His Gly Gly Asp Ala Val 230 235 240 245			835
gcc acc aac ggc atc ctg cac gat gag acg ctg gat cgt tta aaa Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu Asp Arg Leu Lys 250 255 260			880
tagactcccg gggttttgctt ggt			903



&lt;210&gt; 280

&lt;211&gt; 260

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 280

Met Ser Lys Tyr Ala Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu  
 1 5 10 15

Leu Ala Asp Ser Ile Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu  
 20 25 30

Val Ser Ser Lys Pro Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala  
 35 40 45

Thr Glu Glu Ala Leu Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp  
 50 55 60

Ser Ile Leu Gly Glu Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg  
 65 70 75 80

Gln Trp Ile Ile Asp Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly  
 85 90 95

Val Pro Val Trp Ala Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro  
 100 105 110

Val Ala Gly Val Ile Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala  
 115 120 125

Ser Glu Gly Ala Gly Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg  
 130 135 140

Lys Leu Ser Val Ser Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser  
 145 150 155 160

Phe Ser Ser Leu Ser Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe  
 165 170 175

Val Ser Leu Thr Asp Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe  
 180 185 190

Phe Ser Tyr Cys Leu Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu  
 195 200 205

Pro Glu Val Ser Leu Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr  
 210 215 220

Glu Ala Gly Gly Lys Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His  
 225 230 235 240

Gly Gly Asp Ala Val Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu  
 245 250 255

Asp Arg Leu Lys  
 260

&lt;210&gt; 281

&lt;211&gt; 978

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(955)

&lt;223&gt; RXA01570

&lt;400&gt; 281

```

cactgaactc cgtttttgat ctcggcaaaa tcgaagccac cggatttagc gcaccgacct 60

ggcagaccgc cctcaacgac tacctcaagg aactctcaaa gtg aaa ggc atc atc 115
                               Val Lys Gly Ile Ile
                               1 5

ctc gca ggt ggc tcc ggc acc cgg ctc tac ccc atc acc aag ggc atc 163
Leu Ala Gly Gly Ser Gly Thr Arg Leu Tyr Pro Ile Thr Lys Gly Ile
                               10 15 20

tcc aag caa ctg atg ccg att tac gac aaa ccc atg gtc tac tac cca 211
Ser Lys Gln Leu Met Pro Ile Tyr Asp Lys Pro Met Val Tyr Tyr Pro
                               25 30 35

ctg acc acg ctc att cag gcc ggc atc aaa gac atc ctg att atc acc 259
Leu Thr Thr Leu Ile Gln Ala Gly Ile Lys Asp Ile Leu Ile Ile Thr
                               40 45 50

acc cct gaa gac agc gcc tcc ttt gaa cgc ttg ctt ggc gac ggc tcc 307
Thr Pro Glu Asp Ser Ala Ser Phe Glu Arg Leu Leu Gly Asp Gly Ser
                               55 60 65

tcc tgg ggc atc aac ctc acc tac gcc gtc caa ccc tcc ccc gac gga 355
Ser Trp Gly Ile Asn Leu Thr Tyr Ala Val Gln Pro Ser Pro Asp Gly
70 75 80 85

cta gcc caa gca ttc atc atc ggc gag gaa ttc atc ggt gac gac gac 403
Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe Ile Gly Asp Asp Asp
90 95 100

gtc gcg ttg gtg ctt ggc gat aac atc ttc gac ggc gca caa ctt ggc 451
Val Ala Leu Val Leu Gly Asp Asn Ile Phe Asp Gly Ala Gln Leu Gly
105 110 115

cac gca cta aag cag tgc tcc aac ccc gac ggt ggc att gtc ttt gct 499
His Ala Leu Lys Gln Cys Ser Asn Pro Asp Gly Gly Ile Val Phe Ala
120 125 130

tat gag gtc tcc gat cct gag cgt tat ggc gtg gtg gaa ttt gat gct 547
Tyr Glu Val Ser Asp Pro Glu Arg Tyr Gly Val Val Glu Phe Asp Ala
135 140 145

gct aat aag gcg gtg tct att gaa gaa aag ccc acc gcg cca aaa tcc 595
Ala Asn Lys Ala Val Ser Ile Glu Glu Lys Pro Thr Ala Pro Lys Ser
150 155 160 165

aac ttt gcc gtg gta gga cta tat ttc tac gac aat cgc gtg gtg gac 643
Asn Phe Ala Val Val Gly Leu Tyr Phe Tyr Asp Asn Arg Val Val Asp
170 175 180

atc gcc aag tca atc aag cct tcc tcg cgt ggc gaa ctg gaa atc acc 691
Ile Ala Lys Ser Ile Lys Pro Ser Ser Arg Gly Glu Leu Glu Ile Thr
185 190 195

```

tcc gtt aac gat gcc tac ctc cag caa ggt gct tta act gtg cag cgc 739  
 Ser Val Asn Asp Ala Tyr Leu Gln Gln Gly Ala Leu Thr Val Gln Arg  
           200                                  205                                  210

ctg gac cgt ggc gat gtc tgg tta gat acc ggc aca atc gat tcc atg 787  
 Leu Asp Arg Gly Asp Val Trp Leu Asp Thr Gly Thr Ile Asp Ser Met  
           215                                  220                                  225

tcc gag gcg tct tcc tat gtt gag gtc ctg caa aaa cgt acc ggc aac 835  
 Ser Glu Ala Ser Ser Tyr Val Glu Val Leu Gln Lys Arg Thr Gly Asn  
           230                                  235                                  240                                  245

atc atc gga tcc ccc gaa gtc gct gcg tac cgc gaa ggt ttc atc aca 883  
 Ile Ile Gly Ser Pro Glu Val Ala Ala Tyr Arg Glu Gly Phe Ile Thr  
                                   250                                  255                                  260

gct gaa gaa ctc aca gtg ctt ggt gag gaa ctg aag aaa tca ggc tac 931  
 Ala Glu Glu Leu Thr Val Leu Gly Glu Glu Leu Lys Lys Ser Gly Tyr  
                                   265                                  270                                  275

gga aac tac ctg ctg aga gct ttg taatttacgg tgtggtgtg gag 978  
 Gly Asn Tyr Leu Leu Arg Ala Leu  
                                   280                                  285

&lt;210&gt; 282

&lt;211&gt; 285

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 282

Val Lys Gly Ile Ile Leu Ala Gly Gly Ser Gly Thr Arg Leu Tyr Pro  
   1                                  5                                  10                                  15

Ile Thr Lys Gly Ile Ser Lys Gln Leu Met Pro Ile Tyr Asp Lys Pro  
           20                                  25                                  30

Met Val Tyr Tyr Pro Leu Thr Thr Leu Ile Gln Ala Gly Ile Lys Asp  
           35                                  40                                  45

Ile Leu Ile Ile Thr Thr Pro Glu Asp Ser Ala Ser Phe Glu Arg Leu  
           50                                  55                                  60

Leu Gly Asp Gly Ser Ser Trp Gly Ile Asn Leu Thr Tyr Ala Val Gln  
           65                                  70                                  75                                  80

Pro Ser Pro Asp Gly Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe  
           85                                  90                                  95

Ile Gly Asp Asp Asp Val Ala Leu Val Leu Gly Asp Asn Ile Phe Asp  
           100                                  105                                  110

Gly Ala Gln Leu Gly His Ala Leu Lys Gln Cys Ser Asn Pro Asp Gly  
           115                                  120                                  125

Gly Ile Val Phe Ala Tyr Glu Val Ser Asp Pro Glu Arg Tyr Gly Val  
           130                                  135                                  140

Val Glu Phe Asp Ala Ala Asn Lys Ala Val Ser Ile Glu Glu Lys Pro  
           145                                  150                                  155                                  160

Thr Ala Pro Lys Ser Asn Phe Ala Val Val Gly Leu Tyr Phe Tyr Asp  
 165 170 175  
 Asn Arg Val Val Asp Ile Ala Lys Ser Ile Lys Pro Ser Ser Arg Gly  
 180 185 190  
 Glu Leu Glu Ile Thr Ser Val Asn Asp Ala Tyr Leu Gln Gln Gly Ala  
 195 200 205  
 Leu Thr Val Gln Arg Leu Asp Arg Gly Asp Val Trp Leu Asp Thr Gly  
 210 215 220  
 Thr Ile Asp Ser Met Ser Glu Ala Ser Ser Tyr Val Glu Val Leu Gln  
 225 230 235 240  
 Lys Arg Thr Gly Asn Ile Ile Gly Ser Pro Glu Val Ala Ala Tyr Arg  
 245 250 255  
 Glu Gly Phe Ile Thr Ala Glu Glu Leu Thr Val Leu Gly Glu Glu Leu  
 260 265 270  
 Lys Lys Ser Gly Tyr Gly Asn Tyr Leu Leu Arg Ala Leu  
 275 280 285

&lt;210&gt; 283

&lt;211&gt; 891

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(868)

&lt;223&gt; RXA02666

&lt;400&gt; 283

gctcggcgac gaggaagaga agaaggacgc attcgacgac ttcgacgatt ccgacgtgga 60

tcttgacgat ctgagcttcg acgacgaaga ttagacgccc atg tcg tct aca cga 115  
 Met Ser Ser Thr Arg  
 1 5

atc ccc gtc atc gca ctc ctc gcg gcg gcg ggg cgc gga acc cgc ctc 163  
 Ile Pro Val Ile Ala Leu Leu Ala Ala Ala Gly Arg Gly Thr Arg Leu  
 10 15 20

ggc gga ccc atc ccc aaa gca ttc gtc acg ttg cgt gaa cgc aca ctt 211  
 Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu Arg Glu Arg Thr Leu  
 25 30 35

tta gag cgc tcg ctc caa gcc atg ctc acc tcc gaa agc gtc gac gaa 259  
 Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser Glu Ser Val Asp Glu  
 40 45 50

atc atc atc ctc gtc agc ccc gac atg gaa acc tac gcc cgc gat ttg 307  
 Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr Tyr Ala Arg Asp Leu  
 55 60 65

ctg cgc aaa cgc ggt ctt ttg aac gac ccc gaa ggg gta cgc gta cgg 355  
 Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu Gly Val Arg Val Arg

70	75	80	85	
ctc gtg cac ggc ggc ggg gag cgc gcg gac tcg gtc tgg gca ggc ctt				403
Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser Val Trp Ala Gly Leu	90	95	100	
cag gca att tcg ctt gac gac gcc acc ccc gat gca att gtc tta atc				451
Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp Ala Ile Val Leu Ile	105	110	115	
cac gac agc gcc cga gcg ctc aca cca ccc ggc atg att gcg cgc gtg				499
His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly Met Ile Ala Arg Val	120	125	130	
gtg cgc aaa gtc cac gaa ggc gcc acc gca gtc atc cca gta ctg cca				547
Val Arg Lys Val His Glu Gly Ala Thr Ala Val Ile Pro Val Leu Pro	135	140	145	
gta tcg gac acc atc aaa cga gtg tcc cct gat ggc gga gta gtt gtc				595
Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp Gly Gly Val Val Val	150	155	160	165
gac aca ccc aac cgt gca gaa ctt cgc gcc gtc caa acc cca caa ggc				643
Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val Gln Thr Pro Gln Gly	170	175	180	
ttc ctg ctg tcc gaa ctt gtt gca gcg aat gag aaa ttc ttc gcc gac				691
Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu Lys Phe Phe Ala Asp	185	190	195	
ccc aac cca ggc ttc atc cca acc gat gac gcc agc ttg atg gaa tgg				739
Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala Ser Leu Met Glu Trp	200	205	210	
tac ggc gca gat gta gtc tgc gta caa ggc gac cca atg gcg ttt aaa				787
Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp Pro Met Ala Phe Lys	215	220	225	
gta aca acc ccc att gat atg atg ctg gca caa cgc atc acc gac gaa				835
Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln Arg Ile Thr Asp Glu	230	235	240	245
gcc gaa ccc aca ata ttt gag gta cca ggt gac taacc caatc atccccgcg				888
Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp	250	255		
tag				891
<210> 284				
<211> 256				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 284				
Met Ser Ser Thr Arg Ile Pro Val Ile Ala Leu Leu Ala Ala Ala Gly	1	5	10	15
Arg Gly Thr Arg Leu Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu	20	25	30	

```
<210> 285
<211> 1056
<212> DNA
<213> Corynebacterium glutamicum
```

```

<400> 285
cccgttcatg ctgggctttg gtgcggtgat ggcaactatt tgtctgatca ttgtgagttt 60

tagtgcacgc cgattctgag aaacaactaa agtgagccac atg cgc aca gta gtt    115
               Met Arg Thr Val Val

```

1															5	
acc ggc ggt gcc ggc ttc atc gga tcc cat ctc gtt gac ctt ttg atc																163
Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Asp Leu Leu Ile																
10					15					20						
aag gaa ggc cac gag gtc gtt gtg atc gat aac ctc tcc cgc gga cgc																211
Lys Glu Gly His Glu Val Val Val Ile Asp Asn Leu Ser Arg Gly Arg																
25					30					35						
ctg gag aat ctc tcc gat gcg gaa gcc acc gga aaa ctc acc ttt gtg																259
Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly Lys Leu Thr Phe Val																
40					45					50						
gaa gcc gat ctt ctc gac gtt gat ttc aac gag ttt cta gga acc cac																307
Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu Phe Leu Gly Thr His																
55					60					65						
aag cct gag gtt att ttc cac ctg gca gcg caa atc gat gtg cgc cac																355
Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln Ile Asp Val Arg His																
70					75					80					85	
tct gtt gta gat cct ctt cac gac gcc gaa acc aac att ttg tcc acc																403
Ser Val Val Asp Pro Leu His Asp Ala Glu Thr Asn Ile Leu Ser Thr																
90					95					100						
atc cgc atc gct gac gct gcc cgc cag cac ggt gtt cgc aag gtt gtc																451
Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly Val Arg Lys Val Val																
105					110					115						
ttt acc tcc tca ggc ggt tcc att tac ggt gag cct tcg gaa ttc cca																499
Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu Pro Ser Glu Phe Pro																
120					125					130						
gtt gat gaa acc gtg cca gtg gat cca cat tcc cct tat gcg gca tcc																547
Val Asp Glu Thr Val Pro Val Asp Pro His Ser Pro Tyr Ala Ala Ser																
135					140					145						
aag gtg tcc ggt gaa att tac ctg aac acc ttc cgc cac ctg tac ggc																595
Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe Arg His Leu Tyr Gly																
150					155					160					165	
tta gac tgt tct cac atc gca ccg gca aat gtt tac ggc cca cgc caa																643
Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val Tyr Gly Pro Arg Gln																
170					175					180						
gat cca cac ggt gaa gca gga gtt gtg gcc att ttc gcg ctg cga ctt																691
Asp Pro His Gly Glu Ala Gly Val Val Ala Ile Phe Ala Leu Arg Leu																
185					190					195						
ctg gga ggc ctg gac acc aag gta ttc ggc gac ggc gga aac acc cgc																739
Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp Gly Gly Asn Thr Arg																
200					205					210						
gac tac gtc tac gtc ggt gac gta gtt cgt gct ttc tac ctg gct tct																787
Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala Phe Tyr Leu Ala Ser																
215					220					225						
ggg gaa atc ggt ggg gga gag cgc ttc aac att ggc acc tct gtg gaa																835
Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile Gly Thr Ser Val Glu																
230					235					240					245	

acc tct gac cgc cag ctg cac acc ctc gtg gcc act gcg gca ggt tcc 883  
 Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala Thr Ala Ala Gly Ser  
                   250                  255                  260

aaa gat gat cct gaa tat gca cct gca cgt ctc ggc gat gtg cca cgc 931  
 Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu Gly Asp Val Pro Arg  
                   265                  270                  275

agt gca ctc agc ttc ggc aag gcc aaa gag gtg ctt ggt tgg gag cct 979  
 Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val Leu Gly Trp Glu Pro  
                   280                  285                  290

gag gtg aac atc gaa caa ggt gtg gcc aag act gtg gag tac ttc cgc 1027  
 Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr Val Glu Tyr Phe Arg  
                   295                  300                  305

act cac taggggaaaa tccaccacaa atc 1056  
 Thr His  
 310

&lt;210&gt; 286

&lt;211&gt; 311

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 286

Met Arg Thr Val Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu  
   1                  5                  10                  15

Val Asp Leu Leu Ile Lys Glu Gly His Glu Val Val Val Ile Asp Asn  
                   20                  25                  30

Leu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly  
                   35                  40                  45

Lys Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu  
                   50                  55                  60

Phe Leu Gly Thr His Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln  
                   65                  70                  75                  80

Ile Asp Val Arg His Ser Val Val Asp Pro Leu His Asp Ala Glu Thr  
                   85                  90                  95

Asn Ile Leu Ser Thr Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly  
                   100                  105                  110

Val Arg Lys Val Val Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu  
                   115                  120                  125

Pro Ser Glu Phe Pro Val Asp Glu Thr Val Pro Val Asp Pro His Ser  
                   130                  135                  140

Pro Tyr Ala Ala Ser Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe  
                   145                  150                  155                  160

Arg His Leu Tyr Gly Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val  
                   165                  170                  175



Tyr Gly Pro Arg Gln Asp Pro His Gly Glu Ala Gly Val Val Ala Ile  
 180 185 190  
 Phe Ala Leu Arg Leu Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp  
 195 200 205  
 Gly Gly Asn Thr Arg Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala  
 210 215 220  
 Phe Tyr Leu Ala Ser Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile  
 225 230 235 240  
 Gly Thr Ser Val Glu Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala  
 245 250 255  
 Thr Ala Ala Gly Ser Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu  
 260 265 270  
 Gly Asp Val Pro Arg Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val  
 275 280 285  
 Leu Gly Trp Glu Pro Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr  
 290 295 300  
 Val Glu Tyr Phe Arg Thr His  
 305 310

<210> 287  
 <211> 1134  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1111)  
 <223> RXA01887

<400> 287  
 catctttaca ggaaaccctt tgacggcatc aatgggtggt atctagtatc tactagaacg 60  
 ttatagtaga acgttctagt aaaacttgga aggatgaaaa atg tca gtc aaa ctt 115  
 Met Ser Val Lys Leu  
 1 5  
 gcc ctc atc ggt gct gga cgc atc gga tca aat cac gca cgc ctg atc 163  
 Ala Leu Ile Gly Ala Gly Arg Ile Gly Ser Asn His Ala Arg Leu Ile  
 10 15 20  
 aca aac cac gtg atc ggc tct gaa ctg gtc gcc gtc gtt gac cca act 211  
 Thr Asn His Val Ile Gly Ser Glu Leu Val Ala Val Val Asp Pro Thr  
 25 30 35  
 ccc aac gca gaa acc ctc gct gat gaa ttg ggc gcc gtt gcg ttc tct 259  
 Pro Asn Ala Glu Thr Leu Ala Asp Glu Leu Gly Ala Val Ala Phe Ser  
 40 45 50  
 aac cca gat gac gtc ctg acc cgc gat gac att gac gcg gtt ttg att 307  
 Asn Pro Asp Asp Val Leu Thr Arg Asp Asp Ile Asp Ala Val Leu Ile  
 55 60 65

gct aca cca gca cga acc cac gcg gat ctc gtg gtc aaa gca gcg gca	355
Ala Thr Pro Ala Arg Thr His Ala Asp Leu Val Val Lys Ala Ala Ala	
70 75 80 85	
gcg ggc aag cac gtg ttt gtg gaa aag ccc atg gcc gtc acc ctc gag	403
Ala Gly Lys His Val Phe Val Glu Lys Pro Met Ala Val Thr Leu Glu	
90 95 100	
gac gca gat cgt gcc atc aac gca gca cgc gaa gca aac act gtc ctg	451
Asp Ala Asp Arg Ala Ile Asn Ala Ala Arg Glu Ala Asn Thr Val Leu	
105 110 115	
cag gtg ggc ttc aat cgt cgt ttc gcg gca ggt ttc gct gca gca cgc	499
Gln Val Gly Phe Asn Arg Arg Phe Ala Ala Gly Phe Ala Ala Ala Arg	
120 125 130	
gca cgc att gac gca ggc gat atc ggc acc cca cag ctg ctt cgt tcc	547
Ala Arg Ile Asp Ala Gly Asp Ile Gly Thr Pro Gln Leu Leu Arg Ser	
135 140 145	
gtg acc cgc gat cca gga cca ttc acc gct gac ccc aac aag atc cct	595
Val Thr Arg Asp Pro Gly Pro Phe Thr Ala Asp Pro Asn Lys Ile Pro	
150 155 160 165	
cag tgg acc atc ttc ctg gaa acc ctc atc cac gat ttc gat gcg ctg	643
Gln Trp Thr Ile Phe Leu Glu Thr Leu Ile His Asp Phe Asp Ala Leu	
170 175 180	
tgc tac ctc aac cca ggc gca acc cca gtg gaa gta acc gct cac gct	691
Cys Tyr Leu Asn Pro Gly Ala Thr Pro Val Glu Val Thr Ala His Ala	
185 190 195	
gat tgc ctc gtc gtt cca gaa gct gct ggc act ggc ttc ctc gac acc	739
Asp Cys Leu Val Val Pro Glu Ala Ala Gly Thr Gly Phe Leu Asp Thr	
200 205 210	
gca gtg gtg act gtc cgt ttt gat aac gga gca att ggt act gca gaa	787
Ala Val Val Thr Val Arg Phe Asp Asn Gly Ala Ile Gly Thr Ala Glu	
215 220 225	
gca agc ttc agc gca gcc tat ggt tat gac gtt cgc ggt gaa gtc ttc	835
Ala Ser Phe Ser Ala Ala Tyr Gly Tyr Asp Val Arg Gly Glu Val Phe	
230 235 240 245	
gga tcc aag ggc atg atg acc gca ggc gac gcg cgc gca acc aac atg	883
Gly Ser Lys Gly Met Met Thr Ala Gly Asp Ala Arg Ala Thr Asn Met	
250 255 260	
act ttc tac ggc gct gag ggc atc gcg gct gcc acc tca cgc gcg gat	931
Thr Phe Tyr Gly Ala Glu Gly Ile Ala Ala Ala Thr Ser Arg Ala Asp	
265 270 275	
acc gat ctg ctc tcc gat gct tac cga gct gaa ttc caa gct ttc gtc	979
Thr Asp Leu Leu Ser Asp Ala Tyr Arg Ala Glu Phe Gln Ala Phe Val	
280 285 290	
gac tcc atc cgt acc aac acc cct tcc aag gtt cca ggc gaa gct gca	1027
Asp Ser Ile Arg Thr Asn Thr Pro Ser Lys Val Pro Gly Glu Ala Ala	
295 300 305	
cgc acc gca cta ctc atc gca ctc ggc gcc atc cga agc gta gaa acc	1075

Arg Thr Ala Leu Leu Ile Ala Leu Gly Ala Ile Arg Ser Val Glu Thr  
 310 315 320 325  
  
 ggc gca acc atc aac ctt gct gaa agc atc gag gtt taaccatgac 1121  
 Gly Ala Thr Ile Asn Leu Ala Glu Ser Ile Glu Val  
 330 335  
  
 ttttaaactc gca 1134  
  
 <210> 288  
 <211> 337  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
  
 <400> 288  
 Met Ser Val Lys Leu Ala Leu Ile Gly Ala Gly Arg Ile Gly Ser Asn  
 1 5 10 15  
 His Ala Arg Leu Ile Thr Asn His Val Ile Gly Ser Glu Leu Val Ala  
 20 25 30  
 Val Val Asp Pro Thr Pro Asn Ala Glu Thr Leu Ala Asp Glu Leu Gly  
 35 40 45  
 Ala Val Ala Phe Ser Asn Pro Asp Asp Val Leu Thr Arg Asp Asp Ile  
 50 55 60  
 Asp Ala Val Leu Ile Ala Thr Pro Ala Arg Thr His Ala Asp Leu Val  
 65 70 75 80  
 Val Lys Ala Ala Ala Gly Lys His Val Phe Val Glu Lys Pro Met  
 85 90 95  
 Ala Val Thr Leu Glu Asp Ala Asp Arg Ala Ile Asn Ala Ala Arg Glu  
 100 105 110  
 Ala Asn Thr Val Leu Gln Val Gly Phe Asn Arg Arg Phe Ala Ala Gly  
 115 120 125  
 Phe Ala Ala Ala Arg Ala Arg Ile Asp Ala Gly Asp Ile Gly Thr Pro  
 130 135 140  
 Gln Leu Leu Arg Ser Val Thr Arg Asp Pro Gly Pro Phe Thr Ala Asp  
 145 150 155 160  
 Pro Asn Lys Ile Pro Gln Trp Thr Ile Phe Leu Glu Thr Leu Ile His  
 165 170 175  
 Asp Phe Asp Ala Leu Cys Tyr Leu Asn Pro Gly Ala Thr Pro Val Glu  
 180 185 190  
 Val Thr Ala His Ala Asp Cys Leu Val Val Pro Glu Ala Ala Gly Thr  
 195 200 205  
 Gly Phe Leu Asp Thr Ala Val Val Thr Val Arg Phe Asp Asn Gly Ala  
 210 215 220  
 Ile Gly Thr Ala Glu Ala Ser Phe Ser Ala Ala Tyr Gly Tyr Asp Val  
 225 230 235 240

Arg Gly Glu Val Phe Gly Ser Lys Gly Met Met Thr Ala Gly Asp Ala  
 245 250 255

Arg Ala Thr Asn Met Thr Phe Tyr Gly Ala Glu Gly Ile Ala Ala Ala  
 260 265 270

Thr Ser Arg Ala Asp Thr Asp Leu Leu Ser Asp Ala Tyr Arg Ala Glu  
 275 280 285

Phe Gln Ala Phe Val Asp Ser Ile Arg Thr Asn Thr Pro Ser Lys Val  
 290 295 300

Pro Gly Glu Ala Ala Arg Thr Ala Leu Leu Ile Ala Leu Gly Ala Ile  
 305 310 315 320

Arg Ser Val Glu Thr Gly Ala Thr Ile Asn Leu Ala Glu Ser Ile Glu  
 325 330 335

Val

<210> 289  
 <211> 996  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(973)  
 <223> RXN00013

<400> 289  
 ctgcagaaaa ttcgggacgc atgattgcac atattaccgc caccgattgt gattcttaga 60

acgccacctt attcagcaca cttggccgcac ggcattgcaca atg gaa ggc atg act 115  
 Met Glu Gly Met Thr  
 1 5

aat cca gag cag aca cat ccc gct gca agc ctc gaa gac atg atc aaa 163  
 Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu Glu Asp Met Ile Lys  
 10 15 20

acc atc aca aag acc ttc gtg att gct cac gat cag gat tct gat gag 211  
 Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp Gln Asp Ser Asp Glu  
 25 30 35

cat ctt gcg cag gca ctg gtg tac aac gct gga cgt ttg gca tgg cgc 259  
 His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly Arg Leu Ala Trp Arg  
 40 45 50

atg cgc gaa aac ggt gtg gat acg gat tac aag act tct gtg tct gat 307  
 Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys Thr Ser Val Ser Asp  
 55 60 65

gtg gtc acg gat gcc gat cgt gcg gcc gag gcc ttc gtc gca ggc gtt 355  
 Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala Phe Val Ala Gly Val  
 70 75 80 85

ctt gaa gcg ttg cgg cct gag gac ggc gtg ctt ggc gag gaa ggc gcg 403  
 Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu Gly Glu Glu Gly Ala

	90	95	100	
	gac cgg gcg tcg aaa agc gga aaa acc tgg gtc atc gac ccg gtt gat			451
	Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val Ile Asp Pro Val Asp			
	105	110	115	
	ggc acc tac aac ttc acc cag ggc tca gat tat tgg tgc tcg gcg ctc			499
	Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr Trp Cys Ser Ala Leu			
	120	125	130	
	gcg ctg gtc gag ggc gat cca tcc gcg cca tcg cgc gtg ctt ttc ggc			547
	Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser Arg Val Leu Phe Gly			
	135	140	145	
	gcc gta cac cgc cca gcc atg ggt tat acg tgg ttc ggt ggc ccg gga			595
	Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp Phe Gly Gly Pro Gly			
	150	155	160	165
	atc cgc acc acg ctc gac ggc aag gag cta gat ttg ctt gtc gac gcc			643
	Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp Leu Leu Val Asp Ala			
	170	175	180	
	ccc ctc aat caa atc tcc ctg gcc acc tac atc cac ccg tca cgc atc			691
	Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile His Pro Ser Arg Ile			
	185	190	195	
	gcg gaa cct gat att caa aag gcg tgg atg agc gtt gcc acc cac cct			739
	Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser Val Ala Thr His Pro			
	200	205	210	
	gca acg ctg cgc atg ttc ggc gcc ggc tcc atc gat ttg gcc aac atc			787
	Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile Asp Leu Ala Asn Ile			
	215	220	225	
	gcc gac ggc agc atg ggc gca tgg gtg cag cac agc gtc gca gat tgg			835
	Ala Asp Gly Ser Met Gly Ala Trp Val Gln His Ser Val Ala Asp Trp			
	230	235	240	245
	gac tgg cta ccc ggc cgc gca ctc atc gaa ggc gtc ggc gga gca tgc			883
	Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly Val Gly Gly Ala Cys			
	250	255	260	
	atc aaa gtg acc gcc ggc ggc gtc gaa tgg tcc gtt gca gga aac gcg			931
	Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser Val Ala Gly Asn Ala			
	265	270	275	
	gaa gca gtt agt gag atc tcc gaa act tta agc gca cta gac			973
	Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser Ala Leu Asp			
	280	285	290	
	taacaacaca tgagcaaata tgc			996

&lt;210&gt; 290

&lt;211&gt; 291

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 290

Met	Glu	Gly	Met	Thr	Asn	Pro	Glu	Gln	Thr	His	Pro	Ala	Ala	Ser	Leu
1				5					10					15	

Glu Asp Met Ile Lys Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp  
                   20                  25                  30  
 Gln Asp Ser Asp Glu His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly  
                   35                  40                  45  
 Arg Leu Ala Trp Arg Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys  
                   50                  55                  60  
 Thr Ser Val Ser Asp Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala  
                   65                  70                  75                  80  
 Phe Val Ala Gly Val Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu  
                   85                  90                  95  
 Gly Glu Glu Gly Ala Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val  
                   100                  105                  110  
 Ile Asp Pro Val Asp Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr  
                   115                  120                  125  
 Trp Cys Ser Ala Leu Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser  
                   130                  135                  140  
 Arg Val Leu Phe Gly Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp  
                   145                  150                  155                  160  
 Phe Gly Gly Pro Gly Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp  
                   165                  170                  175  
 Leu Leu Val Asp Ala Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile  
                   180                  185                  190  
 His Pro Ser Arg Ile Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser  
                   195                  200                  205  
 Val Ala Thr His Pro Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile  
                   210                  215                  220  
 Asp Leu Ala Asn Ile Ala Asp Gly Ser Met Gly Ala Trp Val Gln His  
                   225                  230                  235                  240  
 Ser Val Ala Asp Trp Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly  
                   245                  250                  255  
 Val Gly Gly Ala Cys Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser  
                   260                  265                  270  
 Val Ala Gly Asn Ala Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser  
                   275                  280                  285  
 Ala Leu Asp  
                   290

&lt;210&gt; 291

&lt;211&gt; 996

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(973)

&lt;223&gt; FRXA00013

&lt;400&gt; 291

ctgcagaaaa ttcgggacgc atgattgcac atattaccgc caccgattgt gattcttaga 60

acgccacctt attcagcaca cttggccgac ggcattgcaca atg gaa ggc atg act 115  
 Met Glu Gly Met Thr  
 1 5

aat cca gag cag aca cat ccc gct gca agc ctc gaa gac atg atc aaa 163  
 Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu Glu Asp Met Ile Lys  
 10 15 20

acc atc aca aag acc ttc gtg att gct cac gat cag gat tct gat gag 211  
 Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp Gln Asp Ser Asp Glu  
 25 30 35

cat ctt gcg cag gca ctg gtg tac aac gct gga cgt ttg gca tgg cgc 259  
 His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly Arg Leu Ala Trp Arg  
 40 45 50

atg cgc gaa aac ggt gtg gat acg gat tac aag act tct gtg tct gat 307  
 Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys Thr Ser Val Ser Asp  
 55 60 65

gtg gtc acg gat gcc gat cgt gcg gcc gag gcc ttc gtc gca ggc gtt 355  
 Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala Phe Val Ala Gly Val  
 70 75 80 85

ctt gaa gcg ttg cgg cct gag gac ggc gtg ctt ggc gag gaa ggc gcg 403  
 Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu Gly Glu Glu Gly Ala  
 90 95 100

gac cgg gcg tcg aaa agc gga aaa acc tgg gtc atc gac ccg gtt gat 451  
 Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val Ile Asp Pro Val Asp  
 105 110 115

ggc acc tac aac ttc acc cag ggc tca gat tat tgg tgc tcg gcg ctc 499  
 Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr Trp Cys Ser Ala Leu  
 120 125 130

gcg ctg gtc gag ggc gat cca tcc gcg cca tcg cgc gtg ctt ttc ggc 547  
 Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser Arg Val Leu Phe Gly  
 135 140 145

gcc gta cac cgc cca gcc atg ggt tat acg tgg ttc ggt ggc ccg gga 595  
 Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp Phe Gly Gly Pro Gly  
 150 155 160 165

atc cgc acc acg ctc gac ggc aag gag cta gat ttg ctt gtc gac gcc 643  
 Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp Leu Leu Val Asp Ala  
 170 175 180

ccc ctc aat caa atc tcc ctg gcc acc tac atc cac ccg tca cgc atc 691  
 Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile His Pro Ser Arg Ile  
 185 190 195

gcg gaa cct gat att caa aag gcg tgg atg agc gtt gcc acc cac cct 739

Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser Val Ala Thr His Pro  
 200 205 210

gca acg ctg cgc atg ttc ggc gcc ggc tcc atc gat ttg gcc aac atc 787  
 Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile Asp Leu Ala Asn Ile  
 215 220 225

gcc gac ggc agc atg ggc gca tgg gtg cag cac agc gtc gca gat tgg 835  
 Ala Asp Gly Ser Met Gly Ala Trp Val Gln His Ser Val Ala Asp Trp  
 230 235 240 245

gac tgg cta ccc ggc cgc gca ctc atc gaa ggc gtc ggc gga gcg tgc 883  
 Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly Val Gly Gly Ala Cys  
 250 255 260

atc aaa gtg acc gcc ggc ggc gtc gaa tgg tcc gtt gca gga aac gcg 931  
 Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser Val Ala Gly Asn Ala  
 265 270 275

gaa gca gtt agt gag atc tcc gaa act tta agc gca cta gac 973  
 Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser Ala Leu Asp  
 280 285 290

tagcaacaca tgagcaaata tgc 996

&lt;210&gt; 292

&lt;211&gt; 291

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 292

Met Glu Gly Met Thr Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu  
 1 5 10 15

Glu Asp Met Ile Lys Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp  
 20 25 30

Gln Asp Ser Asp Glu His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly  
 35 40 45

Arg Leu Ala Trp Arg Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys  
 50 55 60

Thr Ser Val Ser Asp Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala  
 65 70 75 80

Phe Val Ala Gly Val Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu  
 85 90 95

Gly Glu Glu Gly Ala Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val  
 100 105 110

Ile Asp Pro Val Asp Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr  
 115 120 125

Trp Cys Ser Ala Leu Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser  
 130 135 140

Arg Val Leu Phe Gly Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp  
 145 150 155 160



[illegible]

```
<210> 293
<211> 948
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(925)  
<223> RXA01099
```

```

<400> 293
gggatgaggggc attgattccg tcatcattgg caaggcactt tatgagcaca agttcaccct 60

cgaagagggt ttggctgcag tagaaaagct cggttaatac atg gat gct cgt ggg 115
Met Asp Ala Arg Gly
1 5

atg ttg gcc att gcg gag gcc gtt gta gat gat gcc gaa gcc ctc ttc 163
Met Leu Ala Ile Ala Glu Ala Val Val Asp Asp Ala Glu Ala Leu Phe
10 15 20

atg cag ggc ttc gga gct gca cct gcc cat atg aaa tcc ccg ggg gat 211
Met Gln Gly Phe Gly Ala Ala Pro Ala His Met Lys Ser Pro Gly Asp
25 30 35

ttt gcc acg gaa gtg gat atg gcc atc gaa tcc cat atg cgt tcg atg 259
Phe Ala Thr Glu Val Asp Met Ala Ile Glu Ser His Met Arg Ser Met
40 45 50

ctg aac atg atg aca ggc att gct gtc atc ggt gaa gaa ggt ggc ggt 307
Leu Asn Met Met Thr Gly Ile Ala Val Ile Gly Glu Glu Gly Gly Gly
55 60 65

```

```

gcg acc tcc ggc acg cgc tgg gtg att gat ccc atc gac ggc acc gcc 355
Ala Thr Ser Gly Thr Arg Trp Val Ile Asp Pro Ile Asp Gly Thr Ala
 70                      75                      80                      85

aac ttc gcg gcg tcc aac ccg atg agc gcg atc ctg gtg tct ttg ctt 403
Asn Phe Ala Ala Ser Asn Pro Met Ser Ala Ile Leu Val Ser Leu Leu
          90                      95                      100

gtc gac gac cag ccc gtc ctg ggt att acc tcc atg ccc atg ctg ggt 451
Val Asp Asp Gln Pro Val Leu Gly Ile Thr Ser Met Pro Met Leu Gly
          105                      110                      115

aaa cgc ctc acc gct ttt gaa ggt tca ccg ctg atg atc aac ggt gaa 499
Lys Arg Leu Thr Ala Phe Glu Gly Ser Pro Leu Met Ile Asn Gly Glu
          120                      125                      130

cct cag gaa cca ttg caa gaa caa tcc agt ttg gta tcc cac att ggt 547
Pro Gln Glu Pro Leu Gln Glu Ser Ser Leu Val Ser His Ile Gly
          135                      140                      145

ttt agt tcc atg gcc tcc ccg cgc aat aca gcg ttt cct gtg gag ttg 595
Phe Ser Ser Met Ala Ser Pro Arg Asn Thr Ala Phe Pro Val Glu Leu
150                      155                      160                      165

cgt cgg gat ctt ctg acc gag ctc acg gaa tcg tat ctt cgt ccc cgc 643
Arg Arg Asp Leu Leu Thr Glu Leu Thr Glu Ser Tyr Leu Arg Pro Arg
          170                      175                      180

att aca ggt tcg gtg ggt gtt gat ctc gcg ttc act gcg cag ggc att 691
Ile Thr Gly Ser Val Gly Val Asp Leu Ala Phe Thr Ala Gln Gly Ile
          185                      190                      195

ttt gga gca tgc gta tcg ttt agt cct cat gtt tgg gac aat tcc gca 739
Phe Gly Ala Cys Val Ser Phe Ser Pro His Val Trp Asp Asn Ser Ala
          200                      205                      210

ggc gtg atg ttg atg cgc gct gct ggt gca caa gtt act gac acc gaa 787
Gly Val Met Leu Met Arg Ala Ala Gly Ala Gln Val Thr Asp Thr Glu
          215                      220                      225

ggc cat ccg tgg gca cca ggt agg gga gtc gtg gcc gga aca aaa agg 835
Gly His Pro Trp Ala Pro Gly Arg Gly Val Val Ala Gly Thr Lys Arg
230                      235                      240                      245

gct cac gat gtg ctg tta agt aag att gaa aaa gtt cgg ttg atg cat 883
Ala His Asp Val Leu Leu Ser Lys Ile Glu Lys Val Arg Leu Met His
          250                      255                      260

gca gat gca ggt aat gac cag tcg tta aat gag gag tac aag 925
Ala Asp Ala Gly Asn Asp Gln Ser Leu Asn Glu Glu Tyr Lys
          265                      270                      275

taaaatgggc gtggcaattc gag 948

```

&lt;210&gt; 294

&lt;211&gt; 275

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 294

```

Met Asp Ala Arg Gly Met Leu Ala Ile Ala Glu Ala Val Val Asp Asp
 1           5           10           15
Ala Glu Ala Leu Phe Met Gln Gly Phe Gly Ala Ala Pro Ala His Met
          20           25           30
Lys Ser Pro Gly Asp Phe Ala Thr Glu Val Asp Met Ala Ile Glu Ser
          35           40           45
His Met Arg Ser Met Leu Asn Met Met Thr Gly Ile Ala Val Ile Gly
          50           55           60
Glu Glu Gly Gly Gly Ala Thr Ser Gly Thr Arg Trp Val Ile Asp Pro
 65           70           75           80
Ile Asp Gly Thr Ala Asn Phe Ala Ala Ser Asn Pro Met Ser Ala Ile
          85           90           95
Leu Val Ser Leu Leu Val Asp Asp Gln Pro Val Leu Gly Ile Thr Ser
          100          105          110
Met Pro Met Leu Gly Lys Arg Leu Thr Ala Phe Glu Gly Ser Pro Leu
          115          120          125
Met Ile Asn Gly Glu Pro Gln Glu Pro Leu Gln Glu Gln Ser Ser Leu
          130          135          140
Val Ser His Ile Gly Phe Ser Ser Met Ala Ser Pro Arg Asn Thr Ala
          145          150          155          160
Phe Pro Val Glu Leu Arg Arg Asp Leu Leu Thr Glu Leu Thr Glu Ser
          165          170          175
Tyr Leu Arg Pro Arg Ile Thr Gly Ser Val Gly Val Asp Leu Ala Phe
          180          185          190
Thr Ala Gln Gly Ile Phe Gly Ala Cys Val Ser Phe Ser Pro His Val
          195          200          205
Trp Asp Asn Ser Ala Gly Val Met Leu Met Arg Ala Ala Gly Ala Gln
          210          215          220
Val Thr Asp Thr Glu Gly His Pro Trp Ala Pro Gly Arg Gly Val Val
          225          230          235          240
Ala Gly Thr Lys Arg Ala His Asp Val Leu Leu Ser Lys Ile Glu Lys
          245          250          255
Val Arg Leu Met His Ala Asp Ala Gly Asn Asp Gln Ser Leu Asn Glu
          260          265          270
Glu Tyr Lys
          275

```

&lt;210&gt; 295

&lt;211&gt; 576

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(576)

&lt;223&gt; RXN01332

&lt;400&gt; 295

cac atc tct gcc att att gag ccc gac gca gca cgt gcc gct gca gct 48  
 His Ile Ser Ala Ile Ile Glu Pro Asp Ala Ala Arg Ala Ala Ala Ala

1 5 10 15

gca gaa gac gcg ccg ggt gca cag gcc ttc act cgc att gaa gat gct 96  
 Ala Glu Asp Ala Pro Gly Ala Gln Ala Phe Thr Arg Ile Glu Asp Ala

20 25 30

atc gca gcc gat gct gtc gac gca gtg ctg atc gcc gta cca ggt cag 144  
 Ile Ala Ala Asp Ala Val Asp Ala Val Leu Ile Ala Val Pro Gly Gln

35 40 45

ttc cat gag cca gta ctt gtc cca gca cta gaa gca ggc ctt ccc atc 192  
 Phe His Glu Pro Val Leu Val Pro Ala Leu Glu Ala Gly Leu Pro Ile

50 55 60

ctg tgt gaa aag cca ctg acc cca gat tct gaa tcc tca ctg cgc atc 240  
 Leu Cys Glu Lys Pro Leu Thr Pro Asp Ser Glu Ser Ser Leu Arg Ile

65 70 75 80

gtc gag ctg gag cag aag ctg gac aag cca cac atc cag gtt ggt ttc 288  
 Val Glu Leu Glu Gln Lys Leu Asp Lys Pro His Ile Gln Val Gly Phe

85 90 95

atg cgc cgc ttc gac cct gag tac aac aac ttg cgc aaa ttg gtg gaa 336  
 Met Arg Arg Phe Asp Pro Glu Tyr Asn Asn Leu Arg Lys Leu Val Glu

100 105 110

tcc ggc gaa gct ggc gaa ctg ctc atg ctc cgc ggc ctg cac cgc aac 384  
 Ser Gly Glu Ala Gly Glu Leu Leu Met Leu Arg Gly Leu His Arg Asn

115 120 125

cca agt gtt ggt gag agc tac acc cag tcc atg ctg atc acc gac tcc 432  
 Pro Ser Val Gly Glu Ser Tyr Thr Gln Ser Met Leu Ile Thr Asp Ser

130 135 140

gtc gtc cac gaa ttc gat gtc atc cca tgg ctc gca ggc tcc cga gtt 480  
 Val Val His Glu Phe Asp Val Ile Pro Trp Leu Ala Gly Ser Arg Val

145 150 155 160

gtc tcc gtt gaa gtg aag tac cca aag acc tcc tca ctg gcg cac tcc 528  
 Val Ser Val Glu Val Lys Tyr Pro Lys Thr Ser Ser Leu Ala His Ser

165 170 175

ggc ctc aag gaa cca atc ctg gtg atc atg gag ctc gaa aac ggc gtg 576  
 Gly Leu Lys Glu Pro Ile Leu Val Ile Met Glu Leu Glu Asn Gly Val

180 185 190

&lt;210&gt; 296

&lt;211&gt; 192

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 296

His Ile Ser Ala Ile Ile Glu Pro Asp Ala Ala Arg Ala Ala Ala Ala  
 1 5 10 15  
 Ala Glu Asp Ala Pro Gly Ala Gln Ala Phe Thr Arg Ile Glu Asp Ala  
 20 25 30  
 Ile Ala Ala Asp Ala Val Asp Ala Val Leu Ile Ala Val Pro Gly Gln  
 35 40 45  
 Phe His Glu Pro Val Leu Val Pro Ala Leu Glu Ala Gly Leu Pro Ile  
 50 55 60  
 Leu Cys Glu Lys Pro Leu Thr Pro Asp Ser Glu Ser Ser Leu Arg Ile  
 65 70 75 80  
 Val Glu Leu Glu Gln Lys Leu Asp Lys Pro His Ile Gln Val Gly Phe  
 85 90 95  
 Met Arg Arg Phe Asp Pro Glu Tyr Asn Asn Leu Arg Lys Leu Val Glu  
 100 105 110  
 Ser Gly Glu Ala Gly Glu Leu Leu Met Leu Arg Gly Leu His Arg Asn  
 115 120 125  
 Pro Ser Val Gly Glu Ser Tyr Thr Gln Ser Met Leu Ile Thr Asp Ser  
 130 135 140  
 Val Val His Glu Phe Asp Val Ile Pro Trp Leu Ala Gly Ser Arg Val  
 145 150 155 160  
 Val Ser Val Glu Val Lys Tyr Pro Lys Thr Ser Ser Leu Ala His Ser  
 165 170 175  
 Gly Leu Lys Glu Pro Ile Leu Val Ile Met Glu Leu Glu Asn Gly Val  
 180 185 190

<210> 297  
 <211> 549  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(549)  
 <223> FRXA01332

<400> 297  
 gca gca cgt gcc gct gca gct gca gaa gac gcg ccg ggt gca cag gcc 48  
 Ala Ala Arg Ala Ala Ala Ala Glu Asp Ala Pro Gly Ala Gln Ala  
 1 5 10 15  
 ttc act cgc att gaa gat gct atc gca gcc gat gct gtc gac gca gtg 96  
 Phe Thr Arg Ile Glu Asp Ala Ile Ala Ala Asp Ala Val Asp Ala Val  
 20 25 30  
 ctg atc gcc gta cca ggt cag ttc cat gag cca gta ctt gtc cca gca 144  
 Leu Ile Ala Val Pro Gly Gln Phe His Glu Pro Val Leu Val Pro Ala

35	40	45	
cta gaa gca ggc ctt ccc atc ctg tgt gaa aag cca ctg acc cca gat			192
Leu Glu Ala Gly Leu Pro Ile Leu Cys Glu Lys Pro Leu Thr Pro Asp			
50	55	60	
tct gaa tcc tca ctg cgc atc gtc gag ctg gag cag aag ctg gac aag			240
Ser Glu Ser Ser Leu Arg Ile Val Glu Leu Glu Gln Lys Leu Asp Lys			
65	70	75	80
cca cac atc cag gtt ggt ttc atg cgc cgc ttc gac cct gag tac aac			288
Pro His Ile Gln Val Gly Phe Met Arg Arg Phe Asp Pro Glu Tyr Asn			
	85	90	95
aac ttg cgc aaa ttg gtg gaa tcc ggc gaa gct ggc gaa ctg ctc atg			336
Asn Leu Arg Lys Leu Val Glu Ser Gly Glu Ala Gly Glu Leu Leu Met			
	100	105	110
ctc cgc ggc ctg cac cgc aac cca agt gtt ggt gag agc tac acc cag			384
Leu Arg Gly Leu His Arg Asn Pro Ser Val Gly Glu Ser Tyr Thr Gln			
	115	120	125
tcc atg ctg atc acc gac tcc gtc gtc cac gaa ttc gat gtc atc cca			432
Ser Met Leu Ile Thr Asp Ser Val Val His Glu Phe Asp Val Ile Pro			
	130	135	140
tgg ctc gca ggc tcc cga gtt gtc tcc gtt gaa gtg aag tac cca aag			480
Trp Leu Ala Gly Ser Arg Val Val Ser Val Glu Val Lys Tyr Pro Lys			
	145	150	155
acc tcc tca ctg gcg cac tcc ggc ctc aag gaa cca atc ctg gtg atc			528
Thr Ser Ser Leu Ala His Ser Gly Leu Lys Glu Pro Ile Leu Val Ile			
	165	170	175
atg gag ctc gaa aac ggc gtg			549
Met Glu Leu Glu Asn Gly Val			
	180		

&lt;210&gt; 298

&lt;211&gt; 183

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 298

Ala Ala Arg Ala Ala Ala Ala Glu Asp Ala Pro Gly Ala Gln Ala

1

5

10

15

Phe Thr Arg Ile Glu Asp Ala Ile Ala Ala Asp Ala Val Asp Ala Val

20

25

30

Leu Ile Ala Val Pro Gly Gln Phe His Glu Pro Val Leu Val Pro Ala

35

40

45

Leu Glu Ala Gly Leu Pro Ile Leu Cys Glu Lys Pro Leu Thr Pro Asp

50

55

60

Ser Glu Ser Ser Leu Arg Ile Val Glu Leu Glu Gln Lys Leu Asp Lys

65

70

75

80

Pro His Ile Gln Val Gly Phe Met Arg Arg Phe Asp Pro Glu Tyr Asn

85 90 95

Asn Leu Arg Lys Leu Val Glu Ser Gly Glu Ala Gly Glu Leu Leu Met  
100 105 110

Leu Arg Gly Leu His Arg Asn Pro Ser Val Gly Glu Ser Tyr Thr Gln  
115 120 125

Ser Met Leu Ile Thr Asp Ser Val Val His Glu Phe Asp Val Ile Pro  
130 135 140

Trp Leu Ala Gly Ser Arg Val Val Ser Val Glu Val Lys Tyr Pro Lys  
145 150 155 160

Thr Ser Ser Leu Ala His Ser Gly Leu Lys Glu Pro Ile Leu Val Ile  
165 170 175

Met Glu Leu Glu Asn Gly Val  
180

<210> 299  
<211> 1128  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1105)  
<223> RXA01632

<400> 299  
aagggtctgca acgtgctttc gacaccacca tcgcagcgtt tgaacaagct gctcgtctcg 60  
ccccctccac taactgatct ttgaaaggct gaaaaaactc atg act ctt cgt atc 115  
Met Thr Leu Arg Ile  
1 5  
gcc ctt ttc ggc gct ggc cgc atc ggt cac gtc cac gct gcc aac att 163  
Ala Leu Phe Gly Ala Gly Arg Ile Gly His Val His Ala Ala Asn Ile  
10 15 20  
gct gca aac cct gat ctt gaa ctc gtt gtt atc gcc gat cct ttc att 211  
Ala Ala Asn Pro Asp Leu Glu Leu Val Val Ile Ala Asp Pro Phe Ile  
25 30 35  
gaa ggc gca cag cgt ttg gca gaa gcc aat ggg gca gaa gcg gtt gca 259  
Glu Gly Ala Gln Arg Leu Ala Glu Ala Asn Gly Ala Glu Ala Val Ala  
40 45 50  
tca cca gat gag gtg ttc gcc cgc gat gat atc gat ggc atc gtg atc 307  
Ser Pro Asp Glu Val Phe Ala Arg Asp Asp Ile Asp Gly Ile Val Ile  
55 60 65  
ggt tca cca acc agc acc cac gtt gat ctg atc acc cgc gcc gtg gaa 355  
Gly Ser Pro Thr Ser Thr His Val Asp Leu Ile Thr Arg Ala Val Glu  
70 75 80 85  
cgt ggc att cct gca ctg tgc gaa aaa ccc att gat tta gac att gaa 403  
Arg Gly Ile Pro Ala Leu Cys Glu Lys Pro Ile Asp Leu Asp Ile Glu  
90 95 100

atg gtg cgt gcc tgc aaa gag aag atc ggc gac ggc gct tcc aag gtg	451
Met Val Arg Ala Cys Lys Glu Lys Ile Gly Asp Gly Ala Ser Lys Val	
105 110 115	
atg ctg ggg ttt aac cga cgc ttc gat cct tct ttc gct gcc atc aat	499
Met Leu Gly Phe Asn Arg Arg Phe Asp Pro Ser Phe Ala Ala Ile Asn	
120 125 130	
gcg cga gtg gca aac cag gag atc ggc aac ctg gag cag ttg gtg atc	547
Ala Arg Val Ala Asn Gln Glu Ile Gly Asn Leu Glu Gln Leu Val Ile	
135 140 145	
atc agc cgc gat cca gcg ccc gca ccg aag gac tac atc gca ggt tcc	595
Ile Ser Arg Asp Pro Ala Pro Ala Pro Lys Asp Tyr Ile Ala Gly Ser	
150 155 160 165	
ggt gga atc ttc cgc gat atg acc atc cac gat ctg gat atg gcg cgt	643
Gly Gly Ile Phe Arg Asp Met Thr Ile His Asp Leu Asp Met Ala Arg	
170 175 180	
ttc ttt gtg ccc aat atc gtg gaa gtg act gca acc ggc gcc aat gtt	691
Phe Phe Val Pro Asn Ile Val Glu Val Thr Ala Thr Gly Ala Asn Val	
185 190 195	
ttc agc cag gaa atc gcg gag ttc aat gac tac gac cag gtt atc gtc	739
Phe Ser Gln Glu Ile Ala Glu Phe Asn Asp Tyr Asp Gln Val Ile Val	
200 205 210	
acg ctt cgt ggc tca aag ggc gag ttg atc aac atc gtg aac tcc cgc	787
Thr Leu Arg Gly Ser Lys Gly Glu Leu Ile Asn Ile Val Asn Ser Arg	
215 220 225	
cac tgc tcc tac ggc tac gac cag cga ctt gag gct ttc ggc tct aag	835
His Cys Ser Tyr Gly Tyr Asp Gln Arg Leu Glu Ala Phe Gly Ser Lys	
230 235 240 245	
ggc atg ctc gcc gcc gac aac atc agg ccc acc acg gtg cgc aag cac	883
Gly Met Leu Ala Ala Asp Asn Ile Arg Pro Thr Thr Val Arg Lys His	
250 255 260	
aat gcg gaa agc acc gag cag gca gat ccg att ttc aac ttc ttc ctc	931
Asn Ala Glu Ser Thr Glu Gln Ala Asp Pro Ile Phe Asn Phe Phe Leu	
265 270 275	
gag cgc tac gac gcc gct tac aag gca gag ctc gca act ttt gct caa	979
Glu Arg Tyr Asp Ala Ala Tyr Lys Ala Glu Leu Ala Thr Phe Ala Gln	
280 285 290	
gga atc cgc gac gcc caa ggc ttc tca cca aac ttc gag gac ggc gtc	1027
Gly Ile Arg Asp Gly Gln Gly Phe Ser Pro Asn Phe Glu Asp Gly Val	
295 300 305	
atc gcc ctt gaa cta gcg aat gca tgc ctt gaa tca gct caa acc ggc	1075
Ile Ala Leu Glu Leu Ala Asn Ala Cys Leu Glu Ser Ala Gln Thr Gly	
310 315 320 325	
cgc acc gtc acc ctc aac cct gcc aac gtt tagtcaacgt ctagttaatg	1125
Arg Thr Val Thr Leu Asn Pro Ala Asn Val	
330 335	



cct

1128

&lt;210&gt; 300

&lt;211&gt; 335

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 300

Met Thr Leu Arg Ile Ala Leu Phe Gly Ala Gly Arg Ile Gly His Val  
 1 5 10 15

His Ala Ala Asn Ile Ala Ala Asn Pro Asp Leu Glu Leu Val Val Ile  
 20 25 30

Ala Asp Pro Phe Ile Glu Gly Ala Gln Arg Leu Ala Glu Ala Asn Gly  
 35 40 45

Ala Glu Ala Val Ala Ser Pro Asp Glu Val Phe Ala Arg Asp Asp Ile  
 50 55 60

Asp Gly Ile Val Ile Gly Ser Pro Thr Ser Thr His Val Asp Leu Ile  
 65 70 75 80

Thr Arg Ala Val Glu Arg Gly Ile Pro Ala Leu Cys Glu Lys Pro Ile  
 85 90 95

Asp Leu Asp Ile Glu Met Val Arg Ala Cys Lys Glu Lys Ile Gly Asp  
 100 105 110

Gly Ala Ser Lys Val Met Leu Gly Phe Asn Arg Arg Phe Asp Pro Ser  
 115 120 125

Phe Ala Ala Ile Asn Ala Arg Val Ala Asn Gln Glu Ile Gly Asn Leu  
 130 135 140

Glu Gln Leu Val Ile Ile Ser Arg Asp Pro Ala Pro Ala Pro Lys Asp  
 145 150 155 160

Tyr Ile Ala Gly Ser Gly Gly Ile Phe Arg Asp Met Thr Ile His Asp  
 165 170 175

Leu Asp Met Ala Arg Phe Phe Val Pro Asn Ile Val Glu Val Thr Ala  
 180 185 190

Thr Gly Ala Asn Val Phe Ser Gln Glu Ile Ala Glu Phe Asn Asp Tyr  
 195 200 205

Asp Gln Val Ile Val Thr Leu Arg Gly Ser Lys Gly Glu Leu Ile Asn  
 210 215 220

Ile Val Asn Ser Arg His Cys Ser Tyr Gly Tyr Asp Gln Arg Leu Glu  
 225 230 235 240

Ala Phe Gly Ser Lys Gly Met Leu Ala Ala Asp Asn Ile Arg Pro Thr  
 245 250 255

Thr Val Arg Lys His Asn Ala Glu Ser Thr Glu Gln Ala Asp Pro Ile  
 260 265 270

Phe Asn Phe Phe Leu Glu Arg Tyr Asp Ala Ala Tyr Lys Ala Glu Leu

275	280	285	
Ala Thr Phe Ala Gln Gly Ile Arg Asp Gly Gln Gly Phe Ser Pro Asn 290 295 300			
Phe Glu Asp Gly Val Ile Ala Leu Glu Leu Ala Asn Ala Cys Leu Glu 305 310 315 320			
Ser Ala Gln Thr Gly Arg Thr Val Thr Leu Asn Pro Ala Asn Val 325 330 335			
<210> 301			
<211> 1206			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(1183)			
<223> RXA01633			
<400> 301			
gcgaatgcat gccttgaatc agctcaaacc ggccgcaccg tcaccctcaa ccctgccaac	60		
gtttagtcaa cgtctagtta atgcctaagg agaaaaacctc atg aaa aac atc acc	115		
Met Lys Asn Ile Thr	5		
atc gga atg gtc ggc gtc ggc cgc att ggc cgc atg cac gtc gcc aac	163		
Ile Gly Met Val Gly Val Gly Arg Ile Gly Arg Met His Val Ala Asn	20		
atg ctt gcc gtt gct gaa act ttg aag gaa cgc gac ctc aac att gag	211		
Met Leu Ala Val Ala Glu Thr Leu Lys Glu Arg Asp Leu Asn Ile Glu	35		
atc gtg ctc gca gac gca atg ccc ggt ttt gcg gag cag gtg ggc gcg	259		
Ile Val Leu Ala Asp Ala Met Pro Gly Phe Ala Glu Gln Val Gly Ala	50		
gac atg ggc gtg aag gcg gcg gca agc gtc gat aag ctt att gag gac	307		
Asp Met Gly Val Lys Ala Ala Ser Val Asp Lys Leu Ile Glu Asp	65		
ggg gtg gat gcc ctt ttc att gcc acc agc acc gct ggc cac gtc gat	355		
Gly Val Asp Ala Leu Phe Ile Ala Thr Ser Thr Ala Gly His Val Asp	85		
gtt ttg cgc aag ggc atc gcg gca aag ctg ccg atg ttc tgc gag aag	403		
Val Leu Arg Lys Gly Ile Ala Ala Lys Leu Pro Met Phe Cys Glu Lys	95		
ccg atc gcg tcg gat gtg cct gag tcg ctg aac atc atc cgc gaa att	451		
Pro Ile Ala Ser Asp Val Pro Glu Ser Leu Asn Ile Ile Arg Glu Ile	110		
gat gcg gct ggc gcg acg gtt cag gtc ggc cac cag cgc cgt ttt gac	499		
Asp Ala Ala Gly Ala Thr Val Gln Val Gly His Gln Arg Arg Phe Asp	125		

ctc ggt tac cag gaa gct aaa cga cgc cta gat gca ggc gac ctc ggc	547
Leu Gly Tyr Gln Glu Ala Lys Arg Arg Leu Asp Ala Gly Asp Leu Gly	
135 140 145	
tgg ctt cat tcg ctc aag gcc gta tcg agc gat gcg ttt ccg cca ccg	595
Trp Leu His Ser Leu Lys Ala Val Ser Ser Asp Ala Phe Pro Pro Pro	
150 155 160 165	
gtg tcc tac tgc gct acc tct ggt gga ctt ttc cgc gat gtg tcg ctg	643
Val Ser Tyr Cys Ala Thr Ser Gly Gly Leu Phe Arg Asp Val Ser Leu	
170 175 180	
cac gat ttc gac atc att cgc tgg ctg acc ggc cag gat att gtc gag	691
His Asp Phe Asp Ile Ile Arg Trp Leu Thr Gly Gln Asp Ile Val Glu	
185 190 195	
gtg tac gcc aag ggc agc aac aac ggc gac cca gaa atc ggc gca gtc	739
Val Tyr Ala Lys Gly Ser Asn Asn Gly Asp Pro Glu Ile Gly Ala Val	
200 205 210	
ggt gac atc gat acc gga gcg gcc cta ctc acg ctt gcc gac ggc acc	787
Gly Asp Ile Asp Thr Gly Ala Ala Leu Leu Thr Leu Ala Asp Gly Thr	
215 220 225	
ctc gcc acc gcc atc gcc act cgt tac aac ggt gca ggc cac gac gtt	835
Leu Ala Thr Ala Ile Ala Thr Arg Tyr Asn Gly Ala Gly His Asp Val	
230 235 240 245	
cgc ctc gat gtt atg ggc tct aaa gat tcc acg atc gtt ggc ctg gat	883
Arg Leu Asp Val Met Gly Ser Lys Asp Ser Thr Ile Val Gly Leu Asp	
250 255 260	
gaa aag tct gcg ttc gct tct gcg gag gag ggc atc gat ttc cca acc	931
Glu Lys Ser Ala Phe Ala Ser Ala Glu Glu Gly Ile Asp Phe Pro Thr	
265 270 275	
ggc gaa tcg cac cca acg ttt gcc gag cgc ttc gcc gac gca tac aag	979
Gly Glu Ser His Pro Thr Phe Ala Glu Arg Phe Ala Asp Ala Tyr Lys	
280 285 290	
aat gag tgc att gcg ttc gtg gag ttg atc ctg gga gag cgg gaa aac	1027
Asn Glu Cys Ile Ala Phe Val Glu Leu Ile Leu Gly Glu Arg Glu Asn	
295 300 305	
cct tgt acc cct gca gac gct gtg gct gcg gcg att gtt gcc gat gca	1075
Pro Cys Thr Pro Ala Asp Ala Val Ala Ala Ala Ile Val Ala Asp Ala	
310 315 320 325	
gct cag ctg tcg ctg gtc act ggc gag cca gtg aag att cct act gta	1123
Ala Gln Leu Ser Leu Val Thr Gly Glu Pro Val Lys Ile Pro Thr Val	
330 335 340	
cgg gaa att ctt gaa ggt tct gcg cag cca gtt gag gtg cgt gcg ctg	1171
Arg Glu Ile Leu Glu Gly Ser Ala Gln Pro Val Glu Val Arg Ala Leu	
345 350 355	
gtt cca tct gct taaaacctta ctgcttatct aaa	1206
Val Pro Ser Ala	
360	

&lt;210&gt; 302

&lt;211&gt; 361

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 302

Met Lys Asn Ile Thr Ile Gly Met Val Gly Val Gly Arg Ile Gly Arg  
 1 5 10 15

Met His Val Ala Asn Met Leu Ala Val Ala Glu Thr Leu Lys Glu Arg  
 20 25 30

Asp Leu Asn Ile Glu Ile Val Leu Ala Asp Ala Met Pro Gly Phe Ala  
 35 40 45

Glu Gln Val Gly Ala Asp Met Gly Val Lys Ala Ala Ala Ser Val Asp  
 50 55 60

Lys Leu Ile Glu Asp Gly Val Asp Ala Leu Phe Ile Ala Thr Ser Thr  
 65 70 75 80

Ala Gly His Val Asp Val Leu Arg Lys Gly Ile Ala Ala Lys Leu Pro  
 85 90 95

Met Phe Cys Glu Lys Pro Ile Ala Ser Asp Val Pro Glu Ser Leu Asn  
 100 105 110

Ile Ile Arg Glu Ile Asp Ala Ala Gly Ala Thr Val Gln Val Gly His  
 115 120 125

Gln Arg Arg Phe Asp Leu Gly Tyr Gln Glu Ala Lys Arg Arg Leu Asp  
 130 135 140

Ala Gly Asp Leu Gly Trp Leu His Ser Leu Lys Ala Val Ser Ser Asp  
 145 150 155 160

Ala Phe Pro Pro Pro Val Ser Tyr Cys Ala Thr Ser Gly Gly Leu Phe  
 165 170 175

Arg Asp Val Ser Leu His Asp Phe Asp Ile Ile Arg Trp Leu Thr Gly  
 180 185 190

Gln Asp Ile Val Glu Val Tyr Ala Lys Gly Ser Asn Asn Gly Asp Pro  
 195 200 205

Glu Ile Gly Ala Val Gly Asp Ile Asp Thr Gly Ala Ala Leu Leu Thr  
 210 215 220

Leu Ala Asp Gly Thr Leu Ala Thr Ala Ile Ala Thr Arg Tyr Asn Gly  
 225 230 235 240

Ala Gly His Asp Val Arg Leu Asp Val Met Gly Ser Lys Asp Ser Thr  
 245 250 255

Ile Val Gly Leu Asp Glu Lys Ser Ala Phe Ala Ser Ala Glu Glu Gly  
 260 265 270

Ile Asp Phe Pro Thr Gly Glu Ser His Pro Thr Phe Ala Glu Arg Phe  
 275 280 285

Ala Asp Ala Tyr Lys Asn Glu Cys Ile Ala Phe Val Glu Leu Ile Leu

428

Leu Asn Val Phe His Asn Arg Arg Asn Asp Thr His Ile Val Thr Ala	
120 125 130	
ctg gga atc caa gaa gaa ctt ggt gcg atg cgt gga ctg gac ctg cga	547
Leu Gly Ile Gln Glu Glu Leu Gly Ala Met Arg Gly Leu Asp Leu Arg	
135 140 145	
cta gac ctg atc gaa cct gat tcc ttg gag gca ggt cct gaa ggt ggt	595
Leu Asp Leu Ile Glu Pro Asp Ser Leu Glu Ala Gly Pro Glu Gly Gly	
150 155 160 165	
ttg ctg cgc gat ctg ggc tca cac gta gtc gat cag acc ctg gtt ctc	643
Leu Leu Arg Asp Leu Gly Ser His Val Val Asp Gln Thr Leu Val Leu	
170 175 180	
atg ggg ccg gct acc tct gtc acc gcc caa ctt gga tcc atc gac ctt	691
Met Gly Pro Ala Thr Ser Val Thr Ala Gln Leu Gly Ser Ile Asp Leu	
185 190 195	
cca gaa ggc cca acc aac gca agg ttc cgc atc gtg ttg gaa cat gaa	739
Pro Glu Gly Pro Thr Asn Ala Arg Phe Arg Ile Val Leu Glu His Glu	
200 205 210	
tcg ggc gcc gta tcg cac att tct gcc agc aag att gac cgc ttg gag	787
Ser Gly Ala Val Ser His Ile Ser Ala Ser Lys Ile Asp Arg Leu Glu	
215 220 225	
tcc tgg gaa atc cgc ttg gtg ggc gag cgc ggc tcc tac gta tcc aac	835
Ser Trp Glu Ile Arg Leu Val Gly Glu Arg Gly Ser Tyr Val Ser Asn	
230 235 240 245	
tac acc gac gtg cag acc gtg gcg atc aaa cag gga ctt cga cca acc	883
Tyr Thr Asp Val Gln Thr Val Ala Ile Lys Gln Gly Leu Arg Pro Thr	
250 255 260	
aat gac cgc gaa cac tgg ggc tac gaa tcg gag gag cgg tgg ggc acc	931
Asn Asp Arg Glu His Trp Gly Tyr Glu Ser Glu Glu Arg Trp Gly Thr	
265 270 275	
ttg gtt acc gat gaa ggc tca aag gtg att cct tca gca caa ggc gat	979
Leu Val Thr Asp Glu Gly Ser Lys Val Ile Pro Ser Ala Gln Gly Asp	
280 285 290	
tac acc cgc ttc tac gat gcc ttt gcc ttg gct gtg gaa aac ggt ggc	1027
Tyr Thr Arg Phe Tyr Asp Ala Phe Ala Leu Ala Val Glu Asn Gly Gly	
295 300 305	
gca ggg ccg gtg cct gca cgt gaa ggt gtt gca gtg ctc aag gtg ttg	1075
Ala Gly Pro Val Pro Ala Arg Glu Gly Val Ala Val Leu Lys Val Leu	
310 315 320 325	
gat gct gta gcc cag agc gct gcg gaa aaa cgc acc att gag ttg agc	1123
Asp Ala Val Ala Gln Ser Ala Ala Glu Lys Arg Thr Ile Glu Leu Ser	
330 335 340	
taaggagaag tgctgctggc tgc	1146
<210> 304	
<211> 341	
<212> PRT	

<213> *Corynebacterium glutamicum*

&lt;400&gt; 304

Met Thr Ile Arg Ile Gly Leu Val Gly Tyr Gly Val Gly Gly Arg Leu  
 1 5 10 15  
 Phe His Thr Pro Tyr Ile Gln Ala Ser Thr His Cys Glu Leu Val Gly  
 20 25 30  
 Val Val Ala Arg Ser Glu Gly Thr Lys Ala Ala Val Ala Glu Asp Leu  
 35 40 45  
 Pro Asp Val Ala Ile Val Gly Ser Leu Thr Glu Leu Leu Glu Leu Gly  
 50 55 60  
 Val Asp Ala Val Val Ile Ser Thr Pro Pro Ala Thr Arg Arg Glu Leu  
 65 70 75 80  
 Ala Leu Glu Ala Ile Asn Ala Gly Val Ala Val Val Ala Asp Lys Pro  
 85 90 95  
 Phe Ala Pro Ser Ala Ala Asp Ala Met Glu Leu Val Glu Ala Ala Glu  
 100 105 110  
 Lys Ala Gly Val Leu Leu Asn Val Phe His Asn Arg Arg Asn Asp Thr  
 115 120 125  
 His Ile Val Thr Ala Leu Gly Ile Gln Glu Glu Leu Gly Ala Met Arg  
 130 135 140  
 Gly Leu Asp Leu Arg Leu Asp Leu Ile Glu Pro Asp Ser Leu Glu Ala  
 145 150 155 160  
 Gly Pro Glu Gly Gly Leu Leu Arg Asp Leu Gly Ser His Val Val Asp  
 165 170 175  
 Gln Thr Leu Val Leu Met Gly Pro Ala Thr Ser Val Thr Ala Gln Leu  
 180 185 190  
 Gly Ser Ile Asp Leu Pro Glu Gly Pro Thr Asn Ala Arg Phe Arg Ile  
 195 200 205  
 Val Leu Glu His Glu Ser Gly Ala Val Ser His Ile Ser Ala Ser Lys  
 210 215 220  
 Ile Asp Arg Leu Glu Ser Trp Glu Ile Arg Leu Val Gly Glu Arg Gly  
 225 230 235 240  
 Ser Tyr Val Ser Asn Tyr Thr Asp Val Gln Thr Val Ala Ile Lys Gln  
 245 250 255  
 Gly Leu Arg Pro Thr Asn Asp Arg Glu His Trp Gly Tyr Glu Ser Glu  
 260 265 270  
 Glu Arg Trp Gly Thr Leu Val Thr Asp Glu Gly Ser Lys Val Ile Pro  
 275 280 285  
 Ser Ala Gln Gly Asp Tyr Thr Arg Phe Tyr Asp Ala Phe Ala Leu Ala  
 290 295 300  
 Val Glu Asn Gly Gly Ala Gly Pro Val Pro Ala Arg Glu Gly Val Ala

```

305              310              315              320
Val Leu Lys Val Leu Asp Ala Val Ala Gln Ser Ala Ala Glu Lys Arg
              325              330              335

Thr Ile Glu Leu Ser
              340

<210> 305
<211> 1200
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1177)
<223> RXN01630

<400> 305
gtaggtgagt cttcgtgaga taccctcggc cagtcataca gttcaaccaa gctccaccac 60

ccagataaaa acctgcgggt tgcgttttag gagaattccc atg agt gat caa aaa 115
              Met Ser Asp Gln Lys
              1              5

att gtt gtt ggc ctg cta ggc atc acc cac ccg cat gcg tcg gcg cgg 163
Ile Val Val Gly Leu Leu Gly Ile Thr His Pro His Ala Ser Ala Arg
              10              15              20

gtg cgt gcc ctc cgt gaa att gat ggg gta gag gtc gtc gcc gcc gcg 211
Val Arg Ala Leu Arg Glu Ile Asp Gly Val Glu Val Val Ala Ala Ala
              25              30              35

gat act gat tcc cgc ctc cag tac ttc acc gac aaa tat gat gtt gaa 259
Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp Lys Tyr Asp Val Glu
              40              45              50

ccc cgc gag atc gat gac gtc ttg aac gac gat cgc atc aac gcc atc 307
Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp Arg Ile Asn Ala Ile
              55              60              65

atg gtt cac tcc aag agc aag gac atg gtc cct cac gcc aag cgc gcg 355
Met Val His Ser Lys Ser Lys Asp Met Val Pro His Ala Lys Arg Ala
              70              75              80              85

ctc gcg gcc gga aaa tcc gtc gtc gtg gag aag ccc ggc ggg gga aca 403
Leu Ala Ala Gly Lys Ser Val Val Val Glu Lys Pro Gly Gly Gly Thr
              90              95              100

gtg gcg gat ctt gag gag ctc ctg gcc ctc aaa gaa gct gcc gat cct 451
Val Ala Asp Leu Glu Glu Leu Leu Ala Leu Lys Glu Ala Ala Asp Pro
              105              110              115

cag cga atc gtg cag gtc ggg tac aac gtc cgc ctg tct gaa tcg gtt 499
Gln Arg Ile Val Gln Val Gly Tyr Asn Val Arg Leu Ser Glu Ser Val
              120              125              130

cag aga tta aaa gag ctt ctc gac gcc ggc ctc atc ggc gaa gtc gtc 547
Gln Arg Leu Lys Glu Leu Leu Asp Ala Gly Leu Ile Gly Glu Val Val
              135              140              145

```



agc gtg caa gca cgc ggc gcc gca aaa gta ggt gag cat atc acc gag 595  
 Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly Glu His Ile Thr Glu  
 150 155 160 165

cac ctc aac caa ccc gca gac atg ggc ggt gtg ttg tgg att ctt ggc 643  
 His Leu Asn Gln Pro Ala Asp Met Gly Gly Val Leu Trp Ile Leu Gly  
 170 175 180

tgc cac atg ctc gat gca ttg gtg gaa gtc ttc gga gct cca gaa tcc 691  
 Cys His Met Leu Asp Ala Leu Val Glu Val Phe Gly Ala Pro Glu Ser  
 185 190 195

gtg aac gcc cga gtg cat aag acc gca aaa ctc tct gac gac acc agc 739  
 Val Asn Ala Arg Val His Lys Thr Ala Lys Leu Ser Asp Asp Thr Ser  
 200 205 210

cgc gaa gac tca gcc tcc gca ctg ctg tac tac cca gat ttc tcc gtc 787  
 Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr Pro Asp Phe Ser Val  
 215 220 225

agc ttc agc ttc gac ggc cac gat gat ctg gaa tgg ttc gaa agc tcc 835  
 Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu Trp Phe Glu Ser Ser  
 230 235 240 245

cga ctc acg gtc tat gga acc aag ggc atg atc gaa gcc gga atc ctc 883  
 Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile Glu Ala Gly Ile Leu  
 250 255 260

cct cag aca ctg cgc gta tac ctc aat gag tca cgc cag ggc tgg cca 931  
 Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser Arg Gln Gly Trp Pro  
 265 270 275

cag ggt tgg acc gag tgg acc cag agc tac ttc acc cca ccg ttt gct 979  
 Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe Thr Pro Pro Phe Ala  
 280 285 290

cgc aca gaa tcc aac aaa ttc tca gag ctt cca gag cta gaa aac atc 1027  
 Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro Glu Leu Glu Asn Ile  
 295 300 305

agc aac ttc cgc aca gaa atg cag ggg tgg gtg aat tcc att cgc act 1075  
 Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val Asn Ser Ile Arg Thr  
 310 315 320 325

gga tcc cgc aat gtg gcg cca gtt gag gat gct ctc aca gtc gct cgc 1123  
 Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala Leu Thr Val Ala Arg  
 330 335 340

att gtc agt gca tgc tac gaa tcc gac aac aac cag ggc att tcc gta 1171  
 Ile Val Ser Ala Cys Tyr Glu Ser Asp Asn Asn Gln Gly Ile Ser Val  
 345 350 355

aac atc taagaggagc actccatgaa acc 1200  
 Asn Ile

&lt;210&gt; 306

&lt;211&gt; 359

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 306

Met Ser Asp Gln Lys Ile Val Val Gly Leu Leu Gly Ile Thr His Pro  
 1 5 10 15  
 His Ala Ser Ala Arg Val Arg Ala Leu Arg Glu Ile Asp Gly Val Glu  
 20 25 30  
 Val Val Ala Ala Ala Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp  
 35 40 45  
 Lys Tyr Asp Val Glu Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp  
 50 55 60  
 Arg Ile Asn Ala Ile Met Val His Ser Lys Ser Lys Asp Met Val Pro  
 65 70 75 80  
 His Ala Lys Arg Ala Leu Ala Ala Gly Lys Ser Val Val Val Glu Lys  
 85 90 95  
 Pro Gly Gly Gly Thr Val Ala Asp Leu Glu Glu Leu Leu Ala Leu Lys  
 100 105 110  
 Glu Ala Ala Asp Pro Gln Arg Ile Val Gln Val Gly Tyr Asn Val Arg  
 115 120 125  
 Leu Ser Glu Ser Val Gln Arg Leu Lys Glu Leu Leu Asp Ala Gly Leu  
 130 135 140  
 Ile Gly Glu Val Val Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly  
 145 150 155 160  
 Glu His Ile Thr Glu His Leu Asn Gln Pro Ala Asp Met Gly Gly Val  
 165 170 175  
 Leu Trp Ile Leu Gly Cys His Met Leu Asp Ala Leu Val Glu Val Phe  
 180 185 190  
 Gly Ala Pro Glu Ser Val Asn Ala Arg Val His Lys Thr Ala Lys Leu  
 195 200 205  
 Ser Asp Asp Thr Ser Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr  
 210 215 220  
 Pro Asp Phe Ser Val Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu  
 225 230 235 240  
 Trp Phe Glu Ser Ser Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile  
 245 250 255  
 Glu Ala Gly Ile Leu Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser  
 260 265 270  
 Arg Gln Gly Trp Pro Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe  
 275 280 285  
 Thr Pro Pro Phe Ala Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro  
 290 295 300  
 Glu Leu Glu Asn Ile Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val

```

305          310          315          320
Asn Ser Ile Arg Thr Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala
      325          330          335
Leu Thr Val Ala Arg Ile Val Ser Ala Cys Tyr Glu Ser Asp Asn Asn
      340          345          350
Gln Gly Ile Ser Val Asn Ile
      355

<210> 307
<211> 1212
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1189)
<223> RXN00528

<400> 307
ttctgctggg aatccccaca ttttgaacg tagcgtcgat aagcgtgagg cgaagctttt 60
tcggtcgagg ccgttatctt ttttaagagga gaaatttttag atg agc acg tcc acc 115
                                   Met Ser Thr Ser Thr
                                   1          5
atc agg gtt gcc att gcc gga gtc gga aac tgc gcg acc tcc ctc att 163
Ile Arg Val Ala Ile Ala Gly Val Gly Asn Cys Ala Thr Ser Leu Ile
      10          15          20
cag ggt gtg gaa tat tac cga aat gcg gat cct tcc gaa act gtc ccg 211
Gln Gly Val Glu Tyr Tyr Arg Asn Ala Asp Pro Ser Glu Thr Val Pro
      25          30          35
ggt ttg atg cac gtc aaa ttc ggt gat tac cac gtt ggc gac att gaa 259
Gly Leu Met His Val Lys Phe Gly Asp Tyr His Val Gly Asp Ile Glu
      40          45          50
ttc gtg gcc gcg ttc gac gtc gac gcc gaa aaa gta ggc atc gat ctt 307
Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys Val Gly Ile Asp Leu
      55          60          65
gcc gac gcc acc gag gct tca caa aac tgc act atc aaa atc gcc gat 355
Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr Ile Lys Ile Ala Asp
      70          75          80          85
gtc cca cag acc ggc atc aac gtg ctg cgt ggc ccg act ctc gac ggc 403
Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly Pro Thr Leu Asp Gly
      90          95          100
ctg ggc gat cat tac cgc gcg acc atc gac gag tcc acc gcc gag cca 451
Leu Gly Asp His Tyr Arg Ala Thr Ile Asp Glu Ser Thr Ala Glu Pro
      105          110          115
gtc gac gtt gtc cag gcg ctt atc gac gca aaa gcc gat gtt ttg gtg 499
Val Asp Val Val Gln Ala Leu Ile Asp Ala Lys Ala Asp Val Leu Val
      120          125          130

```

tcc tac ctc cca gtg ggc tcc gaa gaa gcc gac aaa ttc tac gca caa	547
Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp Lys Phe Tyr Ala Gln	
135 140 145	
gcc gcc atc gat gca ggc tgc gcc ttt gtc aac gct ctc cca gta ttc	595
Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn Ala Leu Pro Val Phe	
150 155 160 165	
atc gcc tcc gac cct gag tgg gct aag aag ttc act gac gct ggc atc	643
Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe Thr Asp Ala Gly Ile	
170 175 180	
cca att gtt ggc gat gac atc aaa tcc cag atc ggt gca acc atc acc	691
Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile Gly Ala Thr Ile Thr	
185 190 195	
cac cgt gtc ctc gca cgc ctt ttt gaa gaa cgt ggc gtt cgc gta gat	739
His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg Gly Val Arg Val Asp	
200 205 210	
cgc acc atg cag ctc aac gtc ggc ggc aac atg gac ttc aaa aac atg	787
Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met Asp Phe Lys Asn Met	
215 220 225	
ctt gac cgc aat cgc ttg gaa tcc aag aag gtc tcc aaa acc caa gca	835
Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val Ser Lys Thr Gln Ala	
230 235 240 245	
gtg acc tcc aac att cca gat ggt cca ctg tct gga aag gtg gaa gac	883
Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser Gly Lys Val Glu Asp	
250 255 260	
cgc aac gtc cac atc gga cca tcc gac cac gtc caa tgg ctc gat gac	931
Arg Asn Val His Ile Gly Pro Ser Asp His Val Gln Trp Leu Asp Asp	
265 270 275	
cgc aag tgg gct tat gtc cgc ctc gaa ggc acc gca ttc ggt gga gtt	979
Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr Ala Phe Gly Gly Val	
280 285 290	
ccc ctc aac ctt gag tac aaa ctc gag gtg tgg gat tca ccc aac tct	1027
Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp Asp Ser Pro Asn Ser	
295 300 305	
gcc ggc atc atc atc gac gct gtt cgc gcc gcc aag atc gcc ctc gat	1075
Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala Lys Ile Ala Leu Asp	
310 315 320 325	
cgc ggt atc ggc gga ccg atc atg cca gca agc tcc tac ctg atg aag	1123
Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser Ser Tyr Leu Met Lys	
330 335 340	
tcc cca cct gag cag ctt cca gac gat gtt gct tgt gaa cgc cta gag	1171
Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala Cys Glu Arg Leu Glu	
345 350 355	
gca ttc atc atc gag gcg taaaattagg ctaaaaattt ggg	1212
Ala Phe Ile Ile Glu Ala	
360	

<210> 308  
 <211> 363  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 308

```

Met Ser Thr Ser Thr Ile Arg Val Ala Ile Ala Gly Val Gly Asn Cys
 1              5              10              15

Ala Thr Ser Leu Ile Gln Gly Val Glu Tyr Tyr Arg Asn Ala Asp Pro
      20              25              30

Ser Glu Thr Val Pro Gly Leu Met His Val Lys Phe Gly Asp Tyr His
      35              40              45

Val Gly Asp Ile Glu Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys
      50              55              60

Val Gly Ile Asp Leu Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr
      65              70              75              80

Ile Lys Ile Ala Asp Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly
      85              90              95

Pro Thr Leu Asp Gly Leu Gly Asp His Tyr Arg Ala Thr Ile Asp Glu
      100             105             110

Ser Thr Ala Glu Pro Val Asp Val Val Gln Ala Leu Ile Asp Ala Lys
      115             120             125

Ala Asp Val Leu Val Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp
      130             135             140

Lys Phe Tyr Ala Gln Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn
      145             150             155             160

Ala Leu Pro Val Phe Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe
      165             170             175

Thr Asp Ala Gly Ile Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile
      180             185             190

Gly Ala Thr Ile Thr His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg
      195             200             205

Gly Val Arg Val Asp Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met
      210             215             220

Asp Phe Lys Asn Met Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val
      225             230             235             240

Ser Lys Thr Gln Ala Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser
      245             250             255

Gly Lys Val Glu Asp Arg Asn Val His Ile Gly Pro Ser Asp His Val
      260             265             270

Gln Trp Leu Asp Asp Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr
      275             280             285

Ala Phe Gly Gly Val Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp

```

290 295 300

Asp Ser Pro Asn Ser Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala  
305 310 315 320

Lys Ile Ala Leu Asp Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser  
325 330 335

Ser Tyr Leu Met Lys Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala  
340 345 350

Cys Glu Arg Leu Glu Ala Phe Ile Ile Glu Ala  
355 360

<210> 309  
<211> 795  
<212> DNA  
<213> *Corynebacterium glutamicum*

<220>  
<221> CDS  
<222> (101)..(772)  
<223> RXN03057

<400> 309  
catcaacgcc gagtacaact aaggacaact gataatgaca aatgctgcaa ttgtcggatg 60  
aggagacgtc gcaaccgttc atacagaagc gctggaagct ttg gct tcc gat ctt 115  
Leu Ala Ser Asp Leu  
1 5  
ggt att aag ttc gtc gca gtg gtg gat aaa gat cta gag act gct gag 163  
Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp Leu Glu Thr Ala Glu  
10 15 20  
aaa ttt gcg acg gga ctt gga gct gct ggc gat tct tca gaa agc agc 211  
Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp Ser Ser Glu Ser Ser  
25 30 35  
gtc aag gcc cac ggc agc ctg ccg gct ttg ttc tcc aaa aag aag atc 259  
Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe Ser Lys Lys Lys Ile  
40 45 50  
gat gtt cta cac atc acc acc ccc cac gac caa cac att ggt ttg gct 307  
Asp Val Leu His Ile Thr Thr Pro His Asp Gln His Ile Gly Leu Ala  
55 60 65  
ctc gaa gcg cta cac cac ggt gta aat gtc atc ctg gaa aag ccg ttg 355  
Leu Glu Ala Leu His His Gly Val Asn Val Ile Leu Glu Lys Pro Leu  
70 75 80 85  
gct aat gag ttg gac cag gcg cag cgt ctc atc gac tac ttg gat gaa 403  
Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile Asp Tyr Leu Asp Glu  
90 95 100  
aac ccc gat ggt cca aag att gca gtg tgc tat cag aac cgt tac aac 451  
Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr Gln Asn Arg Tyr Asn  
105 110 115  
gtt tcc tcc cag gaa ctg cgt cgt ctg ctc gat tca ggt gac ctc ggt 499

Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp Ser Gly Asp Leu Gly  
 120 125 130

gcc atc aat ggt gca tat tcc tct gtg gtg tgg acc cgc acc cca ggc 547  
 Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp Thr Arg Thr Pro Gly  
 135 140 145

tac tac acc cag aaa cct tgg cgt ggc cag caa gca cac tcc ggt ggt 595  
 Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln Ala His Ser Gly Gly  
 150 155 160 165

ggc ctg ctg atg aac caa gca att cac acc ctg gat ctg ctg cag tgg 643  
 Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu Asp Leu Leu Gln Trp  
 170 175 180

ttc ctt gga aag gca aca gaa gtc aag ggc act gtc tcc acc gat aag 691  
 Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr Val Ser Thr Asp Lys  
 185 190 195

tat gcc gat gtc atc gat gtt gaa gac acc gca cac gca tac atc ggt 739  
 Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala His Ala Tyr Ile Gly  
 200 205 210

cac gag tcc gga gtc cac acc agt gaa gtg agt tgaaccatgc tattggtgat 792  
 His Glu Ser Gly Val His Thr Ser Glu Val Ser  
 215 220

aca 795

&lt;210&gt; 310

&lt;211&gt; 224

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 310

Leu Ala Ser Asp Leu Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp  
 1 5 10 15

Leu Glu Thr Ala Glu Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp  
 20 25 30

Ser Ser Glu Ser Ser Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe  
 35 40 45

Ser Lys Lys Lys Ile Asp Val Leu His Ile Thr Thr Pro His Asp Gln  
 50 55 60

His Ile Gly Leu Ala Leu Glu Ala Leu His His Gly Val Asn Val Ile  
 65 70 75 80

Leu Glu Lys Pro Leu Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile  
 85 90 95

Asp Tyr Leu Asp Glu Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr  
 100 105 110

Gln Asn Arg Tyr Asn Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp  
 115 120 125

Ser Gly Asp Leu Gly Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp

130	135	140
Thr Arg Thr Pro Gly Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln		
145	150	155 160
Ala His Ser Gly Gly Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu		
	165	170 175
Asp Leu Leu Gln Trp Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr		
	180	185 190
Val Ser Thr Asp Lys Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala		
	195	200 205
His Ala Tyr Ile Gly His Glu Ser Gly Val His Thr Ser Glu Val Ser		
	210	215 220

<210> 311  
 <211> 795  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(772)  
 <223> FRXA02902

<400> 311  
 catcaacgcc gagtacaact aaggacaact gataatgaca aatgctgcaa ttgtcggatg 60  
 aggagacgtc gcaaccgttc atacagaagc gctggaagct ttg gct tcc gat ctt 115  
 Leu Ala Ser Asp Leu  
 1 5  
 ggt att aag ttc gtc gca gtg gtg gat aaa gat cta gag act gct gag 163  
 Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp Leu Glu Thr Ala Glu  
 10 15 20  
 aaa ttt gcg acg gga ctt gga gct gct ggc gat tct tca gaa agc agc 211  
 Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp Ser Ser Glu Ser Ser  
 25 30 35  
 gtc aag gcc cac ggc agc ctg ccg gct ttg ttc tcc aaa aag aag atc 259  
 Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe Ser Lys Lys Lys Ile  
 40 45 50  
 gat gtt cta cac atc acc acc ccc cac gac caa cac att ggt ttg gct 307  
 Asp Val Leu His Ile Thr Thr Pro His Asp Gln His Ile Gly Leu Ala  
 55 60 65  
 ctc gaa gcg cta cac cac ggt gta aat gtc atc ctg gaa aag ccg ttg 355  
 Leu Glu Ala Leu His His Gly Val Asn Val Ile Leu Glu Lys Pro Leu  
 70 75 80 85  
 gct aat gag ttg gac cag gcg cag cgt ctc atc gac tac ttg gat gaa 403  
 Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile Asp Tyr Leu Asp Glu  
 90 95 100



```

aac ccc gat ggt cca aag att gca gtg tgc tat cag aac cgt tac aac 451
Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr Gln Asn Arg Tyr Asn
      105                      110                      115

gtt tcc tcc cag gaa ctg cgt cgt ctg ctc gat tca ggt gac ctc ggt 499
Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp Ser Gly Asp Leu Gly
      120                      125                      130

gcc atc aat ggt gca tat tcc tct gtg gtg tgg acc cgc acc cca ggc 547
Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp Thr Arg Thr Pro Gly
      135                      140                      145

tac tac acc cag aaa cct tgg cgt ggc cag caa gca cac tcc ggt ggt 595
Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln Ala His Ser Gly Gly
      150                      155                      160                      165

ggc ctg ctg atg aac caa gca att cac acc ctg gat ctg ctg cag tgg 643
Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu Asp Leu Leu Gln Trp
      170                      175                      180

ttc ctt gga aag gca aca gaa gtc aag ggc act gtc tcc acc gat aag 691
Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr Val Ser Thr Asp Lys
      185                      190                      195

tat gcc gat gtc atc gat gtt gaa gac acc gca cac gca tac atc ggt 739
Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala His Ala Tyr Ile Gly
      200                      205                      210

cac gag tcc gga gtc cac acc agt gaa gtg agt tgaaccatgc tattggtgat 792
His Glu Ser Gly Val His Thr Ser Glu Val Ser
      215                      220

aca 795

```

```

<210> 312
<211> 224
<212> PRT
<213> Corynebacterium glutamicum

```

```

<400> 312
Leu Ala Ser Asp Leu Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp
 1                      5                      10                      15

Leu Glu Thr Ala Glu Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp
      20                      25                      30

Ser Ser Glu Ser Ser Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe
      35                      40                      45

Ser Lys Lys Lys Ile Asp Val Leu His Ile Thr Thr Pro His Asp Gln
      50                      55                      60

His Ile Gly Leu Ala Leu Glu Ala Leu His His Gly Val Asn Val Ile
      65                      70                      75                      80

Leu Glu Lys Pro Leu Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile
      85                      90                      95

Asp Tyr Leu Asp Glu Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr

```

100	105	110
Gln Asn Arg Tyr Asn Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp		
115	120	125
Ser Gly Asp Leu Gly Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp		
130	135	140
Thr Arg Thr Pro Gly Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln		
145	150	155
Ala His Ser Gly Gly Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu		
165	170	175
Asp Leu Leu Gln Trp Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr		
180	185	190
Val Ser Thr Asp Lys Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala		
195	200	205
His Ala Tyr Ile Gly His Glu Ser Gly Val His Thr Ser Glu Val Ser		
210	215	220

<210> 313  
 <211> 831  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(808)  
 <223> RXA00251

<400> 313  
 aaccagcgtt ttcagcgaga tactggacat atcaactaaa atccctgaat aaaacatcta 60  
 acatgggttt tatacagaaa attcatatcga aaggttgatc atg aag aag aag att 115  
 Met Lys Lys Lys Ile  
 1 5  
 gcg gtc gtt acc gga gcg acc gga ggc atg gga att gag atc gtc aaa 163  
 Ala Val Val Thr Gly Ala Thr Gly Gly Met Gly Ile Glu Ile Val Lys  
 10 15 20  
 gac ctc tcc cgc gac cac att gtc tac gcc ttg ggc cga aat cca gag 211  
 Asp Leu Ser Arg Asp His Ile Val Tyr Ala Leu Gly Arg Asn Pro Glu  
 25 30 35  
 cat ctg gca gct ctc gca gag atc gag gga gta gag cct atc gag tcc 259  
 His Leu Ala Ala Leu Ala Glu Ile Glu Gly Val Glu Pro Ile Glu Ser  
 40 45 50  
 gat atc gtg aag gaa gtg ttg gaa gag gga ggc gtc gac aag cta aaa 307  
 Asp Ile Val Lys Glu Val Leu Glu Glu Gly Gly Val Asp Lys Leu Lys  
 55 60 65  
 aac ctc gac cac gtg gat acg ctg gtg cac gcc gcg gcg gtg gcg cgt 355

Asn Leu Asp His Val Asp Thr Leu Val His Ala Ala Ala Val Ala Arg  
 70 75 80 85  
 gac acg acc atc gaa gcc ggc agt gtg gcc gaa tgg cac gca cac ctt 403  
 Asp Thr Thr Ile Glu Ala Gly Ser Val Ala Glu Trp His Ala His Leu  
 90 95 100  
 gat ctc aac gtc att gtc ccg gcc gag ttg agt cgc caa ctc ttg ccc 451  
 Asp Leu Asn Val Ile Val Pro Ala Glu Leu Ser Arg Gln Leu Leu Pro  
 105 110 115  
 gcc ctc cgc gcg gca tcc ggc tgc gtc atc tac atc aac tcc ggc gcc 499  
 Ala Leu Arg Ala Ala Ser Gly Cys Val Ile Tyr Ile Asn Ser Gly Ala  
 120 125 130  
 ggc aac gga cca cac ccc ggc aac acc atc tac gcc gcc agc aaa cac 547  
 Gly Asn Gly Pro His Pro Gly Asn Thr Ile Tyr Ala Ala Ser Lys His  
 135 140 145  
 gcc ctc cgc gga ctc gcc gac gcc ttc cgc aaa gaa gaa gcc aac aac 595  
 Ala Leu Arg Gly Leu Ala Asp Ala Phe Arg Lys Glu Glu Ala Asn Asn  
 150 155 160 165  
 ggc atc cgc gtc agc act gtc agc ccc ggc ccc acc aac acc ccc atg 643  
 Gly Ile Arg Val Ser Thr Val Ser Pro Gly Pro Thr Asn Thr Pro Met  
 170 175 180  
 ctg caa ggc ctc atg gac tca caa ggc acc aac ttc cgc cca gag atc 691  
 Leu Gln Gly Leu Met Asp Ser Gln Gly Thr Asn Phe Arg Pro Glu Ile  
 185 190 195  
 tac atc gaa cca aaa gaa atc gcc aac gca atc aga ttc gtg att gac 739  
 Tyr Ile Glu Pro Lys Glu Ile Ala Asn Ala Ile Arg Phe Val Ile Asp  
 200 205 210  
 gct ggc gaa acc acc cag atc acc aac gtg gac gta cga cca cgt atc 787  
 Ala Gly Glu Thr Thr Gln Ile Thr Asn Val Asp Val Arg Pro Arg Ile  
 215 220 225  
 gaa ctg gcg gac cgg aaa gat tagttctgagg ggccttctg ggc 831  
 Glu Leu Ala Asp Arg Lys Asp  
 230 235

&lt;210&gt; 314

&lt;211&gt; 236

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 314

Met Lys Lys Lys Ile Ala Val Val Thr Gly Ala Thr Gly Gly Met Gly  
 1 5 10 15  
 Ile Glu Ile Val Lys Asp Leu Ser Arg Asp His Ile Val Tyr Ala Leu  
 20 25 30  
 Gly Arg Asn Pro Glu His Leu Ala Ala Leu Ala Glu Ile Glu Gly Val  
 35 40 45  
 Glu Pro Ile Glu Ser Asp Ile Val Lys Glu Val Leu Glu Glu Gly Gly  
 50 55 60

Val Asp Lys Leu Lys Asn Leu Asp His Val Asp Thr Leu Val His Ala  
 65 70 75 80  
 Ala Ala Val Ala Arg Asp Thr Thr Ile Glu Ala Gly Ser Val Ala Glu  
 85 90 95  
 Trp His Ala His Leu Asp Leu Asn Val Ile Val Pro Ala Glu Leu Ser  
 100 105 110  
 Arg Gln Leu Leu Pro Ala Leu Arg Ala Ala Ser Gly Cys Val Ile Tyr  
 115 120 125  
 Ile Asn Ser Gly Ala Gly Asn Gly Pro His Pro Gly Asn Thr Ile Tyr  
 130 135 140  
 Ala Ala Ser Lys His Ala Leu Arg Gly Leu Ala Asp Ala Phe Arg Lys  
 145 150 155 160  
 Glu Glu Ala Asn Asn Gly Ile Arg Val Ser Thr Val Ser Pro Gly Pro  
 165 170 175  
 Thr Asn Thr Pro Met Leu Gln Gly Leu Met Asp Ser Gln Gly Thr Asn  
 180 185 190  
 Phe Arg Pro Glu Ile Tyr Ile Glu Pro Lys Glu Ile Ala Asn Ala Ile  
 195 200 205  
 Arg Phe Val Ile Asp Ala Gly Glu Thr Thr Gln Ile Thr Asn Val Asp  
 210 215 220  
 Val Arg Pro Arg Ile Glu Leu Ala Asp Arg Lys Asp  
 225 230 235

<210> 315  
 <211> 1008  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(985)  
 <223> RXN02654

<400> 315  
 tatttttcgga aatttatataca gcaatcctcg aaatcctaataaagatccct tatcgtggga 60  
 gaggtacggt agttcgttcg aggacaacgt cgagaaaggc atg att tca ttg cta 115  
 Met Ile Ser Leu Leu  
 1 5  
 aat gat cca cgt acg cta ttc ccg aaa gtc gat ccc cca aag caa agc 163  
 Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp Pro Pro Lys Gln Ser  
 10 15 20  
 cag ccg gaa cca ggc cta gat ata aaa ctt tcc ccc caa gcc gat att 211  
 Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser Pro Gln Ala Asp Ile  
 25 30 35  
 ggt ctc tcc agc tat caa gga agt gga agg ctt aag ggc cgc aag gct 259

Gly	Leu	Ser	Ser	Tyr	Gln	Gly	Ser	Gly	Arg	Leu	Lys	Gly	Arg	Lys	Ala		
	40						45					50					
ctt	att	act	ggt	ggc	gat	tct	ggg	att	gga	gct	gcc	gta	gca	atc	gct	307	
Leu	Ile	Thr	Gly	Gly	Asp	Ser	Gly	Ile	Gly	Ala	Ala	Val	Ala	Ile	Ala		
	55						60				65						
tat	gct	cgc	gag	ggg	gca	gat	gtt	gcg	atc	gct	tac	ttg	ccc	gaa	gaa	355	
Tyr	Ala	Arg	Glu	Gly	Ala	Asp	Val	Ala	Ile	Ala	Tyr	Leu	Pro	Glu	Glu		
	70				75				80					85			
caa	gcc	gat	gct	gac	aga	gtg	ctc	caa	gca	atc	gag	gaa	aca	ggt	caa	403	
Gln	Ala	Asp	Ala	Asp	Arg	Val	Leu	Gln	Ala	Ile	Glu	Glu	Thr	Gly	Gln		
				90					95					100			
aaa	gct	ttt	tct	ttc	cct	ggt	gat	ctc	cgt	gat	cca	gaa	tac	tgt	cgc	451	
Lys	Ala	Phe	Ser	Phe	Pro	Gly	Asp	Leu	Arg	Asp	Pro	Glu	Tyr	Cys	Arg		
			105				110						115				
tcg	ctg	gtc	caa	gag	acg	gtg	aac	gct	tta	ggt	ggc	cta	gac	atc	ttg	499	
Ser	Leu	Val	Gln	Glu	Thr	Val	Asn	Ala	Leu	Gly	Gly	Leu	Asp	Ile	Leu		
		120					125					130					
gtc	aac	aac	gcg	tca	cgt	cag	gtg	tgg	gca	cct	ggt	ttg	acc	gaa	att	547	
Val	Asn	Asn	Ala	Ser	Arg	Gln	Val	Trp	Ala	Pro	Gly	Leu	Thr	Glu	Ile		
	135					140					145						
acc	gac	gaa	aac	ttc	gac	cag	act	ttg	cag	gtt	aac	ctc	tat	ggt	agt	595	
Thr	Asp	Glu	Asn	Phe	Asp	Gln	Thr	Leu	Gln	Val	Asn	Leu	Tyr	Gly	Ser		
	150				155				160						165		
ttt	cgg	gtt	acc	aaa	gca	gct	ata	cct	cat	ctg	aag	ccc	gga	tca	tcg	643	
Phe	Arg	Val	Thr	Lys	Ala	Ala	Ile	Pro	His	Leu	Lys	Pro	Gly	Ser	Ser		
				170				175						180			
ata	atc	ttt	aca	tcg	tcc	att	cag	gcg	tac	caa	cct	tcg	gaa	acc	ctc	691	
Ile	Ile	Phe	Thr	Ser	Ser	Ile	Gln	Ala	Tyr	Gln	Pro	Ser	Glu	Thr	Leu		
			185					190					195				
ttg	gat	tac	gcc	atg	act	aag	gcg	gca	ttg	aac	aat	ttg	tca	aag	ggc	739	
Leu	Asp	Tyr	Ala	Met	Thr	Lys	Ala	Ala	Leu	Asn	Asn	Leu	Ser	Lys	Gly		
		200					205					210					
ttg	gca	agt	agt	ctg	ata	ggc	gat	ggc	att	cgg	gta	aat	tct	gta	gcc	787	
Leu	Ala	Ser	Ser	Leu	Ile	Gly	Asp	Gly	Ile	Arg	Val	Asn	Ser	Val	Ala		
	215					220					225						
cca	ggt	cct	ttc	tgg	acg	ccg	ttg	caa	ccc	agc	cat	ggt	cag	cca	caa	835	
Pro	Gly	Pro	Phe	Trp	Thr	Pro	Leu	Gln	Pro	Ser	His	Gly	Gln	Pro	Gln		
				235						240					245		
gag	aaa	ata	gaa	gga	ttt	ggc	cag	cac	gct	ccg	att	gga	aga	gcg	ggt	883	
Glu	Lys	Ile	Glu	Gly	Phe	Gly	Gln	His	Ala	Pro	Ile	Gly	Arg	Ala	Gly		
				250					255					260			
cac	cct	gtt	gag	ttg	gca	ggt	gcg	tac	gtt	ttt	ctc	gct	tct	gac	gaa	931	
His	Pro	Val	Glu	Leu	Ala	Gly	Ala	Tyr	Val	Phe	Leu	Ala	Ser	Asp	Glu		
			265					270					275				
gcc	agc	tat	gtg	gta	gga	gaa	acc	ctg	gga	gtc	aca	ggt	ggg	acg	ccc	979	
Ala	Ser	Tyr	Val	Val	Gly	Glu	Thr	Leu	Gly	Val	Thr	Gly	Gly	Thr	Pro		

280 285 290

acc cca tagtcggtac aagcgggaatc act 1008  
 Thr Pro  
 295

<210> 316  
 <211> 295  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 316  
 Met Ile Ser Leu Leu Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp  
 1 5 10 15  
 Pro Pro Lys Gln Ser Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser  
 20 25 30  
 Pro Gln Ala Asp Ile Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu  
 35 40 45  
 Lys Gly Arg Lys Ala Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala  
 50 55 60  
 Ala Val Ala Ile Ala Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala  
 65 70 75 80  
 Tyr Leu Pro Glu Glu Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile  
 85 90 95  
 Glu Glu Thr Gly Gln Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp  
 100 105 110  
 Pro Glu Tyr Cys Arg Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly  
 115 120 125  
 Gly Leu Asp Ile Leu Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro  
 130 135 140  
 Gly Leu Thr Glu Ile Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val  
 145 150 155 160  
 Asn Leu Tyr Gly Ser Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu  
 165 170 175  
 Lys Pro Gly Ser Ser Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln  
 180 185 190  
 Pro Ser Glu Thr Leu Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn  
 195 200 205  
 Asn Leu Ser Lys Gly Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg  
 210 215 220  
 Val Asn Ser Val Ala Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser  
 225 230 235 240  
 His Gly Gln Pro Gln Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro  
 245 250 255

Ile Gly Arg Ala Gly His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe  
                   260                  265                  270

Leu Ala Ser Asp Glu Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val  
                   275                  280                  285

Thr Gly Gly Thr Pro Thr Pro  
           290                  295

<210> 317  
 <211> 1008  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(985)  
 <223> FRXA02654

<400> 317  
 tatttttcgga aatttatata gcaatcctcg aaatcctaataaagatccct tatcgtggga 60

gaggtacggt agttcgttcg aggacaacgt cgagaaaggc atg att tca ttg cta 115  
   Met Ile Ser Leu Leu  
   1                  5

aat gat cca cgt acg cta ttc ccg aaa gtc gat ccc cca aag caa agc 163  
 Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp Pro Pro Lys Gln Ser  
                                   10                                  15                                  20

cag ccg gaa cca ggc cta gat ata aaa ctt tcc ccc caa gcc gat att 211  
 Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser Pro Gln Ala Asp Ile  
                                   25                                  30                                  35

ggt ctc tcc agc tat caa gga agt gga agg ctt aag ggc cgc aag gct 259  
 Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu Lys Gly Arg Lys Ala  
                                   40                                  45                                  50

ctt att act ggt ggc gat tct ggg att gga gct gcc gta gca atc gct 307  
 Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala Ala Val Ala Ile Ala  
                                   55                                  60                                  65

tat gct cgc gag ggg gca gat gtt gcg atc gct tac ttg ccc gaa gaa 355  
 Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala Tyr Leu Pro Glu Glu  
                   70                                  75                                  80                                  85

caa gcc gat gct gac aga gtg ctc caa gca atc gag gaa aca ggt caa 403  
 Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile Glu Glu Thr Gly Gln  
                                   90                                  95                                  100

aaa gct ttt tct ttc cct ggt gat ctc cgt gat cca gaa tac tgt cgc 451  
 Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp Pro Glu Tyr Cys Arg  
                                   105                                  110                                  115

tcg ctg gtc caa gag acg gtg aac gct tta ggt ggc cta gac atc ttg 499  
 Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly Gly Leu Asp Ile Leu  
                                   120                                  125                                  130

gtc aac aac gcg tca cgt cag gtg tgg gca cct ggt ttg acc gaa att 547  
 Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro Gly Leu Thr Glu Ile

135	140	145	
acc gac gaa aac ttc gac cag act ttg cag gtt aac ctc tat ggt agt			595
Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val Asn Leu Tyr Gly Ser			
150	155	160	165
ttt cgg gtt acc aaa gca gct ata cct cat ctg aag ccc gga tca tcg			643
Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu Lys Pro Gly Ser Ser			
	170	175	180
ata atc ttt aca tcg tcc att cag gcg tac caa cct tcg gaa acc ctc			691
Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln Pro Ser Glu Thr Leu			
	185	190	195
ttg gat tac gcc atg act aag gcg gca ttg aac aat ttg tca aag ggc			739
Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn Asn Leu Ser Lys Gly			
	200	205	210
ttg gca agt agt ctg ata ggc gat ggc att cgg gta aat tct gta gcc			787
Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg Val Asn Ser Val Ala			
	215	220	225
cca ggt cct ttc tgg acg ccg ttg caa ccc agc cat ggt cag cca caa			835
Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser His Gly Gln Pro Gln			
	230	235	240
gag aaa ata gaa gga ttt ggc cag cac gct ccg att gga aga gcg ggt			883
Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro Ile Gly Arg Ala Gly			
	250	255	260
cac cct gtt gag ttg gca ggt gcg tac gtt ttt ctc gct tct gac gaa			931
His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe Leu Ala Ser Asp Glu			
	265	270	275
gcc agc tat gtg gta gga gaa acc ctg gga gtc aca ggt ggg acg ccc			979
Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val Thr Gly Gly Thr Pro			
	280	285	290
acc cca tagtcggtac aagcgggaatc act			1008
Thr Pro			
295			

&lt;210&gt; 318

&lt;211&gt; 295

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 318

Met	Ile	Ser	Leu	Leu	Asn	Asp	Pro	Arg	Thr	Leu	Phe	Pro	Lys	Val	Asp
1				5					10					15	

Pro	Pro	Lys	Gln	Ser	Gln	Pro	Glu	Pro	Gly	Leu	Asp	Ile	Lys	Leu	Ser
			20					25					30		

Pro	Gln	Ala	Asp	Ile	Gly	Leu	Ser	Ser	Tyr	Gln	Gly	Ser	Gly	Arg	Leu
		35					40					45			

Lys	Gly	Arg	Lys	Ala	Leu	Ile	Thr	Gly	Gly	Asp	Ser	Gly	Ile	Gly	Ala
	50					55					60				



Ala Val Ala Ile Ala Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala  
 65 70 75 80  
 Tyr Leu Pro Glu Glu Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile  
 85 90 95  
 Glu Glu Thr Gly Gln Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp  
 100 105 110  
 Pro Glu Tyr Cys Arg Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly  
 115 120 125  
 Gly Leu Asp Ile Leu Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro  
 130 135 140  
 Gly Leu Thr Glu Ile Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val  
 145 150 155 160  
 Asn Leu Tyr Gly Ser Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu  
 165 170 175  
 Lys Pro Gly Ser Ser Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln  
 180 185 190  
 Pro Ser Glu Thr Leu Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn  
 195 200 205  
 Asn Leu Ser Lys Gly Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg  
 210 215 220  
 Val Asn Ser Val Ala Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser  
 225 230 235 240  
 His Gly Gln Pro Gln Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro  
 245 250 255  
 Ile Gly Arg Ala Gly His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe  
 260 265 270  
 Leu Ala Ser Asp Glu Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val  
 275 280 285  
 Thr Gly Gly Thr Pro Thr Pro  
 290 295

<210> 319  
 <211> 1605  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1582)  
 <223> RXN01049

<400> 319  
 aagcacagca attgagcaat actcccatgc atgttttcgc gtgatcacgc tatatcctta 60  
 aagaatattc tttattagtc agaccttttaa aggaaacctt atg gga tca att cca 115  
 Met Gly Ser Ile Pro

	1	5	
aca atg tcc atc cct ttt gat gac tca cgt gga cct tat gtc ctt gct			163
Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly Pro Tyr Val Leu Ala			
	10	20	
atg gat att ggt tcc act gca tca cga ggt gga ctt tat gat gct tcc			211
Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly Leu Tyr Asp Ala Ser			
	25	35	
ggc tgc cca atc aaa ggc acc aag cag cgc gaa tcc cat gaa ttc acc			259
Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu Ser His Glu Phe Thr			
	40	50	
acc ggt gag ggc gtt tcc acc att gat gct gac cag gtg gtt tcg gag			307
Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp Gln Val Val Ser Glu			
	55	65	
atc acc tca gtt att aat ggc att ttg aac gcg gct gat cat cac aac			355
Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala Ala Asp His His Asn			
	70	85	
atc aaa gat cag atc gcc gct gtc gcg cta gat tct ttt gca tcc tca			403
Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp Ser Phe Ala Ser Ser			
	90	100	
tta atc ttg gtc gat ggt gaa ggc aat gcg ctc acc ccg tgc att acc			451
Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu Thr Pro Cys Ile Thr			
	105	115	
tac gcg gat tct cgt tct gca cag tat gtg gag cag ctg cgc gcg gaa			499
Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu Gln Leu Arg Ala Glu			
	120	130	
atc gat gag aag gcc tac cac ggc cgc acc ggc gtc tgc ttg cac acc			547
Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly Val Cys Leu His Thr			
	135	145	
tcc tac cac cca tcg cgc ttg ctg tgg ctg aaa act gag ttc gag aaa			595
Ser Tyr His Pro Ser Arg Leu Leu Trp Leu Lys Thr Glu Phe Glu Lys			
	150	165	
gag ttc aac aaa gcc aag tat gtg atg acc atc ggt gag tac gtc tac			643
Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile Gly Glu Tyr Val Tyr			
	170	180	
ttc aaa ctt gca ggc atc acc gga atg gct act tcg att gcc gcg tgg			691
Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr Ser Ile Ala Ala Trp			
	185	195	
agt ggc att ttg gac gcc cat acc ggc gaa ctt gat ctg act atc ttg			739
Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu Asp Leu Thr Ile Leu			
	200	210	
gag cac atc ggt gtt gat ccg gct ctg ttc ggt gag atc aga aac cct			787
Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly Glu Ile Arg Asn Pro			
	215	225	
gat gaa cca gcc acc gat gcc aaa gtt gtc gac aaa aag tgg aag cac			835
Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp Lys Lys Trp Lys His			
	230	245	

ctg gaa gaa atc cct tgg ttc cat gcc att cca gac ggc tgg cct tcc	883
Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro Asp Gly Trp Pro Ser	
250 255 260	
aac att ggc cca ggc gcc gtg gat tct aaa acc gtc gca gtc gcc gcc	931
Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr Val Ala Val Ala Ala	
265 270 275	
gct aca tcc ggc gcc atg cgc gtg atc ctt ccg agc gtt ccc gaa cag	979
Ala Thr Ser Gly Ala Met Arg Val Ile Leu Pro Ser Val Pro Glu Gln	
280 285 290	
atc ccc tct ggc ctg tgg tgt tac cgc gtt tcc cgc gac cag tgc atc	1027
Ile Pro Ser Gly Leu Trp Cys Tyr Arg Val Ser Arg Asp Gln Cys Ile	
295 300 305	
gtt ggt ggc gca ctc aac gac gtc gga cgc gcc gtc acc tgg ctg gaa	1075
Val Gly Gly Ala Leu Asn Asp Val Gly Arg Ala Val Thr Trp Leu Glu	
310 315 320 325	
cgc acc att atc aag cct gaa aac ctc gac gaa gtg ctg atc cgc gaa	1123
Arg Thr Ile Ile Lys Pro Glu Asn Leu Asp Glu Val Leu Ile Arg Glu	
330 335 340	
ccc ctc gaa ggc acc cca gct gtc ctg ccg ttc ttc tcc ggg gaa cgc	1171
Pro Leu Glu Gly Thr Pro Ala Val Leu Pro Phe Phe Ser Gly Glu Arg	
345 350 355	
tcc atc ggc tgg gca gcc tca gcg cag gcc acg atc acc aac att cag	1219
Ser Ile Gly Trp Ala Ala Ser Ala Gln Ala Thr Ile Thr Asn Ile Gln	
360 365 370	
gaa caa acc ggc cct gaa cac ttg tgg cgc ggc gtt ttc gaa gcc ctc	1267
Glu Gln Thr Gly Pro Glu His Leu Trp Arg Gly Val Phe Glu Ala Leu	
375 380 385	
gca ctc tcc tac cag cgc gtt tgg gaa cac atg ggg aaa gcc ggc gca	1315
Ala Leu Ser Tyr Gln Arg Val Trp Glu His Met Gly Lys Ala Gly Ala	
390 395 400 405	
gcc cct gaa cgg gtc atc gca tca gga cga gtc tcc acc gac cac cca	1363
Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val Ser Thr Asp His Pro	
410 415 420	
gaa ttc ctc gcg atg ctt tcc gac gcc ctc gac acc cca gtc atc cct	1411
Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp Thr Pro Val Ile Pro	
425 430 435	
ctg gaa atg aag cgc gcc acc ctc cgc ggc acc gca ctt atc gtc ctt	1459
Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr Ala Leu Ile Val Leu	
440 445 450	
gag cag ctc gaa cca ggc ggc acg cgc gcg acg cca cca ttc ggc acg	1507
Glu Gln Leu Glu Pro Gly Gly Thr Arg Ala Thr Pro Pro Phe Gly Thr	
455 460 465	
acg cat cag ccg cgc ttt gcg cac cat tac tcc aag gca aga gag ctt	1555
Thr His Gln Pro Arg Phe Ala His His Tyr Ser Lys Ala Arg Glu Leu	
470 475 480 485	

ttc gac gcc ctc tac ctc aag ttg gtc tagcttttcg cagtgggaacg 1602  
 Phe Asp Ala Leu Tyr Leu Lys Leu Val  
 490

cgc 1605

<210> 320

<211> 494

<212> PRT

<213> Corynebacterium glutamicum

<400> 320

Met Gly Ser Ile Pro Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly  
 1 5 10 15  
 Pro Tyr Val Leu Ala Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly  
 20 25 30  
 Leu Tyr Asp Ala Ser Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu  
 35 40 45  
 Ser His Glu Phe Thr Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp  
 50 55 60  
 Gln Val Val Ser Glu Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala  
 65 70 75 80  
 Ala Asp His His Asn Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp  
 85 90 95  
 Ser Phe Ala Ser Ser Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu  
 100 105 110  
 Thr Pro Cys Ile Thr Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu  
 115 120 125  
 Gln Leu Arg Ala Glu Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly  
 130 135 140  
 Val Cys Leu His Thr Ser Tyr His Pro Ser Arg Leu Leu Trp Leu Lys  
 145 150 155 160  
 Thr Glu Phe Glu Lys Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile  
 165 170 175  
 Gly Glu Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr  
 180 185 190  
 Ser Ile Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu  
 195 200 205  
 Asp Leu Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly  
 210 215 220  
 Glu Ile Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp  
 225 230 235 240  
 Lys Lys Trp Lys His Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro  
 245 250 255

<400> 321  
cacagtatgt ggagcagctg cgcgcgga aa tcgatgagaa ggcctaccac ggccgcaccg 60  
gcgtctgctt gcacacctcc taccacccat cgcgcttgct gtg gtg aaa act gag 115  
Val Val.Lys Thr Glu

	1	5	
ttc gag aaa gag ttc aac aaa gcc aag tat gtg atg acc atc ggt gag			163
Phe Glu Lys Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile Gly Glu			
	10	20	
tac gtc tac ttc aaa ctt gca ggc atc acc gga atg gct act tcg att			211
Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr Ser Ile			
	25	35	
gcc gcg tgg agt ggc att ttg gac gcc cat acc ggc gaa ctt gat ctg			259
Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu Asp Leu			
	40	50	
act atc ttg gag cac atc ggt gtt gat ccg gct ctg ttc ggt gag atc			307
Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly Glu Ile			
	55	65	
aga aac cct gat gaa cca gcc acc gat gcc aaa gtt gtc gac aaa aag			355
Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp Lys Lys			
	70	85	
tgg aag cac ctg gaa gaa atc cct tgg ttc cat gcc att cca gac ggc			403
Trp Lys His Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro Asp Gly			
	90	100	
tgg cct tcc aac att ggc cca ggc gcc gtg gat tct aaa acc gtc gca			451
Trp Pro Ser Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr Val Ala			
	105	115	
gtc gcc gcc gct aca tcc ggc gcc atg cgc gtg atc ctt ccg agc gtt			499
Val Ala Ala Ala Thr Ser Gly Ala Met Arg Val Ile Leu Pro Ser Val			
	120	130	
ccc gaa cag atc ccc tct ggc ctg tgg tgt tac cgc gtt tcc cgc gac			547
Pro Glu Gln Ile Pro Ser Gly Leu Trp Cys Tyr Arg Val Ser Arg Asp			
	135	145	
cag tgc atc gtt ggt ggc gca ctc aac gac gtc gga cgc gcc gtc acc			595
Gln Cys Ile Val Gly Gly Ala Leu Asn Asp Val Gly Arg Ala Val Thr			
	150	165	
tgg ctg gaa cgc acc att atc aag cct gaa aac ctc gac gaa gtg ctg			643
Trp Leu Glu Arg Thr Ile Ile Lys Pro Glu Asn Leu Asp Glu Val Leu			
	170	180	
atc cgc gaa ccc ctc gaa ggc acc cca gct gtc ctg ccg ttc ttc tcc			691
Ile Arg Glu Pro Leu Glu Gly Thr Pro Ala Val Leu Pro Phe Phe Ser			
	185	195	
ggg gaa cgc tcc atc ggc tgg gca gcc tca gcg cag gcc acg atc acc			739
Gly Glu Arg Ser Ile Gly Trp Ala Ala Ser Ala Gln Ala Thr Ile Thr			
	200	210	
aac att cag gaa caa acc ggc cct gaa cac ttg tgg cgc ggc gtt ttc			787
Asn Ile Gln Glu Gln Thr Gly Pro Glu His Leu Trp Arg Gly Val Phe			
	215	225	
gaa gcc ctc gca ctc tcc tac cag cgc gtt tgg gaa cac atg ggg aaa			835
Glu Ala Leu Ala Leu Ser Tyr Gln Arg Val Trp Glu His Met Gly Lys			
	230	245	

gcc ggc gca gcc cct gaa cgg gtc atc gca tca gga cga gtc tcc acc 883  
 Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val Ser Thr  
                   250                  255                  260

gac cac cca gaa ttc ctc gcg atg ctt tcc gac gcc ctc gac acc cca 931  
 Asp His Pro Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp Thr Pro  
                   265                  270                  275

gtc atc cct ctg gaa atg aag cgc gcc acc ctc cgc ggc acc gca ctt 979  
 Val Ile Pro Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr Ala Leu  
                   280                  285                  290

atc gtc ctt gag cag ctc gaa cca ggc ggc acg cgc gcg acg cca cca 1027  
 Ile Val Leu Glu Gln Leu Glu Pro Gly Gly Thr Arg Ala Thr Pro Pro  
                   295                  300                  305

ttc ggc acg acg cat cag ccg cgc ttt gcg cac cat tac tcc aag gca 1075  
 Phe Gly Thr Thr His Gln Pro Arg Phe Ala His His Tyr Ser Lys Ala  
 310                  315                  320                  325

aga gag ctt ttc gac gcc ctc tac ctc aag ttg gtc tagcttttcg 1121  
 Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu Val  
                   330                  335

cagtggaacg cgc 1134

<210> 322  
 <211> 337  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 322  
 Val Val Lys Thr Glu Phe Glu Lys Glu Phe Asn Lys Ala Lys Tyr Val  
   1                  5                  10                  15

Met Thr Ile Gly Glu Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly  
                   20                  25                  30

Met Ala Thr Ser Ile Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr  
                   35                  40                  45

Gly Glu Leu Asp Leu Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala  
                   50                  55                  60

Leu Phe Gly Glu Ile Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys  
                   65                  70                  75                  80

Val Val Asp Lys Lys Trp Lys His Leu Glu Glu Ile Pro Trp Phe His  
                   85                  90                  95

Ala Ile Pro Asp Gly Trp Pro Ser Asn Ile Gly Pro Gly Ala Val Asp  
                   100                  105                  110

Ser Lys Thr Val Ala Val Ala Ala Thr Ser Gly Ala Met Arg Val  
                   115                  120                  125

Ile Leu Pro Ser Val Pro Glu Gln Ile Pro Ser Gly Leu Trp Cys Tyr  
                   130                  135                  140

Arg Val Ser Arg Asp Gln Cys Ile Val Gly Gly Ala Leu Asn Asp Val  
 145 150 155 160  
 Gly Arg Ala Val Thr Trp Leu Glu Arg Thr Ile Ile Lys Pro Glu Asn  
 165 170 175  
 Leu Asp Glu Val Leu Ile Arg Glu Pro Leu Glu Gly Thr Pro Ala Val  
 180 185 190  
 Leu Pro Phe Phe Ser Gly Glu Arg Ser Ile Gly Trp Ala Ala Ser Ala  
 195 200 205  
 Gln Ala Thr Ile Thr Asn Ile Gln Glu Gln Thr Gly Pro Glu His Leu  
 210 215 220  
 Trp Arg Gly Val Phe Glu Ala Leu Ala Leu Ser Tyr Gln Arg Val Trp  
 225 230 235 240  
 Glu His Met Gly Lys Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser  
 245 250 255  
 Gly Arg Val Ser Thr Asp His Pro Glu Phe Leu Ala Met Leu Ser Asp  
 260 265 270  
 Ala Leu Asp Thr Pro Val Ile Pro Leu Glu Met Lys Arg Ala Thr Leu  
 275 280 285  
 Arg Gly Thr Ala Leu Ile Val Leu Glu Gln Leu Glu Pro Gly Gly Thr  
 290 295 300  
 Arg Ala Thr Pro Pro Phe Gly Thr Thr His Gln Pro Arg Phe Ala His  
 305 310 315 320  
 His Tyr Ser Lys Ala Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu  
 325 330 335

Val

<210> 323  
 <211> 597  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(574)  
 <223> FRXA01050

<400> 323  
 aagcacagca attgagcaat actcccatgc atgttttcgc gtgatcacgc tatatcctta 60  
 aagaatattc tttattagtc agacctttaa aggaaacctt atg gga tca att cca 115  
 Met Gly Ser Ile Pro  
 1 5  
 aca atg tcc atc cct ttt gat gac tca cgt gga cct tat gtc ctt gct 163  
 Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly Pro Tyr Val Leu Ala  
 10 15 20



atg gat att ggt tcc act gca tca cga ggt gga ctt tat gat gct tcc 211  
 Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly Leu Tyr Asp Ala Ser  
                   25                  30                  35  
  
 ggc tgc cca atc aaa ggc acc aag cag cgc gaa tcc cat gaa ttc acc 259  
 Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu Ser His Glu Phe Thr  
                   40                  45                  50  
  
 acc ggt gag ggc gtt tcc acc att gat gct gac cag gtg gtt tcg gag 307  
 Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp Gln Val Val Ser Glu  
                   55                  60                  65  
  
 atc acc tca gtt att aat ggc att ttg aac gcg gct gat cat cac aac 355  
 Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala Ala Asp His His Asn  
                   70                  75                  80                  85  
  
 atc aaa gat cag atc gcc gct gtc gcg cta gat tct ttt gca tcc tca 403  
 Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp Ser Phe Ala Ser Ser  
                   90                  95                  100  
  
 tta atc ttg gtc gat ggt gaa ggc aat gcg ctc acc ccg tgc att acc 451  
 Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu Thr Pro Cys Ile Thr  
                   105                  110                  115  
  
 tac gcg gat tct cgt tct gca cag tat gtg gag cag ctg cgc gcg gaa 499  
 Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu Gln Leu Arg Ala Glu  
                   120                  125                  130  
  
 atc gat gag aag gcc tac cac ggc cgc acc ggc gtc tgc ttg cac acc 547  
 Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly Val Cys Leu His Thr  
                   135                  140                  145  
  
 tcc tac cac cca tcg cgc ttg ctg tgg tgaaaaactga gttcgagaaa 594  
 Ser Tyr His Pro Ser Arg Leu Leu Trp  
                   150                  155  
  
 gag 597

&lt;210&gt; 324

&lt;211&gt; 158

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 324

Met Gly Ser Ile Pro Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly  
   1                  5                  10                  15  
  
 Pro Tyr Val Leu Ala Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly  
                   20                  25                  30  
  
 Leu Tyr Asp Ala Ser Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu  
                   35                  40                  45  
  
 Ser His Glu Phe Thr Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp  
                   50                  55                  60  
  
 Gln Val Val Ser Glu Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala  
                   65                  70                  75                  80  
  
 Ala Asp His His Asn Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp

				85						90									95
Ser	Phe	Ala	Ser	Ser	Leu	Ile	Leu	Val	Asp	Gly	Glu	Gly	Asn	Ala	Leu				
			100					105					110						
Thr	Pro	Cys	Ile	Thr	Tyr	Ala	Asp	Ser	Arg	Ser	Ala	Gln	Tyr	Val	Glu				
		115					120					125							
Gln	Leu	Arg	Ala	Glu	Ile	Asp	Glu	Lys	Ala	Tyr	His	Gly	Arg	Thr	Gly				
		130				135					140								
Val	Cys	Leu	His	Thr	Ser	Tyr	His	Pro	Ser	Arg	Leu	Leu	Trp						
145					150					155									

<210> 325  
<211> 1065  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1042)  
<223> RXA00202

<400> 325  
ctggcagcag attgtcatcg gttgtgtcat cgcgcttgcg gtgggcttcg atgtcatccg 60  
aaacaaaacc tctaagtaat tcctgaaagg aaattttcac atg tac gct cgt aaa 115  
Met Tyr Ala Arg Lys  
1 5  
ctt att gct ctg tcc gct tct gtc gtt ttg gct ttc agc ttg tct gct 163  
Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala Phe Ser Leu Ser Ala  
10 15 20  
tgc aac cgt gaa tct tct ggc acc agc gca gac ggc ggt tct gcg gat 211  
Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp Gly Gly Ser Ala Asp  
25 30 35  
ggg tcg atc acc ttg gct ctg tct acc cag acc aac ccg ttc ttt gtg 259  
Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr Asn Pro Phe Phe Val  
40 45 50  
cag ctt cgt gat ggt gcc cag gaa aag gct gat gaa ttg ggc gtg acc 307  
Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp Glu Leu Gly Val Thr  
55 60 65  
ctc aat gtt cag gat gct tcc gat gac gct gca acg cag gcc aac cag 355  
Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala Thr Gln Ala Asn Gln  
70 75 80 85  
ctc aac aac gct gtc acc acc ggt gct ggc gtg gtg att gtc aac cca 403  
Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val Val Ile Val Asn Pro  
90 95 100  
act gat tct gat gct gtg gtg ccg tcg gtg gaa gct ctc aac cag gct 451  
Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu Ala Leu Asn Gln Ala  
105 110 115  
gac att cct gtt gtg gct gtc gac cgt tcc tcc aat ggt gcc gag gtg 499

```

Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser Asn Gly Gly Glu Val
    120                      125                      130

gcg tcc ttc gtg gca tct gac aac gtt gct ggc ggc gcg cag gct gct 547
Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly Gly Ala Gln Ala Ala
    135                      140                      145

gca gcc ctg gca gag gcg atc ggt ggc gaa ggt gaa atc ctc atg ctg 595
Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly Glu Ile Leu Met Leu
    150                      155                      160                      165

caa ggc att gcg gga tcc tct gca tca cgt gat cgt gga cag gga ttt 643
Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp Arg Gly Gln Gly Phe
    170                      175                      180

gaa gag gag atc gct aag cat gag ggc att tcc att gtg gct aag cag 691
Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser Ile Val Ala Lys Gln
    185                      190                      195

acc gcc aac ttt gac cgc ggt gag ggc ctg gac gtg gca act aac ctg 739
Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp Val Ala Thr Asn Leu
    200                      205                      210

ctg cag gca cac ccc aat gtg aag gcg atc ttc gcg gaa aac gat gag 787
Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe Ala Glu Asn Asp Glu
    215                      220                      225

atg gcg ttg ggc gca atc gaa gcc ctg ggt gct cgt gct ggt gaa gat 835
Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala Arg Ala Gly Glu Asp
    230                      235                      240                      245

gtc atc gtt gtc ggt ttc gat ggc acc aat gat ggt ctg gca gcg gtt 883
Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp Gly Leu Ala Ala Val
    250                      255                      260

gaa gat gga cgc atg ttg gcc acc gtt gct cag cag cca gaa gag ctg 931
Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln Gln Pro Glu Glu Leu
    265                      270                      275

gga gca aag gct gtg gaa gaa gca gct aag ctc ctg cgc ggt gag gac 979
Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu Leu Arg Gly Glu Asp
    280                      285                      290

gct gaa aca gag gta cca gtt gag gtt gtc act gtg aag ctc gac aac 1027
Ala Glu Thr Glu Val Pro Val Glu Val Val Thr Val Lys Leu Asp Asn
    295                      300                      305

gtc gcg gac ttc aag tagtcggcga tgaaaaagtc cgt 1065
Val Ala Asp Phe Lys
310

```

&lt;210&gt; 326

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 326

```

Met Tyr Ala Arg Lys Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala
  1                      5                      10                      15

```

Phe Ser Leu Ser Ala Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp  
                   20                                  25                                  30  
 Gly Gly Ser Ala Asp Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr  
                   35                                  40                                  45  
 Asn Pro Phe Phe Val Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp  
                   50                                  55                                  60  
 Glu Leu Gly Val Thr Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala  
                   65                                  70                                  75                                  80  
 Thr Gln Ala Asn Gln Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val  
                                   85                                  90                                  95  
 Val Ile Val Asn Pro Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu  
                                   100                                  105                                  110  
 Ala Leu Asn Gln Ala Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser  
                   115                                  120                                  125  
 Asn Gly Gly Glu Val Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly  
                   130                                  135                                  140  
 Gly Ala Gln Ala Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly  
                   145                                  150                                  155                                  160  
 Glu Ile Leu Met Leu Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp  
                                   165                                  170                                  175  
 Arg Gly Gln Gly Phe Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser  
                                   180                                  185                                  190  
 Ile Val Ala Lys Gln Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp  
                   195                                  200                                  205  
 Val Ala Thr Asn Leu Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe  
                   210                                  215                                  220  
 Ala Glu Asn Asp Glu Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala  
                   225                                  230                                  235                                  240  
 Arg Ala Gly Glu Asp Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp  
                                   245                                  250                                  255  
 Gly Leu Ala Ala Val Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln  
                   260                                  265                                  270  
 Gln Pro Glu Glu Leu Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu  
                   275                                  280                                  285  
 Leu Arg Gly Glu Asp Ala Glu Thr Glu Val Pro Val Glu Val Val Thr  
                   290                                  295                                  300  
 Val Lys Leu Asp Asn Val Ala Asp Phe Lys  
                   305                                  310

&lt;210&gt; 327

&lt;211&gt; 1077

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1054)

&lt;223&gt; RXN00872

&lt;400&gt; 327

```

gaaatgtatt gctttgtcag gacaatgtgt tattgtcatg acatgcgatc gtgaggggtcg 60

ccacattcca tcaaaaatga gtgaagggtt gcatcgccac atg act aac ttg acg 115
                                   Met Thr Asn Leu Thr
                                   1 5

agc act cac gaa gtc cta gct atc ggc cgc ttg ggc gta gat att tac 163
Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu Gly Val Asp Ile Tyr
                                   10 15 20

cca ctt caa agt gga gta gga ctg gcc gat gtt caa tct ttc ggc aag 211
Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val Gln Ser Phe Gly Lys
                                   25 30 35

tac ctc ggc gga agc gca gca aac gtt tct gtt gca gcc gcc cgc cat 259
Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val Ala Ala Ala Arg His
                                   40 45 50

gga cac aat tcc gca ctg ctg tcc cgt gtg gga aat gat cct ttc ggc 307
Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly Asn Asp Pro Phe Gly
                                   55 60 65

gag tac ctg ctt gct gag ctg gag cgt ttg ggc gtg gac aac cag tac 355
Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly Val Asp Asn Gln Tyr
                                   70 75 80 85

gtt gcc acc gat cag act ttt aag acc cca gtg acc ttc tgt gaa att 403
Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val Thr Phe Cys Glu Ile
                                   90 95 100

ttc cca ccg gat gat ttc cca ctg tac ttc tac cgc gaa cca aag gct 451
Phe Pro Pro Asp Phe Pro Leu Tyr Phe Tyr Arg Glu Pro Lys Ala
                                   105 110 115

ccg gat ctc aat att gaa tcc gca gac gtc agc ctg gac gat gtg cgc 499
Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser Leu Asp Asp Val Arg
                                   120 125 130

gaa gcc gat att ttg tgg ttc aca ctc act ggt ttc agt gaa gag cca 547
Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly Phe Ser Glu Glu Pro
                                   135 140 145

agc cgc ggc aca cac cgc gag atc ttg act act cgt gcg aac cgt cgc 595
Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr Arg Ala Asn Arg Arg
                                   150 155 160 165

cac acc atc ttt gat ctg gac tac cga cca atg ttc tgg gaa tcc cca 643
His Thr Ile Phe Asp Leu Asp Tyr Arg Pro Met Phe Trp Glu Ser Pro
                                   170 175 180

gaa gag gcc acc aag cag gcg gaa tgg gcg ttg cag cat tcc acg gtg 691
Glu Glu Ala Thr Lys Gln Ala Glu Trp Ala Leu Gln His Ser Thr Val
                                   185 190 195

```

gcg gtt ggc aac aag gaa gaa tgc gaa atc gca gtg ggc gag acc gag 739  
 Ala Val Gly Asn Lys Glu Glu Cys Glu Ile Ala Val Gly Glu Thr Glu  
           200                                  205                                  210

cca gag cgc gcg ggc cga gca ctg ttg gaa cgc ggt gtg gag ttg gcc 787  
 Pro Glu Arg Ala Gly Arg Ala Leu Leu Glu Arg Gly Val Glu Leu Ala  
           215                                  220                                  225

atc gtc aag cag gga cct aag ggt gtc atg gcg atg acc aag gac gaa 835  
 Ile Val Lys Gln Gly Pro Lys Gly Val Met Ala Met Thr Lys Asp Glu  
           230                                  235                                  240                                  245

acc gta gaa gtt cct ccg ttc ttc gtc gat gtc atc aac ggt ctt ggt 883  
 Thr Val Glu Val Pro Pro Phe Phe Val Asp Val Ile Asn Gly Leu Gly  
                                   250                                  255                                  260

gcc ggc gat gca ttc ggc ggc gcg ctg tgc cac ggt ctg ctc tct gaa 931  
 Ala Gly Asp Ala Phe Gly Gly Ala Leu Cys His Gly Leu Leu Ser Glu  
                                   265                                  270                                  275

tgg ccg ttg gaa aag gtt ctc cgt ttt gcc aac acc gcg ggt gcg ctt 979  
 Trp Pro Leu Glu Lys Val Leu Arg Phe Ala Asn Thr Ala Gly Ala Leu  
                                   280                                  285                                  290

gtg gcg tcc cgt ctt gaa tgc tcc acc gca atg cct act acc gat gag 1027  
 Val Ala Ser Arg Leu Glu Cys Ser Thr Ala Met Pro Thr Thr Asp Glu  
           295                                  300                                  305

gtg gaa gcc tcc ctc aac cag aaa gtc tgatatgact cctccgatta 1074  
 Val Glu Ala Ser Leu Asn Gln Lys Val  
           310                                  315

tct 1077

&lt;210&gt; 328

&lt;211&gt; 318

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 328

Met Thr Asn Leu Thr Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu  
   1                                  5                                  10                                  15

Gly Val Asp Ile Tyr Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val  
           20                                  25                                  30

Gln Ser Phe Gly Lys Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val  
           35                                  40                                  45

Ala Ala Ala Arg His Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly  
           50                                  55                                  60

Asn Asp Pro Phe Gly Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly  
   65                                  70                                  75                                  80

Val Asp Asn Gln Tyr Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val  
                                   85                                  90                                  95

Thr Phe Cys Glu Ile Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr

100 105 110  
 Arg Glu Pro Lys Ala Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser  
 115 120 125  
 Leu Asp Asp Val Arg Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly  
 130 135 140  
 Phe Ser Glu Glu Pro Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr  
 145 150 155 160  
 Arg Ala Asn Arg Arg His Thr Ile Phe Asp Leu Asp Tyr Arg Pro Met  
 165 170 175  
 Phe Trp Glu Ser Pro Glu Glu Ala Thr Lys Gln Ala Glu Trp Ala Leu  
 180 185 190  
 Gln His Ser Thr Val Ala Val Gly Asn Lys Glu Glu Cys Glu Ile Ala  
 195 200 205  
 Val Gly Glu Thr Glu Pro Glu Arg Ala Gly Arg Ala Leu Leu Glu Arg  
 210 215 220  
 Gly Val Glu Leu Ala Ile Val Lys Gln Gly Pro Lys Gly Val Met Ala  
 225 230 235 240  
 Met Thr Lys Asp Glu Thr Val Glu Val Pro Pro Phe Phe Val Asp Val  
 245 250 255  
 Ile Asn Gly Leu Gly Ala Gly Asp Ala Phe Gly Gly Ala Leu Cys His  
 260 265 270  
 Gly Leu Leu Ser Glu Trp Pro Leu Glu Lys Val Leu Arg Phe Ala Asn  
 275 280 285  
 Thr Ala Gly Ala Leu Val Ala Ser Arg Leu Glu Cys Ser Thr Ala Met  
 290 295 300  
 Pro Thr Thr Asp Glu Val Glu Ala Ser Leu Asn Gln Lys Val  
 305 310 315  
  
 <210> 329  
 <211> 622  
 <212> DNA  
 <213> Corynebacterium glutamicum  
  
 <220>  
 <221> CDS  
 <222> (101)..(622)  
 <223> FRXA00872  
  
 <400> 329  
 gaaatgtatt gctttgtcag gacaatgtgt tattgtcatg acatgcgatac gtgagggtcg 60  
  
 ccacattcca tcaaaaatga gtgaagggtt gcatcgccac atg act aac ttg acg 115  
 Met Thr Asn Leu Thr  
 1 5  
  
 agc act cac gaa gtc cta gct atc ggc cgc ttg ggc gta gat att tac 163  
 Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu Gly Val Asp Ile Tyr

	10	15	20	
cca ctt caa agt gga gta gga ctg gcc gat gtt caa tct ttc ggc aag				211
Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val Gln Ser Phe Gly Lys				
	25	30	35	
tac ctc ggc gga agc gca gca aac gtt tct gtt gca gcc gcc cgc cat				259
Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val Ala Ala Ala Arg His				
	40	45	50	
gga cac aat tcc gca ctg ctg tcc cgt gtg gga aat gat cct ttc ggc				307
Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly Asn Asp Pro Phe Gly				
	55	60	65	
gag tac ctg ctt gct gag ctg gag cgt ttg ggc gtg gac aac cag tac				355
Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly Val Asp Asn Gln Tyr				
	70	75	80	85
gtt gcc acc gat cag act ttt aag acc cca gtg acc ttc tgt gaa att				403
Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val Thr Phe Cys Glu Ile				
	90	95	100	
ttc cca ccg gat gat ttc cca ctg tac ttc tac cgc gaa cca aag gct				451
Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr Arg Glu Pro Lys Ala				
	105	110	115	
ccg gat ctc aat att gaa tcc gca gac gtc agc ctg gac gat gtg cgc				499
Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser Leu Asp Asp Val Arg				
	120	125	130	
gaa gcc gat att ttg tgg ttc aca ctc act ggt ttc agt gaa gag cca				547
Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly Phe Ser Glu Glu Pro				
	135	140	145	
agc cgc ggc aca cac cgc gag atc ttg act act cgt gcg aac cgt cgc				595
Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr Arg Ala Asn Arg Arg				
	150	155	160	165
cac acc atc ttt gat ctg gac tac cga				622
His Thr Ile Phe Asp Leu Asp Tyr Arg				
	170			

&lt;210&gt; 330

&lt;211&gt; 174

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 330

Met	Thr	Asn	Leu	Thr	Ser	Thr	His	Glu	Val	Leu	Ala	Ile	Gly	Arg	Leu
1				5					10					15	

Gly	Val	Asp	Ile	Tyr	Pro	Leu	Gln	Ser	Gly	Val	Gly	Leu	Ala	Asp	Val
			20					25					30		

Gln	Ser	Phe	Gly	Lys	Tyr	Leu	Gly	Gly	Ser	Ala	Ala	Asn	Val	Ser	Val
		35					40					45			

Ala	Ala	Ala	Arg	His	Gly	His	Asn	Ser	Ala	Leu	Leu	Ser	Arg	Val	Gly
	50					55					60				



Asn Asp Pro Phe Gly Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly  
 65 70 75 80  
 Val Asp Asn Gln Tyr Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val  
 85 90 95  
 Thr Phe Cys Glu Ile Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr  
 100 105 110  
 Arg Glu Pro Lys Ala Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser  
 115 120 125  
 Leu Asp Asp Val Arg Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly  
 130 135 140  
 Phe Ser Glu Glu Pro Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr  
 145 150 155 160  
 Arg Ala Asn Arg Arg His Thr Ile Phe Asp Leu Asp Tyr Arg  
 165 170

<210> 331  
 <211> 1767  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(1744)  
 <223> RXN00799

<400> 331  
 ttgtctaacc ccgtataggt gagaaatggt ggacaagtgt ctgttttttg tgggggaaat 60  
 ctgactacga tggttaagaaa taaggaaaga gattaccatt atg tct caa gag cgg 115  
 Met Ser Gln Glu Arg 5  
 cct caa atc ggc tcc cgc ctc tct cgt gtc att gaa caa gac ggc cta 163  
 Pro Gln Ile Gly Ser Arg Leu Ser Arg Val Ile Glu Gln Asp Gly Leu 20  
 caa ttc cgc gat ctc gac ggc gac ggc gta ctt gca cct tat gaa gat 211  
 Gln Phe Arg Asp Leu Asp Gly Asp Gly Val Leu Ala Pro Tyr Glu Asp 35  
 tgg cgt cta acc cca gca gag cgt gcc gct gac ctg gtg aaa cgt atg 259  
 Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp Leu Val Lys Arg Met 50  
 aat gtg gaa gaa aaa gcg ggc ctg atg atc atc ggt tcg cac tac ccc 307  
 Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile Gly Ser His Tyr Pro 65  
 gga tac tcg cct ttg gcg ccg gag agt gaa ggc aaa gac gcg gaa aag 355  
 Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly Lys Asp Ala Glu Lys 85  
 tgc gag cct ttg ctg aac cct gtc gat atg tgg cgt gag gat aac ccg 403  
 Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn Pro

90										95										100									
atc	acg	ggg	gtt	cct	ttc	acc	gag	cct	gtg	ctg	gca	act	tct	tcc	act					451									
Ile	Thr	Gly	Val	Pro	Phe	Thr	Glu	Pro	Val	Leu	Ala	Thr	Ser	Ser	Thr														
			105																										
gaa	aat	gcc	att	aac	ctg	cgc	aat	cag	cgt	tac	tta	att	gtt	cgt	gac					499									
Glu	Asn	Ala	Ile	Asn	Leu	Arg	Asn	Gln	Arg	Tyr	Leu	Ile	Val	Arg	Asp														
			120																										
aac	ctg	cca	gct	cgt	ggg	ctt	gct	act	tgg	acc	aat	gct	gtt	cag	gaa					547									
Asn	Leu	Pro	Ala	Arg	Gly	Leu	Ala	Thr	Trp	Thr	Asn	Ala	Val	Gln	Glu														
			135																										
gtc	gcg	gag	cga	tcc	cgt	ttg	ggg	att	cct	gtt	gcg	ttt	gcg	tcg	aat					595									
Val	Ala	Glu	Arg	Ser	Arg	Leu	Gly	Ile	Pro	Val	Ala	Phe	Ala	Ser	Asn														
cct	cgt	aac	cac	gtc	gcg	ctc	gtt	gcg	cag	ttc	ggg	gtg	aac	gag	tcc					643									
Pro	Arg	Asn	His	Val	Ala	Leu	Val	Ala	Gln	Phe	Gly	Val	Asn	Glu	Ser														
gcg	ggg	gtg	ttc	tct	gag	tgg	cct	ggc	gag	ctg	ggg	ctt	gct	gcg	ctt					691									
Ala	Gly	Val	Phe	Ser	Glu	Trp	Pro	Gly	Glu	Leu	Gly	Leu	Ala	Ala	Leu														
cgc	gat	gct	gaa	ctg	atg	gag	act	ttc	ggg	acc	gag	gct	gct	aaa	gaa					739									
Arg	Asp	Ala	Glu	Leu	Met	Glu	Thr	Phe	Gly	Thr	Glu	Ala	Ala	Lys	Glu														
tgg	cgt	gcc	ggg	ggg	gtg	cac	aag	ctg	tac	ggg	tac	atg	gct	gac	ctc					787									
Trp	Arg	Ala	Gly	Gly	Val	His	Lys	Leu	Tyr	Gly	Tyr	Met	Ala	Asp	Leu														
gct	tct	gag	cct	cgt	tgg	tcc	cgc	ttc	aac	ggg	act	ttt	ggg	gag	gat					835									
Ala	Ser	Glu	Pro	Arg	Trp	Ser	Arg	Phe	Asn	Gly	Thr	Phe	Gly	Glu	Asp														
ccg	gag	ttg	atc	tct	gat	tac	atc	gct	gct	gtt	gtg	cgt	ggg	ttg	cag					883									
Pro	Glu	Leu	Ile	Ser	Asp	Tyr	Ile	Ala	Ala	Val	Val	Arg	Gly	Leu	Gln														
ggc	cct	gag	ctg	tcc	aag	aat	tcc	gtg	tcg	acc	acc	att	aag	cac	ttc					931									
Gly	Pro	Glu	Leu	Ser	Lys	Asn	Ser	Val	Ser	Thr	Thr	Ile	Lys	His	Phe														
cca	ggg	ggc	ggc	gtg	cgc	ctc	gac	ggc	cac	gat	cct	cac	ttc	cac	tgg					979									
Pro	Gly	Gly	Gly	Val	Arg	Leu	Asp	Gly	His	Asp	Pro	His	Phe	His	Trp														
ggg	cag	acc	aat	gag	tac	cca	acc	gaa	gat	gcg	ctg	ggc	aag	tac	cat					1027									
Gly	Gln	Thr	Asn	Glu	Tyr	Pro	Thr	Glu	Asp	Ala	Leu	Gly	Lys	Tyr	His														
ctg	cct	cct	ttc	cag	gca	gct	atc	gac	gct	ggc	tgc	gcc	tcg	atc	atg					1075									
Leu	Pro	Pro	Phe	Gln	Ala	Ala	Ile	Asp	Ala	Gly	Cys	Ala	Ser	Ile	Met														
cct	tac	tac	gca	cgg	cca	atg	aac	aac	tcc	ggc	aac	cag	ctc	gat	cag					1123									
Pro	Tyr	Tyr	Ala	Arg	Pro	Met	Asn	Asn	Ser	Ala	Asn	Gln	Leu	Asp	Gln														

cag ctg tgg caa aac ccg acc acg cag ttc gaa gag gtt gcg ttt gcc 1171  
 Gln Leu Trp Gln Asn Pro Thr Thr Gln Phe Glu Glu Val Ala Phe Ala  
 345 350 355  
 tac aac cgc acc ttc att cag gat ttg ctt cgc gac gcc atg ggc cac 1219  
 Tyr Asn Arg Thr Phe Ile Gln Asp Leu Leu Arg Asp Ala Met Gly His  
 360 365 370  
 cgt ggg tac gtc aac tcc gac tcc ggc gtc atc gac gcc atg atg tgg 1267  
 Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile Asp Ala Met Met Trp  
 375 380 385  
 ggc gtg gag gaa ctg agc gag cca gaa cgc ttc gcc gca gca gtg cgt 1315  
 Gly Val Glu Glu Leu Ser Glu Pro Glu Arg Phe Ala Ala Ala Val Arg  
 390 395 400 405  
 gca ggc acc gac att ttc tcc gac atg gct aac cca cgt cga ctg ctc 1363  
 Ala Gly Thr Asp Ile Phe Ser Asp Met Ala Asn Pro Arg Arg Leu Leu  
 410 415 420  
 gaa gca gtt gct gag gga cac ctt gat gag tca gag ctg aat cag cca 1411  
 Glu Ala Val Ala Glu Gly His Leu Asp Glu Ser Glu Leu Asn Gln Pro  
 425 430 435  
 gtc cag cga ctg ctg gag gaa atc ttc cag ctt ggt ctg ttt gag aac 1459  
 Val Gln Arg Leu Leu Glu Glu Ile Phe Gln Leu Gly Leu Phe Glu Asn  
 440 445 450  
 cca tat gtc tct gaa gat gaa gca gaa aag atc att ggt gcg cca gag 1507  
 Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile Ile Gly Ala Pro Glu  
 455 460 465  
 gtt tct gca ttg ggc aac aaa gca cag ctt gat tcc gtc acc ttg ctg 1555  
 Val Ser Ala Leu Gly Asn Lys Ala Gln Leu Asp Ser Val Thr Leu Leu  
 470 475 480 485  
 cgt aac aac ccc atc cgt gct gcc act gga tcc tgc agc aag cct gaa 1603  
 Arg Asn Asn Pro Ile Arg Ala Ala Thr Gly Ser Cys Ser Lys Pro Glu  
 490 495 500  
 gat cta ccc att ggt tac tgg ccg tac caa gat cga cga ggt tca act 1651  
 Asp Leu Pro Ile Gly Tyr Trp Pro Tyr Gln Asp Arg Arg Gly Ser Thr  
 505 510 515  
 aca gct gga agc agc cat tcg cgc aga act ccc agg ggt aac ctt ggt 1699  
 Thr Ala Gly Ser Ser His Ser Arg Arg Thr Pro Arg Gly Asn Leu Gly  
 520 525 530  
 gtc ttc cga gtc aga agc aga tct tgc aat cgt gtg ggc tcg ccc 1744  
 Val Phe Arg Val Arg Ser Arg Ser Cys Asn Arg Val Gly Ser Pro  
 535 540 545  
 tgaaattgca ctgtttgaag atg 1767

&lt;210&gt; 332

&lt;211&gt; 548

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 332

```

Met Ser Gln Glu Arg Pro Gln Ile Gly Ser Arg Leu Ser Arg Val Ile
 1             5             10             15

Glu Gln Asp Gly Leu Gln Phe Arg Asp Leu Asp Gly Asp Gly Val Leu
      20             25             30

Ala Pro Tyr Glu Asp Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp
      35             40             45

Leu Val Lys Arg Met Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile
      50             55             60

Gly Ser His Tyr Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly
      65             70             75             80

Lys Asp Ala Glu Lys Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp
      85             90             95

Arg Glu Asp Asn Pro Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu
      100            105            110

Ala Thr Ser Ser Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr
      115            120            125

Leu Ile Val Arg Asp Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr
      130            135            140

Asn Ala Val Gln Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val
      145            150            155            160

Ala Phe Ala Ser Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe
      165            170            175

Gly Val Asn Glu Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu
      180            185            190

Gly Leu Ala Ala Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr
      195            200            205

Glu Ala Ala Lys Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly
      210            215            220

Tyr Met Ala Asp Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly
      225            230            235            240

Thr Phe Gly Glu Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val
      245            250            255

Val Arg Gly Leu Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr
      260            265            270

Thr Ile Lys His Phe Pro Gly Gly Gly Val Arg Leu Asp Gly His Asp
      275            280            285

Pro His Phe His Trp Gly Gln Thr Asn Glu Tyr Pro Thr Glu Asp Ala
      290            295            300

Leu Gly Lys Tyr His Leu Pro Pro Phe Gln Ala Ala Ile Asp Ala Gly
      305            310            315            320

```

Cys Ala Ser Ile Met Pro Tyr Tyr Ala Arg Pro Met Asn Asn Ser Ala  
                           325                          330                          335  
 Asn Gln Leu Asp Gln Gln Leu Trp Gln Asn Pro Thr Thr Gln Phe Glu  
                           340                          345                          350  
 Glu Val Ala Phe Ala Tyr Asn Arg Thr Phe Ile Gln Asp Leu Leu Arg  
                           355                          360                          365  
 Asp Ala Met Gly His Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile  
                           370                          375                          380  
 Asp Ala Met Met Trp Gly Val Glu Glu Leu Ser Glu Pro Glu Arg Phe  
                           385                          390                          395                          400  
 Ala Ala Ala Val Arg Ala Gly Thr Asp Ile Phe Ser Asp Met Ala Asn  
                           405                          410                          415  
 Pro Arg Arg Leu Leu Glu Ala Val Ala Glu Gly His Leu Asp Glu Ser  
                           420                          425                          430  
 Glu Leu Asn Gln Pro Val Gln Arg Leu Leu Glu Glu Ile Phe Gln Leu  
                           435                          440                          445  
 Gly Leu Phe Glu Asn Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile  
                           450                          455                          460  
 Ile Gly Ala Pro Glu Val Ser Ala Leu Gly Asn Lys Ala Gln Leu Asp  
                           465                          470                          475                          480  
 Ser Val Thr Leu Leu Arg Asn Asn Pro Ile Arg Ala Ala Thr Gly Ser  
                           485                          490                          495  
 Cys Ser Lys Pro Glu Asp Leu Pro Ile Gly Tyr Trp Pro Tyr Gln Asp  
                           500                          505                          510  
 Arg Arg Gly Ser Thr Thr Ala Gly Ser Ser His Ser Arg Arg Thr Pro  
                           515                          520                          525  
 Arg Gly Asn Leu Gly Val Phe Arg Val Arg Ser Arg Ser Cys Asn Arg  
                           530                          535                          540  
 Val Gly Ser Pro  
 545

<210> 333  
 <211> 1607  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1584)  
 <223> FRXA00799

<400> 333  
 cta caa ttc cgc gat ctc gac ggc gac ggc gta ctt gca cct tat gaa 48  
 Leu Gln Phe Arg Asp Leu Asp Gly Asp Gly Val Leu Ala Pro Tyr Glu  
   1                          5                          10                          15

gat tgg cgt cta acc cca gca gag cgt gcc gct gac ctg gtg aaa cgt	96
Asp Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp Leu Val Lys Arg	
20 25 30	
atg aat gtg gaa gaa aaa gcg ggc ctg atg atc atc ggt tcg cac tac	144
Met Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile Gly Ser His Tyr	
35 40 45	
ccc gga tac tcg cct ttg gcg ccg gag agt gaa ggc aaa gac gcg gaa	192
Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly Lys Asp Ala Glu	
50 55 60	
aag tgc gag cct ttg ctg aac cct gtc gat atg tgg cgt gag gat aac	240
Lys Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn	
65 70 75 80	
ccg atc acg ggt gtt cct ttc acc gag cct gtg ctg gca act tct tcc	288
Pro Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu Ala Thr Ser Ser	
85 90 95	
act gaa aat gcc att aac ctg cgc aat cag cgt tac tta att gtt cgt	336
Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr Leu Ile Val Arg	
100 105 110	
gac aac ctg cca gct cgt ggg ctt gct act tgg acc aat gct gtt cag	384
Asp Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr Asn Ala Val Gln	
115 120 125	
gaa gtc gcg gag cga tcc cgt ttg ggt att cct gtt gcg ttt gcg tcg	432
Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val Ala Phe Ala Ser	
130 135 140	
aat cct cgt aac cac gtc gcg ctc gtt gcg cag ttc ggt gtg aac gag	480
Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe Gly Val Asn Glu	
145 150 155 160	
tcc gcg ggt gtg ttc tct gag tgg cct ggc gag ctg ggt ctt gct gcg	528
Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu Gly Leu Ala Ala	
165 170 175	
ctt cgc gat gct gaa ctg atg gag act ttc ggt acc gag gct gct aaa	576
Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr Glu Ala Ala Lys	
180 185 190	
gaa tgg cgt gcc ggt ggt gtg cac aag ctg tac ggt tac atg gct gac	624
Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly Tyr Met Ala Asp	
195 200 205	
ctc gct tct gag cct cgt tgg tcc cgc ttc aac ggt act ttt ggt gag	672
Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly Thr Phe Gly Glu	
210 215 220	
gat ccg gag ttg atc tct gat tac atc gct gct gtt gtg cgt ggt ttg	720
Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val Val Arg Gly Leu	
225 230 235 240	
cag ggc cct gag ctg tcc aag aat tcc gtg tcg acc acc att aag cac	768
Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr Thr Ile Lys His	
245 250 255	
ttc cca ggt ggc ggc gtg cgc ctc gac ggc cac gat cct cac ttc cac	816

Phe	Pro	Gly	Gly	Gly	Val	Arg	Leu	Asp	Gly	His	Asp	Pro	His	Phe	His		
			260					265					270				
tgg	ggt	cag	acc	aat	gag	tac	cca	acc	gaa	gat	gcg	ctg	ggc	aag	tac	864	
Trp	Gly	Gln	Thr	Asn	Glu	Tyr	Pro	Thr	Glu	Asp	Ala	Leu	Gly	Lys	Tyr		
		275					280					285					
cat	ctg	cct	cct	ttc	cag	gca	gct	atc	gac	gct	ggc	tgc	gcc	tcg	atc	912	
His	Leu	Pro	Pro	Phe	Gln	Ala	Ala	Ile	Asp	Ala	Gly	Cys	Ala	Ser	Ile		
	290					295					300						
atg	cct	tac	tac	gca	cgg	cca	atg	aac	aac	tcc	gcc	aac	cag	ctc	gat	960	
Met	Pro	Tyr	Tyr	Ala	Arg	Pro	Met	Asn	Asn	Ser	Ala	Asn	Gln	Leu	Asp		
305					310					315					320		
cag	cag	ctg	tgg	caa	aac	ccg	acc	acg	cag	ttc	gaa	gag	gtt	gcg	ttt	1008	
Gln	Gln	Leu	Trp	Gln	Asn	Pro	Thr	Thr	Gln	Phe	Glu	Glu	Val	Ala	Phe		
				325					330					335			
gcc	tac	aac	cgc	acc	ttc	att	cag	gat	ttg	ctt	cgc	gac	gcc	atg	ggc	1056	
Ala	Tyr	Asn	Arg	Thr	Phe	Ile	Gln	Asp	Leu	Leu	Arg	Asp	Ala	Met	Gly		
			340					345					350				
cac	cgt	ggg	tac	gtc	aac	tcc	gac	tcc	ggc	gtc	atc	gac	gcc	atg	atg	1104	
His	Arg	Gly	Tyr	Val	Asn	Ser	Asp	Ser	Gly	Val	Ile	Asp	Ala	Met	Met		
	355					360						365					
tgg	ggc	gtg	gag	gaa	ctc	agc	gag	cca	gaa	cgc	ttc	gcc	gca	gca	gtg	1152	
Trp	Gly	Val	Glu	Glu	Leu	Ser	Glu	Pro	Glu	Arg	Phe	Ala	Ala	Ala	Val		
	370					375					380						
cgt	gca	ggc	acc	gac	att	ttc	tcc	gac	atg	gct	aac	cca	cgt	cga	ctg	1200	
Arg	Ala	Gly	Thr	Asp	Ile	Phe	Ser	Asp	Met	Ala	Asn	Pro	Arg	Arg	Leu		
385					390					395					400		
ctc	gaa	gca	gtt	gct	gag	gga	cac	ctt	gat	gag	tca	gag	ctg	aat	cag	1248	
Leu	Glu	Ala	Val	Ala	Glu	Gly	His	Leu	Asp	Glu	Ser	Glu	Leu	Asn	Gln		
				405					410					415			
cca	gtc	cag	cga	ctc	ctg	gag	gaa	atc	ttc	cag	ctt	ggc	ctg	ttt	gag	1296	
Pro	Val	Gln	Arg	Leu	Leu	Glu	Glu	Ile	Phe	Gln	Leu	Gly	Leu	Phe	Glu		
			420					425					430				
aac	cca	tat	gtc	tct	gaa	gat	gaa	gca	gaa	aag	atc	att	ggc	gcg	cca	1344	
Asn	Pro	Tyr	Val	Ser	Glu	Asp	Glu	Ala	Glu	Lys	Ile	Ile	Gly	Ala	Pro		
		435					440					445					
gag	gtt	tct	gca	ttg	ggc	aac	aaa	gca	cag	ctt	gat	tcc	gtc	acc	ttg	1392	
Glu	Val	Ser	Ala	Leu	Gly	Asn	Lys	Ala	Gln	Leu	Asp	Ser	Val	Thr	Leu		
	450					455					460						
ctg	cgt	aac	aac	ccc	atc	cgt	gct	gcc	act	gga	tcc	tgc	agc	aag	cct	1440	
Leu	Arg	Asn	Asn	Pro	Ile	Arg	Ala	Ala	Thr	Gly	Ser	Cys	Ser	Lys	Pro		
465					470					475					480		
gaa	gat	cta	ccc	att	ggc	tac	tgg	ccg	tac	caa	gat	cga	cga	ggc	tca	1488	
Glu	Asp	Leu	Pro	Ile	Gly	Tyr	Trp	Pro	Tyr	Gln	Asp	Arg	Arg	Gly	Ser		
				485					490					495			
act	aca	gct	gga	agc	agc	cat	tcg	cgc	aga	act	ccc	agg	ggc	aac	ctt	1536	
Thr	Thr	Ala	Gly	Ser	Ser	His	Ser	Arg	Arg	Thr	Pro	Arg	Gly	Asn	Leu		

500 505 510  
 ggt gtc ttc cga gtc aga agc aga tct tgc aat cgt gtg ggc tcg ccc 1584  
 Gly Val Phe Arg Val Arg Ser Arg Ser Cys Asn Arg Val Gly Ser Pro  
 515 520 525  
 tgaaattgca ctgtttgaag atg 1607  
  
 <210> 334  
 <211> 528  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
  
 <400> 334  
 Leu Gln Phe Arg Asp Leu Asp Gly Asp Gly Val Leu Ala Pro Tyr Glu  
 1 5 10 15  
 Asp Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp Leu Val Lys Arg  
 20 25 30  
 Met Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile Gly Ser His Tyr  
 35 40 45  
 Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly Lys Asp Ala Glu  
 50 55 60  
 Lys Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn  
 65 70 75 80  
 Pro Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu Ala Thr Ser Ser  
 85 90 95  
 Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr Leu Ile Val Arg  
 100 105 110  
 Asp Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr Asn Ala Val Gln  
 115 120 125  
 Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val Ala Phe Ala Ser  
 130 135 140  
 Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe Gly Val Asn Glu  
 145 150 155 160  
 Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu Gly Leu Ala Ala  
 165 170 175  
 Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr Glu Ala Ala Lys  
 180 185 190  
 Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly Tyr Met Ala Asp  
 195 200 205  
 Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly Thr Phe Gly Glu  
 210 215 220  
 Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val Val Arg Gly Leu  
 225 230 235 240  
 Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr Thr Ile Lys His



245										250				255			
Phe	Pro	Gly	Gly	Gly	Val	Arg	Leu	Asp	Gly	His	Asp	Pro	His	Phe	His		
			260					265					270				
Trp	Gly	Gln	Thr	Asn	Glu	Tyr	Pro	Thr	Glu	Asp	Ala	Leu	Gly	Lys	Tyr		
		275					280					285					
His	Leu	Pro	Pro	Phe	Gln	Ala	Ala	Ile	Asp	Ala	Gly	Cys	Ala	Ser	Ile		
	290					295					300						
Met	Pro	Tyr	Tyr	Ala	Arg	Pro	Met	Asn	Asn	Ser	Ala	Asn	Gln	Leu	Asp		
305					310					315					320		
Gln	Gln	Leu	Trp	Gln	Asn	Pro	Thr	Thr	Gln	Phe	Glu	Glu	Val	Ala	Phe		
				325					330					335			
Ala	Tyr	Asn	Arg	Thr	Phe	Ile	Gln	Asp	Leu	Leu	Arg	Asp	Ala	Met	Gly		
			340					345					350				
His	Arg	Gly	Tyr	Val	Asn	Ser	Asp	Ser	Gly	Val	Ile	Asp	Ala	Met	Met		
		355					360					365					
Trp	Gly	Val	Glu	Glu	Leu	Ser	Glu	Pro	Glu	Arg	Phe	Ala	Ala	Ala	Val		
	370					375					380						
Arg	Ala	Gly	Thr	Asp	Ile	Phe	Ser	Asp	Met	Ala	Asn	Pro	Arg	Arg	Leu		
385					390					395					400		
Leu	Glu	Ala	Val	Ala	Glu	Gly	His	Leu	Asp	Glu	Ser	Glu	Leu	Asn	Gln		
				405					410					415			
Pro	Val	Gln	Arg	Leu	Leu	Glu	Glu	Ile	Phe	Gln	Leu	Gly	Leu	Phe	Glu		
			420					425					430				
Asn	Pro	Tyr	Val	Ser	Glu	Asp	Glu	Ala	Glu	Lys	Ile	Ile	Gly	Ala	Pro		
		435					440					445					
Glu	Val	Ser	Ala	Leu	Gly	Asn	Lys	Ala	Gln	Leu	Asp	Ser	Val	Thr	Leu		
	450					455					460						
Leu	Arg	Asn	Asn	Pro	Ile	Arg	Ala	Ala	Thr	Gly	Ser	Cys	Ser	Lys	Pro		
465					470					475					480		
Glu	Asp	Leu	Pro	Ile	Gly	Tyr	Trp	Pro	Tyr	Gln	Asp	Arg	Arg	Gly	Ser		
				485					490					495			
Thr	Thr	Ala	Gly	Ser	Ser	His	Ser	Arg	Arg	Thr	Pro	Arg	Gly	Asn	Leu		
			500					505					510				
Gly	Val	Phe	Arg	Val	Arg	Ser	Arg	Ser	Cys	Asn	Arg	Val	Gly	Ser	Pro		
		515					520					525					

```
<210> 335
<211> 1632
<212> DNA
<213> Corynebacterium glutamicum
```

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1609)

&lt;223&gt; RXA00032

&lt;400&gt; 335

cacttgctga agacgcccac atcgaagacc ttgcagatgt aaacgcaaac gcctaactgt 60

ttttcgagct	aaacccatcc	ttgaaaggat	cttttccacc	atg	aac	acc	cca	ctc	115
				Met	Asn	Thr	Pro	Leu	
				1				5	

cag	ctc	aac	act	gaa	aac	ctg	cag	gaa	atc	gct	tcg	act	tcc	gga	gtg	163
Gln	Leu	Asn	Thr	Glu	Asn	Leu	Gln	Glu	Ile	Ala	Ser	Thr	Ser	Gly	Val	
				10				15						20		

cag	atc	cca	gcg	ttc	aac	cgc	gct	gac	gtc	gcc	ccg	ggc	att	gtc	cac	211
Gln	Ile	Pro	Ala	Phe	Asn	Arg	Ala	Asp	Val	Ala	Pro	Gly	Ile	Val	His	
			25				30						35			

ttc	ggt	gtt	ggc	gga	ttc	cat	cgc	gct	cac	caa	gcg	atg	tac	ctc	aat	259
Phe	Gly	Val	Gly	Gly	Phe	His	Arg	Ala	His	Gln	Ala	Met	Tyr	Leu	Asn	
		40					45					50				

gaa	ttg	atg	aat	gag	ggc	aag	gcc	ttg	gat	tgg	ggc	atc	atc	ggc	atg	307
Glu	Leu	Met	Asn	Glu	Gly	Lys	Ala	Leu	Asp	Trp	Gly	Ile	Ile	Gly	Met	
	55					60					65					

ggt	gtc	atg	cct	tcc	gat	gtg	cgc	atg	cgc	gat	gcc	ctg	gcc	agc	caa	355
Gly	Val	Met	Pro	Ser	Asp	Val	Arg	Met	Arg	Asp	Ala	Leu	Ala	Ser	Gln	
	70				75					80					85	

gat	cac	ctt	tat	acc	ctg	acc	act	aaa	gct	cct	gat	gga	act	ctt	gat	403
Asp	His	Leu	Tyr	Thr	Leu	Thr	Thr	Lys	Ala	Pro	Asp	Gly	Thr	Leu	Asp	
				90					95					100		

caa	aaa	atc	atc	gga	tcc	atc	att	gac	tac	gtg	ttc	gct	ccc	gag	gac	451
Gln	Lys	Ile	Ile	Gly	Ser	Ile	Ile	Asp	Tyr	Val	Phe	Ala	Pro	Glu	Asp	
			105					110					115			

cca	gca	cgg	gcc	gtt	gca	acc	ctc	gcg	cag	gac	tcc	atc	cgc	att	gtt	499
Pro	Ala	Arg	Ala	Val	Ala	Thr	Leu	Ala	Gln	Asp	Ser	Ile	Arg	Ile	Val	
		120					125					130				

tcc	ctc	acg	gtg	act	gaa	ggc	gga	tac	aac	atc	gat	ccg	gcg	aca	gaa	547
Ser	Leu	Thr	Val	Thr	Glu	Gly	Gly	Tyr	Asn	Ile	Asp	Pro	Ala	Thr	Glu	
	135					140					145					

gat	ttc	gac	cac	acc	aac	cct	cga	atc	gtt	gct	gac	cgc	gaa	gcc	ctg	595
Asp	Phe	Asp	His	Thr	Asn	Pro	Arg	Ile	Val	Ala	Asp	Arg	Glu	Ala	Leu	
	150				155					160					165	

cag	gcg	ggc	gat	act	tcc	act	ttg	cag	acc	ttc	ttt	ggg	ttg	atc	act	643
Gln	Ala	Gly	Asp	Thr	Ser	Thr	Leu	Gln	Thr	Phe	Phe	Gly	Leu	Ile	Thr	
				170					175					180		

gcc	gca	ttg	att	tcc	cga	aaa	gaa	tca	gga	tct	acg	cca	ttt	acc	atc	691
Ala	Ala	Leu	Ile	Ser	Arg	Lys	Glu	Ser	Gly	Ser	Thr	Pro	Phe	Thr	Ile	
		185						190					195			

atg agc tgc gat aac atc caa ggc aac ggc gat ctg gct aag cgt ttc	739
Met Ser Cys Asp Asn Ile Gln Gly Asn Gly Asp Leu Ala Lys Arg Phe	
200 205 210	
ttc ctc gcc ttc gca cat tcc gtg tct tct gag ctc ggc gaa tgg gtg	787
Phe Leu Ala Phe Ala His Ser Val Ser Ser Glu Leu Gly Glu Trp Val	
215 220 225	
gaa aac aac gtg gcc ttc ccc aac tcc atg gtg gac cgc atc acc cct	835
Glu Asn Asn Val Ala Phe Pro Asn Ser Met Val Asp Arg Ile Thr Pro	
230 235 240 245	
gaa acc acc gac ggc gac cgc gat gac atc aag gaa atc ggc tac atc	883
Glu Thr Thr Asp Gly Asp Arg Asp Ile Lys Glu Ile Gly Tyr Ile	
250 255 260	
gat gcg tgg cca gtg gtt tct gaa gat ttc acc caa tgg gtc ctc gag	931
Asp Ala Trp Pro Val Val Ser Glu Asp Phe Thr Gln Trp Val Leu Glu	
265 270 275	
gat gcc ttc acc cag ggc cgc ccc gcg tac gag gag gtt ggc gtg cag	979
Asp Ala Phe Thr Gln Gly Arg Pro Ala Tyr Glu Glu Val Gly Val Gln	
280 285 290	
gtc gtc tcc gac gtg gag cct tat gaa tta atg aag ctg cgc ctg ctc	1027
Val Val Ser Asp Val Glu Pro Tyr Glu Leu Met Lys Leu Arg Leu Leu	
295 300 305	
aac gcc tcc cac cag gga ctt tgc tac ttc ggc cac ttg gct ggc cac	1075
Asn Ala Ser His Gln Gly Leu Cys Tyr Phe Gly His Leu Ala Gly His	
310 315 320 325	
cac atg gtc cac gac gtc atg gcg gat acc cgc ttc cag gat ttc ctc	1123
His Met Val His Asp Val Met Ala Asp Thr Arg Phe Gln Asp Phe Leu	
330 335 340	
ctg gct tac atg gag cgc gaa gcc acc cct acc ctc aag gaa ctt cca	1171
Leu Ala Tyr Met Glu Arg Glu Ala Thr Pro Thr Leu Lys Glu Leu Pro	
345 350 355	
ggt gtc gat cta gat gct tat cga cgc caa ctc atc gcg cga ttc ggc	1219
Gly Val Asp Leu Asp Ala Tyr Arg Arg Gln Leu Ile Ala Arg Phe Gly	
360 365 370	
aac gcc gca gtc aaa gac acc gta ccg cgc ctg tgt gcg gaa tcc tcc	1267
Asn Ala Ala Val Lys Asp Thr Val Pro Arg Leu Cys Ala Glu Ser Ser	
375 380 385	
gac cgc att cca aag tgg ctg ttg cca gtc gta cgc gaa aac ctc gca	1315
Asp Arg Ile Pro Lys Trp Leu Leu Pro Val Val Arg Glu Asn Leu Ala	
390 395 400 405	
gca ggc cgc gac gtc aca ctt tct gca gcc atc gtc gca tcc tgg gcg	1363
Ala Gly Arg Asp Val Thr Leu Ser Ala Ala Ile Val Ala Ser Trp Ala	
410 415 420	
cgc tac gca gaa ggc acc gac gag cag ggc aac cca ata aag att gtt	1411
Arg Tyr Ala Glu Gly Thr Asp Glu Gln Gly Asn Pro Ile Lys Ile Val	
425 430 435	
gac cgt ttg agt gag cgc gtc caa gaa aac gca tca gga aat cgc acc	1459

Asp Arg Leu Ser Glu Arg Val Gln Glu Asn Ala Ser Gly Asn Arg Thr  
           440                          445                          450  
  
 gat att ttg tca ttc atc cgc gac cgt gga atc ttc gga gac ttg gtc 1507  
 Asp Ile Leu Ser Phe Ile Arg Asp Arg Gly Ile Phe Gly Asp Leu Val  
           455                          460                          465  
  
 gat gct gaa cca ttc acc aag gca tac tcc gag aca ctg tcc tcc ctt 1555  
 Asp Ala Glu Pro Phe Thr Lys Ala Tyr Ser Glu Thr Leu Ser Ser Leu  
           470                          475                          480                          485  
  
 cat gac cgt ggc gcg gaa gca acc atc gat gca ctt ctt acg cag gta 1603  
 His Asp Arg Gly Ala Glu Ala Thr Ile Asp Ala Leu Leu Thr Gln Val  
                           490                          495                          500  
  
 act gtc taaatccggtt gcgcgctagg gtt 1632  
 Thr Val

<210> 336  
 <211> 503  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 336  
 Met Asn Thr Pro Leu Gln Leu Asn Thr Glu Asn Leu Gln Glu Ile Ala  
       1                          5                          10                          15  
  
 Ser Thr Ser Gly Val Gln Ile Pro Ala Phe Asn Arg Ala Asp Val Ala  
           20                          25                          30  
  
 Pro Gly Ile Val His Phe Gly Val Gly Gly Phe His Arg Ala His Gln  
           35                          40                          45  
  
 Ala Met Tyr Leu Asn Glu Leu Met Asn Glu Gly Lys Ala Leu Asp Trp  
           50                          55                          60  
  
 Gly Ile Ile Gly Met Gly Val Met Pro Ser Asp Val Arg Met Arg Asp  
       65                          70                          75                          80  
  
 Ala Leu Ala Ser Gln Asp His Leu Tyr Thr Leu Thr Thr Lys Ala Pro  
                           85                          90                          95  
  
 Asp Gly Thr Leu Asp Gln Lys Ile Ile Gly Ser Ile Ile Asp Tyr Val  
           100                          105                          110  
  
 Phe Ala Pro Glu Asp Pro Ala Arg Ala Val Ala Thr Leu Ala Gln Asp  
           115                          120                          125  
  
 Ser Ile Arg Ile Val Ser Leu Thr Val Thr Glu Gly Gly Tyr Asn Ile  
           130                          135                          140  
  
 Asp Pro Ala Thr Glu Asp Phe Asp His Thr Asn Pro Arg Ile Val Ala  
       145                          150                          155                          160  
  
 Asp Arg Glu Ala Leu Gln Ala Gly Asp Thr Ser Thr Leu Gln Thr Phe  
           165                          170                          175  
  
 Phe Gly Leu Ile Thr Ala Ala Leu Ile Ser Arg Lys Glu Ser Gly Ser  
           180                          185                          190

Thr Pro Phe Thr Ile Met Ser Cys Asp Asn Ile Gln Gly Asn Gly Asp  
 195 200 205  
 Leu Ala Lys Arg Phe Phe Leu Ala Phe Ala His Ser Val Ser Ser Glu  
 210 215 220  
 Leu Gly Glu Trp Val Glu Asn Asn Val Ala Phe Pro Asn Ser Met Val  
 225 230 235 240  
 Asp Arg Ile Thr Pro Glu Thr Thr Asp Gly Asp Arg Asp Asp Ile Lys  
 245 250 255  
 Glu Ile Gly Tyr Ile Asp Ala Trp Pro Val Val Ser Glu Asp Phe Thr  
 260 265 270  
 Gln Trp Val Leu Glu Asp Ala Phe Thr Gln Gly Arg Pro Ala Tyr Glu  
 275 280 285  
 Glu Val Gly Val Gln Val Val Ser Asp Val Glu Pro Tyr Glu Leu Met.  
 290 295 300  
 Lys Leu Arg Leu Leu Asn Ala Ser His Gln Gly Leu Cys Tyr Phe Gly  
 305 310 315 320  
 His Leu Ala Gly His His Met Val His Asp Val Met Ala Asp Thr Arg  
 325 330 335  
 Phe Gln Asp Phe Leu Leu Ala Tyr Met Glu Arg Glu Ala Thr Pro Thr  
 340 345 350  
 Leu Lys Glu Leu Pro Gly Val Asp Leu Asp Ala Tyr Arg Arg Gln Leu  
 355 360 365  
 Ile Ala Arg Phe Gly Asn Ala Ala Val Lys Asp Thr Val Pro Arg Leu  
 370 375 380  
 Cys Ala Glu Ser Ser Asp Arg Ile Pro Lys Trp Leu Leu Pro Val Val  
 385 390 395 400  
 Arg Glu Asn Leu Ala Ala Gly Arg Asp Val Thr Leu Ser Ala Ala Ile  
 405 410 415  
 Val Ala Ser Trp Ala Arg Tyr Ala Glu Gly Thr Asp Glu Gln Gly Asn  
 420 425 430  
 Pro Ile Lys Ile Val Asp Arg Leu Ser Glu Arg Val Gln Glu Asn Ala  
 435 440 445  
 Ser Gly Asn Arg Thr Asp Ile Leu Ser Phe Ile Arg Asp Arg Gly Ile  
 450 455 460  
 Phe Gly Asp Leu Val Asp Ala Glu Pro Phe Thr Lys Ala Tyr Ser Glu  
 465 470 475 480  
 Thr Leu Ser Ser Leu His Asp Arg Gly Ala Glu Ala Thr Ile Asp Ala  
 485 490 495  
 Leu Leu Thr Gln Val Thr Val  
 500

```
<220>
<221> CDS
<222> (101)..(1075)
<223> RXA02528
```

477

gaa tca ctt tcc acc acg cag gaa cga atg cgc ggt att agt cat gcg 691  
 Glu Ser Leu Ser Thr Thr Gln Glu Arg Met Arg Gly Ile Ser His Ala  
 185 190 195

gcg tcg ata tat ggg gct gag gtg acg ttc cat ttt ggc cac tat tct 739  
 Ala Ser Ile Tyr Gly Ala Glu Val Thr Phe His Phe Gly His Tyr Ser  
 200 205 210

gtc gaa tct ggc gaa gag atg gct cag gtg gtg ttt aac aac ggc ctt 787  
 Val Glu Ser Gly Glu Glu Met Ala Gln Val Val Phe Asn Asn Gly Leu  
 215 220 225

ccc gat gca ttg att gtg gcg tct cct cgg ctg atg gct ggg gtg atg 835  
 Pro Asp Ala Leu Ile Val Ala Ser Pro Arg Leu Met Ala Gly Val Met  
 230 235 240 245

cgt gct ttt act cgc ctg aat gtc cgc gtt ccc cac gat gtg gtg att 883  
 Arg Ala Phe Thr Arg Leu Asn Val Arg Val Pro His Asp Val Val Ile  
 250 255 260

ggt ggt tat gac gat cct gag tgg tac agc ttt gtc ggc gcg ggg att 931  
 Gly Gly Tyr Asp Asp Pro Glu Trp Tyr Ser Phe Val Gly Ala Gly Ile  
 265 270 275

acc acg ttt gtt cca ccg cat gag gag atg ggg aaa gag gcc gtg cgc 979  
 Thr Thr Phe Val Pro Pro His Glu Glu Met Gly Lys Glu Ala Val Arg  
 280 285 290

ttg ttg gta gat ctg att gaa aat ccc gaa ctt ccc acc ggc gat gtg 1027  
 Leu Leu Val Asp Leu Ile Glu Asn Pro Glu Leu Pro Thr Gly Asp Val  
 295 300 305

gtt ttg cag ggg cag gtg atc ctt cgg ggg tcg agc aca cat tcc ggg 1075  
 Val Leu Gln Gly Gln Val Ile Leu Arg Gly Ser Ser Thr His Ser Gly  
 310 315 320 325

tagaattgcc caaatgtcat caa 1098

&lt;210&gt; 338

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 338

Met Ser Ala Lys Ser Ser Leu Lys Glu Val Ala Glu Leu Ala Gly Val  
 1 5 10 15

Gly Tyr Ala Thr Ala Ser Arg Ala Leu Ser Gly Lys Gly Tyr Val Ser  
 20 25 30

Pro Gln Thr Arg Glu Lys Val Gln Ala Ala Ala Lys Glu Leu Asn Tyr  
 35 40 45

Val Pro Asn Gln Leu Ala Lys Ala Leu Arg Glu His Arg Ser Ala Leu  
 50 55 60

Val Gly Val Ile Val Pro Asp Leu Ser Asn Glu Tyr Tyr Ser Glu Ser  
 65 70 75 80

Leu Gln Thr Ile Gln Gln Asp Leu Lys Ala Ala Gly Tyr Gln Met Leu  
                             85                            90                            95  
 Val Ala Glu Ala Asn Ser Val Gln Ala Gln Asp Val Val Met Glu Ser  
                             100                            105                            110  
 Leu Ile Ser Ile Gln Ala Ala Gly Ile Ile His Val Pro Val Val Gly  
                             115                            120                            125  
 Ser Ile Ala Pro Glu Gly Ile Pro Met Val Gln Leu Thr Arg Gly Glu  
                             130                            135                            140  
 Leu Gly Pro Gly Phe Pro Arg Val Leu Cys Asp Asp Glu Ala Gly Phe  
                             145                            150                            155                            160  
 Phe Gln Leu Thr Glu Ser Val Leu Gly Gly Ser Gly Met Asn Ile Ala  
                             165                            170                            175  
 Ala Leu Val Gly Glu Glu Ser Leu Ser Thr Thr Gln Glu Arg Met Arg  
                             180                            185                            190  
 Gly Ile Ser His Ala Ala Ser Ile Tyr Gly Ala Glu Val Thr Phe His  
                             195                            200                            205  
 Phe Gly His Tyr Ser Val Glu Ser Gly Glu Glu Met Ala Gln Val Val  
                             210                            215                            220  
 Phe Asn Asn Gly Leu Pro Asp Ala Leu Ile Val Ala Ser Pro Arg Leu  
                             225                            230                            235                            240  
 Met Ala Gly Val Met Arg Ala Phe Thr Arg Leu Asn Val Arg Val Pro  
                             245                            250                            255  
 His Asp Val Val Ile Gly Gly Tyr Asp Asp Pro Glu Trp Tyr Ser Phe  
                             260                            265                            270  
 Val Gly Ala Gly Ile Thr Thr Phe Val Pro Pro His Glu Glu Met Gly  
                             275                            280                            285  
 Lys Glu Ala Val Arg Leu Leu Val Asp Leu Ile Glu Asn Pro Glu Leu  
                             290                            295                            300  
 Pro Thr Gly Asp Val Val Leu Gln Gly Gln Val Ile Leu Arg Gly Ser  
                             305                            310                            315                            320  
 Ser Thr His Ser Gly  
                             325

&lt;210&gt; 339

&lt;211&gt; 1246

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1246)

&lt;223&gt; RXN00316

&lt;400&gt; 339

agcgcacatgat cgcgcctgc gagtcgcgcag gggccaact tggcgtgctc ttccagcgcc 60



gcttctggcc	cgcggtcaa	aaaatgaaaa	aggagccgtc	atg	ggc	caa	tgc	acg	115
				Met	Gly	Gln	Cys	Thr	
				1				5	
gta	gcg	ctt	tac	cga	gag	cat	tcc	tat	163
Val	Ala	Leu	Tyr	Arg	Glu	His	Ser	Tyr	
				10				15	
									20
gga	acc	tgg	gca	gcc	gat	ggc	ggt	gga	211
Gly	Thr	Trp	Ala	Ala	Asp	Gly	Gly	Val	
				25				30	
									35
cac	tac	atc	gat	ctt	ttg	tac	tgg	ctg	259
His	Tyr	Ile	Asp	Leu	Leu	Tyr	Trp	Leu	
				40				45	
									50
ttc	ggc	tac	acc	aac	tcc	ttc	aaa	cac	307
Phe	Gly	Tyr	Thr	Asn	Ser	Phe	Lys	His	
				55				60	
									65
gac	agc	gcc	gtt	gcc	act	gtg	cgt	ttt	355
Asp	Ser	Ala	Val	Ala	Thr	Val	Arg	Phe	
				70				75	
									80
									85
att	tca	gcc	acc	acc	gcc	gca	gag	cca	403
Ile	Ser	Ala	Thr	Thr	Ala	Ala	Glu	Pro	
				90				95	
									100
gtg	atg	gga	aca	aag	ggt	gcc	acc	atg	451
Val	Met	Gly	Thr	Lys	Gly	Ala	Thr	Met	
				105				110	
									115
ggt	acc	gac	ggc	agg	ctc	att	gtt	cgc	499
Gly	Thr	Asp	Gly	Arg	Leu	Ile	Val	Arg	
				120				125	
									130
aac	cac	ccc	att	cca	ccc	cgc	gga	tct	547
Asn	His	Pro	Ile	Pro	Pro	Arg	Gly	Ser	
				135				140	
									145
cat	cat	caa	cgg	tgc	ttt	gat	ccc	gta	595
His	His	Gln	Arg	Cys	Phe	Asp	Pro	Val	
				150				155	
									160
									165
ctt	tat	cga	tgc	gct	caa	cga	agg	ccg	643
Leu	Tyr	Arg	Cys	Ala	Gln	Arg	Arg	Pro	
				170				175	
									180
cga	tgc	cac	cag	agc	tct	gaa	agt	tct	691
Arg	Cys	His	Gln	Ser	Ser	Glu	Ser	Pro	
				185				190	
									195
agc	cac	cca	cca	gcc	ggt	ctc	ttt	gat	739
Ser	His	Pro	Pro	Ala	Gly	Leu	Phe	Asp	
				200				205	
									210
tca	cgc	caa	atc	ggt	ctt	gca	cct	tta	787
Ser	Arg	Gln	Ile	Gly	Leu	Ala	Pro	Leu	
				215				220	
									225

gat caa cta gtg cgc ctc gca gct gcc act ggt ttc tcc ttt gtc ggt 835  
 Asp Gln Leu Val Arg Leu Ala Ala Ala Thr Gly Phe Ser Phe Val Gly  
 230 235 240 245  
  
 ctg cgc gtc atc gca gta acc ccc aac gaa cgt gta tat gac ctt tcc 883  
 Leu Arg Val Ile Ala Val Thr Pro Asn Glu Arg Val Tyr Asp Leu Ser  
 250 255 260  
  
 cca gga tcc cca ctg ctg gct gca acc caa caa gcg ttg aaa gaa acc 931  
 Pro Gly Ser Pro Leu Leu Ala Ala Thr Gln Gln Ala Leu Lys Glu Thr  
 265 270 275  
  
 gcc ctg tat gtg ctc gac act gaa ttc cta cag gta aac gca gac acc 979  
 Ala Leu Tyr Val Leu Asp Thr Glu Phe Leu Gln Val Asn Ala Asp Thr  
 280 285 290  
  
 acc cgc gag gcc tgg ctt ccc gca cta gaa gcc gcc gga gca ctg gga 1027  
 Thr Arg Glu Ala Trp Leu Pro Ala Leu Glu Ala Ala Gly Ala Leu Gly  
 295 300 305  
  
 gct aaa acc ttc acc atc gcc gcc ggt gat gac aac att gcg ccc ctg 1075  
 Ala Lys Thr Phe Thr Ile Ala Ala Gly Asp Asp Asn Ile Ala Pro Leu  
 310 315 320 325  
  
 acc gac acg atc ggt gcc atg gtt gac gat gcc cgt gat ttc gga gtc 1123  
 Thr Asp Thr Ile Gly Ala Met Val Asp Asp Ala Arg Asp Phe Gly Val  
 330 335 340  
  
 acc cca gcc cta gag cca atc tct tac cgc agc gtg cat tcc att ccg 1171  
 Thr Pro Ala Leu Glu Pro Ile Ser Tyr Arg Ser Val His Ser Ile Pro  
 345 350 355  
  
 cag gca gca gca atc gcc aga gac tcc ggc gga aaa gtc gtg gcg gac 1219  
 Gln Ala Ala Ala Ile Ala Arg Asp Ser Gly Gly Lys Val Val Ala Asp  
 360 365 370  
  
 acc ttg cac atg gcc agg ttc gga gcc 1246  
 Thr Leu His Met Ala Arg Phe Gly Ala  
 375 380

&lt;210&gt; 340

&lt;211&gt; 382

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 340

Met Gly Gln Cys Thr Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr  
 1 5 10 15

Ala Thr Pro Trp Arg Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu  
 20 25 30

Met Thr Gln Ala Ile His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly  
 35 40 45

Glu Pro Val Glu Val Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp  
 50 55 60

Asn Ile Glu Val Glu Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser  
 65 70 75 80

Gly Ala Leu Ala Thr Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu  
                             85                            90                            95  
 Gly Ala Gln Val Gln Val Met Gly Thr Lys Gly Ala Thr Met Thr Ile  
                             100                            105                            110  
 Leu Glu Phe Pro Glu Gly Thr Asp Gly Arg Leu Ile Val Arg Ser Glu  
                             115                            120                            125  
 Asn Asp Thr Arg Arg Asn His Pro Ile Pro Pro Arg Gly Ser Leu Ser  
                             130                            135                            140  
 Gln Cys Arg Ser Phe His His Gln Arg Cys Phe Asp Pro Val Ser His  
                             145                            150                            155                            160  
 Arg Pro Asp Arg Arg Leu Tyr Arg Cys Ala Gln Arg Arg Pro Pro Thr  
                             165                            170                            175  
 Thr Asp His Arg Pro Arg Cys His Gln Ser Ser Glu Ser Ser Pro Trp  
                             180                            185                            190  
 Cys Leu Arg Ile Ser Ser His Pro Pro Ala Gly Leu Phe Asp Leu Thr  
                             195                            200                            205  
 Glu Ala Phe Lys Thr Ser Arg Gln Ile Gly Leu Ala Pro Leu Ser Ser  
                             210                            215                            220  
 Leu Ser Thr Pro Pro Asp Gln Leu Val Arg Leu Ala Ala Ala Thr Gly  
                             225                            230                            235                            240  
 Phe Ser Phe Val Gly Leu Arg Val Ile Ala Val Thr Pro Asn Glu Arg  
                             245                            250                            255  
 Val Tyr Asp Leu Ser Pro Gly Ser Pro Leu Leu Ala Ala Thr Gln Gln  
                             260                            265                            270  
 Ala Leu Lys Glu Thr Ala Leu Tyr Val Leu Asp Thr Glu Phe Leu Gln  
                             275                            280                            285  
 Val Asn Ala Asp Thr Thr Arg Glu Ala Trp Leu Pro Ala Leu Glu Ala  
                             290                            295                            300  
 Ala Gly Ala Leu Gly Ala Lys Thr Phe Thr Ile Ala Ala Gly Asp Asp  
                             305                            310                            315                            320  
 Asn Ile Ala Pro Leu Thr Asp Thr Ile Gly Ala Met Val Asp Asp Ala  
                             325                            330                            335  
 Arg Asp Phe Gly Val Thr Pro Ala Leu Glu Pro Ile Ser Tyr Arg Ser  
                             340                            345                            350  
 Val His Ser Ile Pro Gln Ala Ala Ala Ile Ala Arg Asp Ser Gly Gly  
                             355                            360                            365  
 Lys Val Val Ala Asp Thr Leu His Met Ala Arg Phe Gly Ala  
                             370                            375                            380

&lt;210&gt; 341

&lt;211&gt; 412

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(412)

&lt;223&gt; FRXA00309

&lt;400&gt; 341

agcgcatgat cgatgcctgc gagtccgcag ggggtccaact tggcgtgctc ttccagcgcc 60

gcttctggcc cgcggtctcaa aaaatgaaaa aggagccgctc atg ggc caa tgc acg 115  
 Met Gly Gln Cys Thr  
 1 5

gta gcg ctt tac cga gag cat tcc tat tac aca gca acc cca tgg cga 163  
 Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr Ala Thr Pro Trp Arg  
 10 15 20

gga acc tgg gca gcc gat ggc ggt gga gtg ctc atg act caa gcc atc 211  
 Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu Met Thr Gln Ala Ile  
 25 30 35

cac tac atc gat ctt ttg tac tgg ctg ttg ggc gaa ccc gtg gaa gtt 259  
 His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly Glu Pro Val Glu Val  
 40 45 50

ttc ggc tac acc aac tcc ttc aaa cac ggc gac aac atc gaa gtc gaa 307  
 Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp Asn Ile Glu Val Glu  
 55 60 65

gac agc gcc gtt gcc act gtg cgt ttt gaa tcg ggc gcg ttg gcc aca 355  
 Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser Gly Ala Leu Ala Thr  
 70 75 80 85

att tca gcc acc acc gcc gca gag cca gca ctc ggc gca caa gtg cag 403  
 Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu Gly Ala Gln Val Gln  
 90 95 100

gtg atg gga 412  
 Val Met Gly

&lt;210&gt; 342

&lt;211&gt; 104

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 342

Met Gly Gln Cys Thr Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr  
 1 5 10 15

Ala Thr Pro Trp Arg Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu  
 20 25 30

Met Thr Gln Ala Ile His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly  
 35 40 45

Glu Pro Val Glu Val Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp  
 50 55 60

Asn Ile Glu Val Glu Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser  
 65 70 75 80  
 Gly Ala Leu Ala Thr Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu  
 85 90 95  
 Gly Ala Gln Val Gln Val Met Gly  
 100

<210> 343  
 <211> 558  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(535)  
 <223> RXN00310

<400> 343  
 ttgcgggatt catcatcggc gcaatcgcac tgtctgccgc agttattttg accaccaagg 60  
 aaaccgcctt caccaagctt gaagatctag ggaagaaata atg tct gac aag atc 115  
 Met Ser Asp Lys Ile  
 1 5  
 tgg aaa gtc ggc atc atc ggt tgc ggt gca atc agc cga aac cat atc 163  
 Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile Ser Arg Asn His Ile  
 10 15 20  
 gaa gca gtt cag gca atc ccc ggc gca gaa gtc agc gca gtc tgt gat 211  
 Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val Ser Ala Val Cys Asp  
 25 30 35  
 gtg gat ggt gcg aaa gca tcg gaa acc gca gcg aaa tat gga att tct 259  
 Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala Lys Tyr Gly Ile Ser  
 40 45 50  
 ccc agt ttc acg tct gtc gat gag atc ctc gcc tcc ggg gtg gac att 307  
 Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala Ser Gly Val Asp Ile  
 55 60 65  
 gtc gca gtc tgc acc cca cat cca acc cac gaa aca gtg gtc ctc gcc 355  
 Val Ala Val Cys Thr Pro His Pro Thr His Glu Thr Val Val Leu Ala  
 70 75 80 85  
 gct gct gcc gcc gga gtg cac gtg ctt tgt gag aag cca atc gcc atc 403  
 Ala Ala Ala Ala Gly Val His Val Leu Cys Glu Lys Pro Ile Ala Ile  
 90 95 100  
 gaa ctc gat tcc gca cag cgc atg atc gat gcc tgc gag tcc gca ggg 451  
 Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala Cys Glu Ser Ala Gly  
 105 110 115  
 gtc caa ctt ggc gtg ctc ttc cag cgc cgc ttc tgg ccc gcg gct caa 499  
 Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe Trp Pro Ala Ala Gln  
 120 125 130  
 aaa atg aaa aag gag ccg tca tgg gcc aat gca cgg tagcgcttta 545

Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala Arg  
 135 140 145

ccgagagcat tcc

558

<210> 344

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 344

Met Ser Asp Lys Ile Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile  
 1 5 10 15

Ser Arg Asn His Ile Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val  
 20 25 30

Ser Ala Val Cys Asp Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala  
 35 40 45

Lys Tyr Gly Ile Ser Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala  
 50 55 60

Ser Gly Val Asp Ile Val Ala Val Cys Thr Pro His Pro Thr His Glu  
 65 70 75 80

Thr Val Val Leu Ala Ala Ala Ala Gly Val His Val Leu Cys Glu  
 85 90 95

Lys Pro Ile Ala Ile Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala  
 100 105 110

Cys Glu Ser Ala Gly Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe  
 115 120 125

Trp Pro Ala Ala Gln Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala  
 130 135 140

Arg  
 145

<210> 345

<211> 558

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> FRXA00310

<400> 345

ttgcgggatt catcatcggc gcaatcgac tgtctgcgc agttattttg accaccaagg 60

aaaccgcctt caccaagctt gaagatctag ggaagaaata atg tct gac aag atc 115  
 Met Ser Asp Lys Ile  
 1 5

tgg aaa gtc ggc atc atc ggt tgc ggt gca atc agc cga aac cat atc 163

Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile Ser Arg Asn His Ile  
                             10                            15                            20  
 gaa gca gtt cag gca atc ccc ggc gca gaa gtc agc gca gtc tgt gat 211  
 Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val Ser Ala Val Cys Asp  
                             25                            30                            35  
 gtg gat ggt gcg aaa gca tcg gaa acc gca gcg aaa tat gga att tct 259  
 Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala Lys Tyr Gly Ile Ser  
                             40                            45                            50  
 ccc agt ttc acg tct gtc gat gag atc ctc gcc tcc ggg gtg gac att 307  
 Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala Ser Gly Val Asp Ile  
                             55                            60                            65  
 gtc gca gtc tgc acc cca cat cca acc cac gaa aca gtg gtc ctc gcc 355  
 Val Ala Val Cys Thr Pro His Pro Thr His Glu Thr Val Val Leu Ala  
                             70                            75                            80                            85  
 gct gct gcc gcc gga gtg cac gtg ctt tgt gag aag cca atc gcc atc 403  
 Ala Ala Ala Ala Gly Val His Val Leu Cys Glu Lys Pro Ile Ala Ile  
                             90                            95                            100  
 gaa ctc gat tcc gca cag cgc atg atc gat gcc tgc gag tcc gca ggg 451  
 Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala Cys Glu Ser Ala Gly  
                             105                            110                            115  
 gtc caa ctt ggc gtg ctc ttc cag cgc cgc ttc tgg ccc gcg gct caa 499  
 Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe Trp Pro Ala Ala Gln  
                             120                            125                            130  
 aaa atg aaa aag gag ccg tca tgg gcc aat gca cgg tagcgcttta 545  
 Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala Arg  
                             135                            140                            145  
 ccgagagcat tcc 558

&lt;210&gt; 346

&lt;211&gt; 145

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 346

Met Ser Asp Lys Ile Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile  
                             1                            5                            10                            15  
 Ser Arg Asn His Ile Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val  
                             20                            25                            30  
 Ser Ala Val Cys Asp Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala  
                             35                            40                            45  
 Lys Tyr Gly Ile Ser Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala  
                             50                            55                            60  
 Ser Gly Val Asp Ile Val Ala Val Cys Thr Pro His Pro Thr His Glu  
                             65                            70                            75                            80  
 Thr Val Val Leu Ala Ala Ala Ala Ala Gly Val His Val Leu Cys Glu  
                             85                            90                            95

Lys Pro Ile Ala Ile Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala  
 100 105 110  
 Cys Glu Ser Ala Gly Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe  
 115 120 125  
 Trp Pro Ala Ala Gln Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala  
 130 135 140

Arg  
 145

<210> 347  
 <211> 1342  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1342)  
 <223> RXA00041

<400> 347  
 atgaagcagc agcatccaag ctggaaaacg ctgatcacta ccgtctcatg gagcaattaa 60  
 agctgcgcta gaaacaaaaa ggaaagtagt gtgtggggct atg cac aca gaa ctt 115  
 Met His Thr Glu Leu  
 1 5  
 tcc agt ttg cgc cct gcg tac cat gtg act cct ccg cag ggc agg ctc 163  
 Ser Ser Leu Arg Pro Ala Tyr His Val Thr Pro Pro Gln Gly Arg Leu  
 10 15 20  
 aat gat ccc aac gga atg tac gtc gat ggc gat acc ctc cac gtc tac 211  
 Asn Asp Pro Asn Gly Met Tyr Val Asp Gly Asp Thr Leu His Val Tyr  
 25 30 35  
 tac cag cac gat cca ggt ttc ccc ttc gca cca aag cgc acc ggc tgg 259  
 Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly Trp  
 40 45 50  
 gct cac acc acc acg ccg ttg acc gga ccg cag cga ttg cag tgg acg 307  
 Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp Thr  
 55 60 65  
 cac ctg ccc gac gct ctt tac ccg gat gca tcc tat gac ctg gat gga 355  
 His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser Tyr Asp Leu Asp Gly  
 70 75 80 85  
 tgc tat tcc ggt gga gcc gta ttt act gac ggc aca ctt aaa ctt ttc 403  
 Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly Thr Leu Lys Leu Phe  
 90 95 100  
 tac acc ggc aac cta aaa att gac ggc aag cgc cgc gcc acc caa aac 451  
 Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln Asn  
 105 110 115  
 ctc gtc gaa gtc gag gac cca act ggg ctg atg ggc ggc att cat cgc 499  
 Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His Arg



120	125	130	
cgt tcg cct aaa aat ccg ctt atc gac gga ccc gcc agc ggt ttc aca			547
Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe Thr			
135	140	145	
ccc cat tac cgc gat ccc atg atc agc cct gat ggt gat ggt tgg aaa			595
Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp Lys			
150	155	160	165
atg gtt ctt ggg gcc caa cgc gaa aac ctc acc ggt gca gcg gtt cta			643
Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val Leu			
	170	175	180
tac cgc tcg aca gat ctt gaa aac tgg gaa ttc tcc ggt gaa atc acc			691
Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu Ile Thr			
	185	190	195
ttt gac ctc agt gat gca caa cct ggt tct gct cct gat ctc gtt ccc			739
Phe Asp Leu Ser Asp Ala Gln Pro Gly Ser Ala Pro Asp Leu Val Pro			
	200	205	210
ggt ggc tac atg tgg gaa tgc ccc aac ctt ttt acg ctt cgc gat gaa			787
Gly Gly Tyr Met Trp Glu Cys Pro Asn Leu Phe Thr Leu Arg Asp Glu			
	215	220	225
gaa act ggc gaa gat ctc gac gtg ctg att ttc tgt cca caa gga ttg			835
Glu Thr Gly Glu Asp Leu Asp Val Leu Ile Phe Cys Pro Gln Gly Leu			
	230	235	240
gac cga atc cac gat gag gtt act cac tac gca agc tct gac cag tgc			883
Asp Arg Ile His Asp Glu Val Thr His Tyr Ala Ser Ser Asp Gln Cys			
	250	255	260
gga tat gtc gtc ggc aag ctt gaa gga acg acc ttc cgc gtc ttg cga			931
Gly Tyr Val Val Gly Lys Leu Glu Gly Thr Thr Phe Arg Val Leu Arg			
	265	270	275
gga ttc agc gag ctg gat ttc ggc cat gaa ttc tac gca ccg cag gtt			979
Gly Phe Ser Glu Leu Asp Phe Gly His Glu Phe Tyr Ala Pro Gln Val			
	280	285	290
gca gta aac ggt tct gat gcc tgg ctc gtg ggc tgg atg ggg ctg ccc			1027
Ala Val Asn Gly Ser Asp Ala Trp Leu Val Gly Trp Met Gly Leu Pro			
	295	300	305
gcg cag gat gat cac cca aca gtt gca cgg gaa gga tgg gtg cac tgc			1075
Ala Gln Asp Asp His Pro Thr Val Ala Arg Glu Gly Trp Val His Cys			
	310	315	320
ctg act gtg ccc cgc aag ctt cat ttg cgc aac cac gcg atc tat caa			1123
Leu Thr Val Pro Arg Lys Leu His Leu Arg Asn His Ala Ile Tyr Gln			
	330	335	340
gag ctt ctt ctc cca gag ggg gag tca ggg gta atc aga tct gta tta			1171
Glu Leu Leu Leu Pro Glu Gly Glu Ser Gly Val Ile Arg Ser Val Leu			
	345	350	355
ggt tct gaa cct gtc cga gta gac atc cga ggc aat att tcc ctc gag			1219
Gly Ser Glu Pro Val Arg Val Asp Ile Arg Gly Asn Ile Ser Leu Glu			
	360	365	370

tgg gat ggt gtc cgt ttg tct gtg gat cgt ggt ggt gat cgt cgc gta 1267  
 Trp Asp Gly Val Arg Leu Ser Val Asp Arg Gly Gly Asp Arg Arg Val  
 375 380 385  
  
 gct gag gta aaa cct ggc gaa tta gtg atc gcg gac gat aat aca gcc 1315  
 Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala Asp Asp Asn Thr Ala  
 390 395 400 405  
  
 att gag ata act gca ggt gat gga cag 1342  
 Ile Glu Ile Thr Ala Gly Asp Gly Gln  
 410

&lt;210&gt; 348

&lt;211&gt; 414

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 348

Met His Thr Glu Leu Ser Ser Leu Arg Pro Ala Tyr His Val Thr Pro  
 1 5 10 15  
  
 Pro Gln Gly Arg Leu Asn Asp Pro Asn Gly Met Tyr Val Asp Gly Asp  
 20 25 30  
  
 Thr Leu His Val Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro  
 35 40 45  
  
 Lys Arg Thr Gly Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln  
 50 55 60  
  
 Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser  
 65 70 75 80  
  
 Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly  
 85 90 95  
  
 Thr Leu Lys Leu Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg  
 100 105 110  
  
 Arg Ala Thr Gln Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met  
 115 120 125  
  
 Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro  
 130 135 140  
  
 Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp  
 145 150 155 160  
  
 Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr  
 165 170 175  
  
 Gly Ala Ala Val Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe  
 180 185 190  
  
 Ser Gly Glu Ile Thr Phe Asp Leu Ser Asp Ala Gln Pro Gly Ser Ala  
 195 200 205  
  
 Pro Asp Leu Val Pro Gly Gly Tyr Met Trp Glu Cys Pro Asn Leu Phe  
 210 215 220

Thr Leu Arg Asp Glu Glu Thr Gly Glu Asp Leu Asp Val Leu Ile Phe  
 225 230 235 240  
 Cys Pro Gln Gly Leu Asp Arg Ile His Asp Glu Val Thr His Tyr Ala  
 245 250 255  
 Ser Ser Asp Gln Cys Gly Tyr Val Val Gly Lys Leu Glu Gly Thr Thr  
 260 265 270  
 Phe Arg Val Leu Arg Gly Phe Ser Glu Leu Asp Phe Gly His Glu Phe  
 275 280 285  
 Tyr Ala Pro Gln Val Ala Val Asn Gly Ser Asp Ala Trp Leu Val Gly  
 290 295 300  
 Trp Met Gly Leu Pro Ala Gln Asp Asp His Pro Thr Val Ala Arg Glu  
 305 310 315 320  
 Gly Trp Val His Cys Leu Thr Val Pro Arg Lys Leu His Leu Arg Asn  
 325 330 335  
 His Ala Ile Tyr Gln Glu Leu Leu Leu Pro Glu Gly Glu Ser Gly Val  
 340 345 350  
 Ile Arg Ser Val Leu Gly Ser Glu Pro Val Arg Val Asp Ile Arg Gly  
 355 360 365  
 Asn Ile Ser Leu Glu Trp Asp Gly Val Arg Leu Ser Val Asp Arg Gly  
 370 375 380  
 Gly Asp Arg Arg Val Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala  
 385 390 395 400  
 Asp Asp Asn Thr Ala Ile Glu Ile Thr Ala Gly Asp Gly Gln  
 405 410

&lt;210&gt; 349

&lt;211&gt; 720

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(720)

&lt;223&gt; RXA02026

&lt;400&gt; 349

cca ttt cat ata caa cca gaa aca ggt tta tta aat gat ccc aac gga 48  
 Pro Phe His Ile Gln Pro Glu Thr Gly Leu Leu Asn Asp Pro Asn Gly  
 1 5 10 15  
 ctt att ttt tat aaa ggg aag tat tat gtt tca cat caa tgg ttc cca 96  
 Leu Ile Phe Tyr Lys Gly Lys Tyr Tyr Val Ser His Gln Trp Phe Pro  
 20 25 30  
 tta ggc gca gta cat ggc tta aag tat tgg tat aac tac acg agt gat 144  
 Leu Gly Ala Val His Gly Leu Lys Tyr Trp Tyr Asn Tyr Thr Ser Asp  
 35 40 45

gac tta ata aac ttt aaa cct gaa ggg cca ata tta aat cca gat act 192  
 Asp Leu Ile Asn Phe Lys Pro Glu Gly Pro Ile Leu Asn Pro Asp Thr  
 50 55 60

aaa tat gac agc cat ggt gtt tat agc ggt agc gct ttt gaa tat aac 240  
 Lys Tyr Asp Ser His Gly Val Tyr Ser Gly Ser Ala Phe Glu Tyr Asn  
 65 70 75 80

ggg cat tta tat tat atg tac aca gga aat cat cga gat aat cat tgg 288  
 Gly His Leu Tyr Tyr Met Tyr Thr Gly Asn His Arg Asp Asn His Trp  
 85 90 95

caa cga cat gcg agt cag atg atc gca cga ttg aaa gaa gac ggt tca 336  
 Gln Arg His Ala Ser Gln Met Ile Ala Arg Leu Lys Glu Asp Gly Ser  
 100 105 110

gtt gaa aag ttt cca aag cca gta att agc cag caa cca gaa gga tat 384  
 Val Glu Lys Phe Pro Lys Pro Val Ile Ser Gln Gln Pro Glu Gly Tyr  
 115 120 125

aca agt cat ttt aga gat cct aaa gtt ttt aaa tat ggt gag aaa tat 432  
 Thr Ser His Phe Arg Asp Pro Lys Val Phe Lys Tyr Gly Glu Lys Tyr  
 130 135 140

tat gca atc att ggc gca caa aat aat gat cag caa ggt cga tta tta 480  
 Tyr Ala Ile Ile Gly Ala Gln Asn Asn Asp Gln Gln Gly Arg Leu Leu  
 145 150 155 160

ctt tat aat act gaa gat ata att aat tgg cat tat tta ggt gaa ata 528  
 Leu Tyr Asn Thr Glu Asp Ile Ile Asn Trp His Tyr Leu Gly Glu Ile  
 165 170 175

aat aca gag tta gat gat ttt gga tat atg tgg gaa tgc cca gat tac 576  
 Asn Thr Glu Leu Asp Asp Phe Gly Tyr Met Trp Glu Cys Pro Asp Tyr  
 180 185 190

ttt aat tta gat aat caa gat gtc ata ctt att tgt cca caa ggt att 624  
 Phe Asn Leu Asp Asn Gln Asp Val Ile Leu Ile Cys Pro Gln Gly Ile  
 195 200 205

gaa cca aaa ggc aat cag ttc aaa aat att tat caa agt ggt tat ata 672  
 Glu Pro Lys Gly Asn Gln Phe Lys Asn Ile Tyr Gln Ser Gly Tyr Ile  
 210 215 220

ctt gga aag ttt gat att gaa aag tta aca tat gaa cat gaa aat ttt 720  
 Leu Gly Lys Phe Asp Ile Glu Lys Leu Thr Tyr Glu His Glu Asn Phe  
 225 230 235 240

&lt;210&gt; 350

&lt;211&gt; 240

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 350

Pro Phe His Ile Gln Pro Glu Thr Gly Leu Leu Asn Asp Pro Asn Gly  
 1 5 10 15

Leu Ile Phe Tyr Lys Gly Lys Tyr Tyr Val Ser His Gln Trp Phe Pro  
 20 25 30

```
<210> 351
<211> 1617
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1594)  
<223> RXA02061
```

<400> 351  
taacctgcct tcacctggga ttatccaccc atgtgtgatg aaatcgctac cctgaatcaa 60

agacactggc gtaattgagt gaaggcagga caataaagag atg acg aac gtt tcc 115  
Met Thr Asn Val Ser  
1 5

ggg tat cac cga cca gag ctg cac atc acc gct gaa agt ggt gtt ttg 163

Gly Tyr His Arg	Pro Glu Leu His Ile Thr Ala Glu Ser Gly Val Leu	
	10 15 20	
ttt gca cct gca ggc gtt ctg ttg gat gac gac acg tgg cat ttc ttc	211	
Phe Ala Pro Ala Gly Val Leu Leu Asp Asp Thr Trp His Phe Phe		
	25 30 35	
cac cag tac cgt ccc tca cca gat cac ggc ccc agg tgg gcg cac caa	259	
His Gln Tyr Arg Pro Ser Pro Asp His Gly Pro Arg Trp Ala His Gln		
	40 45 50	
ttc gca gag cgc act cca ttt gtg tgg gat atc tgc gat gac gtg cta	307	
Phe Ala Glu Arg Thr Pro Phe Val Trp Asp Ile Cys Asp Asp Val Leu		
	55 60 65	
gcc cct gaa ggc gat gaa acc cag gtt cgc gct ggc tca gtg gtg tcc	355	
Ala Pro Glu Gly Asp Glu Thr Gln Val Arg Ala Gly Ser Val Val Ser		
	70 75 80 85	
aac aac ggt ggc gtt gat ctg tac ttc acc tcg gtt gtt ggc ccc act	403	
Asn Asn Gly Gly Val Asp Leu Tyr Phe Thr Ser Val Val Gly Pro Thr		
	90 95 100	
tcc act atc cag ttg gca cac atc aac aac atc cgt ggc acc acc gaa	451	
Ser Thr Ile Gln Leu Ala His Ile Asn Asn Ile Arg Gly Thr Thr Glu		
	105 110 115	
ctg atc aat gag gac gag ctg ggg ctc gat cca gat gtc tcc cga atc	499	
Leu Ile Asn Glu Asp Glu Leu Gly Leu Asp Pro Asp Val Ser Arg Ile		
	120 125 130	
ggc gaa gtg gtt ggc aac act gat ggt tat gta aag ttc cgc tca ccg	547	
Gly Glu Val Val Gly Asn Thr Asp Gly Tyr Val Lys Phe Arg Ser Pro		
	135 140 145	
tgc gtt atc cca ggt tgg gaa gac caa gga aac cgc gat gaa ggc cac	595	
Cys Val Ile Pro Gly Trp Glu Asp Gln Gly Asn Arg Asp Glu Gly His		
	150 155 160 165	
tca gga tgg ttg atg ctc gca gtt act ggc cca gtt gaa gcc cca aca	643	
Ser Gly Trp Leu Met Leu Ala Val Thr Gly Pro Val Glu Ala Pro Thr		
	170 175 180	
gta gtg gtc ctc gac tcg cca gat gga aga gaa tgg tcc att aca ggt	691	
Val Val Val Leu Asp Ser Pro Asp Gly Arg Glu Trp Ser Ile Thr Gly		
	185 190 195	
ccc ctg tct ctc aac ggc ctc tct gga tta gag tca gac gaa gtt cta	739	
Pro Leu Ser Leu Asn Gly Leu Ser Gly Leu Glu Ser Asp Glu Val Leu		
	200 205 210	
gtt gct cct cgc atg att cgt ctg cgc gat gaa gtg gat cat gaa atc	787	
Val Ala Pro Arg Met Ile Arg Leu Arg Asp Glu Val Asp His Glu Ile		
	215 220 225	
tac gat gtc ctc att gtc acc att gaa caa gac ggg att gac att tcg	835	
Tyr Asp Val Leu Ile Val Thr Ile Glu Gln Asp Gly Ile Asp Ile Ser		
	230 235 240 245	
gga tac ctg gta ggc cag ctc aac ggc tca gaa ttc gat gtg aag act	883	
Gly Tyr Leu Val Gly Gln Leu Asn Gly Ser Glu Phe Asp Val Lys Thr		

250	255	260	
cca ttt acc cgc atc gat ttt ggc cat gat ttc tct cgc ccc cgc aac Pro Phe Thr Arg Ile Asp Phe Gly His Asp Phe Ser Arg Pro Arg Asn 265 270 275			931
acc aac tac gcc gaa acc acc atc ggc tac gac ttc gcc cac atc ttt Thr Asn Tyr Ala Glu Thr Thr Ile Gly Tyr Asp Phe Ala His Ile Phe 280 285 290			979
ggc ctc atg aat ggc gta ggt cgt ttg gac tcc ccc act gag cat ctc Gly Leu Met Asn Gly Val Gly Arg Leu Asp Ser Pro Thr Glu His Leu 295 300 305			1027
agt tgg aag gaa gaa ggc tgg gca aac gct att tct ttc cca cgt att Ser Trp Lys Glu Glu Gly Trp Ala Asn Ala Ile Ser Phe Pro Arg Ile 310 315 320 325			1075
gtc acg ctc cag gac ggt acg gtc ttc cag acc cct cca gaa gga ttg Val Thr Leu Gln Asp Gly Thr Val Phe Gln Thr Pro Pro Glu Gly Leu 330 335 340			1123
ctt gat gcc att cat gaa tcc gag gca gcg gca ggt tgg acc gga ctg Leu Asp Ala Ile His Glu Ser Glu Ala Ala Ala Gly Trp Thr Gly Leu 345 350 355			1171
tgc gaa atc cca tca aac agc gca gtt gaa gtg gcg ttg aag gac caa Cys Glu Ile Pro Ser Asn Ser Ala Val Glu Val Ala Leu Lys Asp Gln 360 365 370			1219
gaa ggt gaa atc gct gca aca atc act cac cgc cac aat cag cta gtc Glu Gly Glu Ile Ala Ala Thr Ile Thr His Arg His Asn Gln Leu Val 375 380 385			1267
gtt gat cgg tcc atg aac ccc aac cac gcg ggt gat cca cac gcg att Val Asp Arg Ser Met Asn Pro Asn His Ala Gly Asp Pro His Ala Ile 390 395 400 405			1315
gca cca ttg act gat gat gaa aca gat tca ctg ttc att gtc gtt gac Ala Pro Leu Thr Asp Asp Glu Thr Asp Ser Leu Phe Ile Val Val Asp 410 415 420			1363
ggc tct aca gta gaa gtt ttt gct gat ggc ggt tat gta tca atg gca Gly Ser Thr Val Glu Val Phe Ala Asp Gly Gly Tyr Val Ser Met Ala 425 430 435			1411
agc cgt gtg tat ttc aac aac gga cca ttc agc gaa ttt gag gtc acc Ser Arg Val Tyr Phe Asn Asn Gly Pro Phe Ser Glu Phe Glu Val Thr 440 445 450			1459
acc acc ggt gac gca agc att att cgc cag gaa agt cac ttc cct gtt Thr Thr Gly Asp Ala Ser Ile Ile Arg Gln Glu Ser His Phe Pro Val 455 460 465			1507
gat ttc agt tcg gtg tcc cta gat ata gat gat ctc act gcg ctc atg Asp Phe Ser Ser Val Ser Leu Asp Ile Asp Asp Leu Thr Ala Leu Met 470 475 480 485			1555
cag ttc gat gaa aac gaa ccg cat gaa ggc cca gtg aga taagagttag Gln Phe Asp Glu Asn Glu Pro His Glu Gly Pro Val Arg 490 495			1604

atgcgttcca gcc

1617

&lt;210&gt; 352

&lt;211&gt; 498

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 352

Met Thr Asn Val Ser Gly Tyr His Arg Pro Glu Leu His Ile Thr Ala  
 1 5 10 15

Glu Ser Gly Val Leu Phe Ala Pro Ala Gly Val Leu Leu Asp Asp Asp  
 20 25 30

Thr Trp His Phe Phe His Gln Tyr Arg Pro Ser Pro Asp His Gly Pro  
 35 40 45

Arg Trp Ala His Gln Phe Ala Glu Arg Thr Pro Phe Val Trp Asp Ile  
 50 55 60

Cys Asp Asp Val Leu Ala Pro Glu Gly Asp Glu Thr Gln Val Arg Ala  
 65 70 75 80

Gly Ser Val Val Ser Asn Asn Gly Gly Val Asp Leu Tyr Phe Thr Ser  
 85 90 95

Val Val Gly Pro Thr Ser Thr Ile Gln Leu Ala His Ile Asn Asn Ile  
 100 105 110

Arg Gly Thr Thr Glu Leu Ile Asn Glu Asp Glu Leu Gly Leu Asp Pro  
 115 120 125

Asp Val Ser Arg Ile Gly Glu Val Val Gly Asn Thr Asp Gly Tyr Val  
 130 135 140

Lys Phe Arg Ser Pro Cys Val Ile Pro Gly Trp Glu Asp Gln Gly Asn  
 145 150 155 160

Arg Asp Glu Gly His Ser Gly Trp Leu Met Leu Ala Val Thr Gly Pro  
 165 170 175

Val Glu Ala Pro Thr Val Val Val Leu Asp Ser Pro Asp Gly Arg Glu  
 180 185 190

Trp Ser Ile Thr Gly Pro Leu Ser Leu Asn Gly Leu Ser Gly Leu Glu  
 195 200 205

Ser Asp Glu Val Leu Val Ala Pro Arg Met Ile Arg Leu Arg Asp Glu  
 210 215 220

Val Asp His Glu Ile Tyr Asp Val Leu Ile Val Thr Ile Glu Gln Asp  
 225 230 235 240

Gly Ile Asp Ile Ser Gly Tyr Leu Val Gly Gln Leu Asn Gly Ser Glu  
 245 250 255

Phe Asp Val Lys Thr Pro Phe Thr Arg Ile Asp Phe Gly His Asp Phe  
 260 265 270



Ser Arg Pro Arg Asn Thr Asn Tyr Ala Glu Thr Thr Ile Gly Tyr Asp  
 275 280 285  
 Phe Ala His Ile Phe Gly Leu Met Asn Gly Val Gly Arg Leu Asp Ser  
 290 295 300  
 Pro Thr Glu His Leu Ser Trp Lys Glu Glu Gly Trp Ala Asn Ala Ile  
 305 310 315 320  
 Ser Phe Pro Arg Ile Val Thr Leu Gln Asp Gly Thr Val Phe Gln Thr  
 325 330 335  
 Pro Pro Glu Gly Leu Leu Asp Ala Ile His Glu Ser Glu Ala Ala Ala  
 340 345 350  
 Gly Trp Thr Gly Leu Cys Glu Ile Pro Ser Asn Ser Ala Val Glu Val  
 355 360 365  
 Ala Leu Lys Asp Gln Glu Gly Glu Ile Ala Ala Thr Ile Thr His Arg  
 370 375 380  
 His Asn Gln Leu Val Val Asp Arg Ser Met Asn Pro Asn His Ala Gly  
 385 390 395 400  
 Asp Pro His Ala Ile Ala Pro Leu Thr Asp Asp Glu Thr Asp Ser Leu  
 405 410 415  
 Phe Ile Val Val Asp Gly Ser Thr Val Glu Val Phe Ala Asp Gly Gly  
 420 425 430  
 Tyr Val Ser Met Ala Ser Arg Val Tyr Phe Asn Asn Gly Pro Phe Ser  
 435 440 445  
 Glu Phe Glu Val Thr Thr Thr Gly Asp Ala Ser Ile Ile Arg Gln Glu  
 450 455 460  
 Ser His Phe Pro Val Asp Phe Ser Ser Val Ser Leu Asp Ile Asp Asp  
 465 470 475 480  
 Leu Thr Ala Leu Met Gln Phe Asp Glu Asn Glu Pro His Glu Gly Pro  
 485 490 495

Val Arg

<210> 353  
 <211> 1305  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1282)  
 <223> RXN01369

<400> 353  
 ctgcgacgga cctagcaaag gggcgctgac acaagcactg cgtttgctgg tgcgcggaca 60  
 gtcagccacg acctattcca ttgaagaaaa ggacttgtaa atg gag cta ttg gaa 115  
 Met Glu Leu Leu Glu

	1	5	
ggc tca ctg cgc acc tac cca tgg ggt tca aga aca ctg atc gct gat			163
Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg Thr Leu Ile Ala Asp	10	20	
ctc aaa ggc gaa gaa tca cca tcg tct cgc cca gag gcc gaa gtc tgg			211
Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro Glu Ala Glu Val Trp	25	35	
ttc ggt gcc cac cca gga tca cca tca acc atc ggt gga aac gca ctc			259
Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile Gly Gly Asn Ala Leu	40	50	
aac gaa gtc atc gca gcg aac ccc gaa gaa gca ttg gcc acg cgt gtt			307
Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala Leu Gly Thr Arg Val	55	65	
gcc gaa gcg ttt gaa aat gag ctt cca ttc ctc ctc aaa atc ctc gca			355
Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu Leu Lys Ile Leu Ala	70	85	
gcg gga gca ccc cta tca ctg cag gcc cac cca tcg ctg gaa cag gcc			403
Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro Ser Leu Glu Gln Ala	90	100	
cgt gaa gga ttc gcc cgc gaa aac tca gca gga att gac ctc ggc gca			451
Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly Ile Asp Leu Gly Ala	105	115	
ccg aac cgc aac tac cgc gac cca aac cac aag cca gag ctg atc gtt			499
Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys Pro Glu Leu Ile Val	120	130	
gct ctc acg gaa ttc atc gcg atg gca ggc ttc cgc cca ctg cgg aac			547
Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe Arg Pro Leu Arg Asn	135	145	
acc ctc acc att ttc gac gcc ctc gcc tgc gaa ccc ctc gac cgc tac			595
Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu Pro Leu Asp Arg Tyr	150	165	
cgc agc atg ctc acc gtc gac aac gag gaa gaa tcc ctc cgc gca ctg			643
Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu Ser Leu Arg Ala Leu	170	180	
ttt acc acc tgg atc acc atc ccc atc ggt aaa cga cac gaa ctc atc			691
Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys Arg His Glu Leu Ile	185	195	
gat gcc ctc atc agc aac gcc cac acc tac ctt gag gca agc gat cgt			739
Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu Glu Ala Ser Asp Arg	200	210	
gac gag gac atc gca ttc gtg ctc tca cac atc atc gag ctc aac gaa			787
Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile Ile Glu Leu Asn Glu	215	225	
cag tac ccc gcc gat gtc gcc gtt ctg ggt gct ctg ctg ttg aac ttc			835
Gln Tyr Pro Gly Asp Val Gly Val Leu Gly Ala Leu Leu Leu Asn Phe	230	245	

tac aaa ctt gcc cca ggc gaa gcc ctc tac ctc gac gcc gca aac ctt 883  
 Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala Asn Leu  
                   250                  255                  260

cac gca tac atc agc ggc ctc ggc gta gag atc atg gcg aac tcc gac 931  
 His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn Ser Asp  
                   265                  270                  275

aac gtg ctc cgc ggt gga ctg aca tcc aaa tac gtc gac gtc ccg gag 979  
 Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val Pro Glu  
                   280                  285                  290

ctt gtg cgc gtg ttg gat ttc aac tct ttg gaa aac gct cgc gtg gac 1027  
 Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg Val Asp  
                   295                  300                  305

gtt gaa gaa gac ggt gca acg acc cac tac cca gtt cca atc aac gaa 1075  
 Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile Asn Glu  
 310                  315                  320                  325

ttc caa ctc gat cgc gtt gca gtt cag ggc gaa gca gaa gcc aac cac 1123  
 Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala Asn His  
                   330                  335                  340

gat ggt ccc atg att gtt ctg tgc acc tcc gga act gtt tcc ttg gaa 1171  
 Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser Leu Glu  
                   345                  350                  355

gca ggg gag aag acc ctc gaa gta gca gca ggt cac gcc gca tgg gtt 1219  
 Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala Trp Val  
                   360                  365                  370

cca gca aac gac cca acc att gcg atg cgt tct gag gac gca gaa gta 1267  
 Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala Glu Val  
                   375                  380                  385

ttc ctc gct agg gtt tagatctttt tagattaaaa tca 1305  
 Phe Leu Ala Arg Val  
 390

&lt;210&gt; 354

&lt;211&gt; 394

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 354

Met Glu Leu Leu Glu Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg  
 1                  5                  10                  15

Thr Leu Ile Ala Asp Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro  
                   20                  25                  30

Glu Ala Glu Val Trp Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile  
                   35                  40                  45

Gly Gly Asn Ala Leu Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala  
                   50                  55                  60

Leu Gly Thr Arg Val Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu

65	70	75	80
Leu Lys Ile Leu Ala Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro	85	90	95
Ser Leu Glu Gln Ala Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly	100	105	110
Ile Asp Leu Gly Ala Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys	115	120	125
Pro Glu Leu Ile Val Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe	130	135	140
Arg Pro Leu Arg Asn Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu	145	150	155
Pro Leu Asp Arg Tyr Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu	165	170	175
Ser Leu Arg Ala Leu Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys	180	185	190
Arg His Glu Leu Ile Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu	195	200	205
Glu Ala Ser Asp Arg Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile	210	215	220
Ile Glu Leu Asn Glu Gln Tyr Pro Gly Asp Val Gly Val Leu Gly Ala	225	230	235
Leu Leu Leu Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu	245	250	255
Asp Ala Ala Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile	260	265	270
Met Ala Asn Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr	275	280	285
Val Asp Val Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu	290	295	300
Asn Ala Arg Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro	305	310	315
Val Pro Ile Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu	325	330	335
Ala Glu Ala Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly	340	345	350
Thr Val Ser Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly	355	360	365
His Ala Ala Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser	370	375	380
Glu Asp Ala Glu Val Phe Leu Ala Arg Val	385	390	

<210> 355  
 <211> 524  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(501)  
 <223> FRXA01369

<400> 355  
 aac gaa cag tgc ctc ggc gat gtc ggc gtt ctg ggt gct ctg ctg ttg 48  
 Asn Glu Gln Cys Leu Gly Asp Val Gly Val Leu Gly Ala Leu Leu Leu  
 1 \ 5 10 15  
 aac ttc tac aaa ctt gcc cca ggc gaa gcc ctc tac ctc gac gcc gca 96  
 Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala  
 20 25 30  
 aac ctt cac gca tac atc agc ggc ctc ggc gta gag atc atg gcg aac 144  
 Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn  
 35 40 45  
 tcc gac aac gtg ctc cgc ggt gga ctg aca tcc aaa tac gtc gac gtc 192  
 Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val  
 50 55 60  
 ccg gag ctt gtg cgc gtg ttg gat ttc aac tct ttg gaa aac gct cgc 240  
 Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg  
 65 70 75 80  
 gtg gac gtt gaa gaa gac ggt gca acg acc cac tac cca gtt cca atc 288  
 Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile  
 85 90 95  
 aac gaa ttc caa ctc gat cgc gtt gca gtt cag ggc gaa gca gaa gcc 336  
 Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala  
 100 105 110  
 aac cac gat ggt ccc atg att gtt ctg tgc acc tcc gga act gtt tcc 384  
 Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser  
 115 120 125  
 ttg gaa gca ggg gag aag acc ctc gaa gta gca gca ggt cac gcc gca 432  
 Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala  
 130 135 140  
 tgg gtt cca gca aac gac cca acc att gcg atg cgt tct gag gac gca 480  
 Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala  
 145 150 155 160  
 gaa gta ttc ctc gct agg gtt tagatctttt tagattaataa tca 524  
 Glu Val Phe Leu Ala Arg Val  
 165

<210> 356  
 <211> 167  
 <212> PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 356

Asn Glu Gln Cys Leu Gly Asp Val Gly Val Leu Gly Ala Leu Leu Leu  
 1 5 10 15

Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala  
 20 25 30

Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn  
 35 40 45

Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val  
 50 55 60

Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg  
 65 70 75 80

Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile  
 85 90 95

Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala  
 100 105 110

Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser  
 115 120 125

Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala  
 130 135 140

Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala  
 145 150 155 160

Glu Val Phe Leu Ala Arg Val  
 165

&lt;210&gt; 357

&lt;211&gt; 808

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(808)

&lt;223&gt; FRXA01373

&lt;400&gt; 357

ctgcgacgga cctagcaaag gggcgctgac acaagcactg cgtttgctgg tgcgcggaca 60

gtcagccacg acctattcca ttgaagaaaa ggacttgtaa atg gag cta ttg gaa 115  
 Met Glu Leu Leu Glu  
 1 5

ggc tca ctg cgc acc tac cca tgg ggt tca aga aca ctg atc gct gat 163  
 Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg Thr Leu Ile Ala Asp  
 10 15 20

ctc aaa ggc gaa gaa tca cca tcg tct cgc cca gag gcc gaa gtc tgg 211  
 Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro Glu Ala Glu Val Trp  
 25 30 35

```

ttc ggt gcc cac cca gga tca cca tca acc atc ggt gga aac gca ctc 259
Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile Gly Gly Asn Ala Leu
      40                      45                      50

aac gaa gtc atc gca gcg aac ccc gaa gaa gca ttg ggc acg cgt gtt 307
Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala Leu Gly Thr Arg Val
      55                      60                      65

gcc gaa gcg ttt gaa aat gag ctt cca ttc ctc ctc aaa atc ctc gca 355
Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu Leu Lys Ile Leu Ala
      70                      75                      80                      85

gcg gga gca ccc cta tca ctg cag gcc cac cca tcg ctg gaa cag gcc 403
Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro Ser Leu Glu Gln Ala
      90                      95                      100

cgt gaa gga ttc gcc cgc gaa aac tca gca gga att gac ctc ggc gca 451
Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly Ile Asp Leu Gly Ala
      105                      110                      115

ccg aac cgc aac tac cgc gac cca aac cac aag cca gag ctg atc gtt 499
Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys Pro Glu Leu Ile Val
      120                      125                      130

gct ctc acg gaa ttc atc gcg atg gca ggc ttc cgc cca ctg cgg aac 547
Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe Arg Pro Leu Arg Asn
      135                      140                      145

acc ctc acc att ttc gac gcc ctc gcc tgc gaa ccc ctc gac cgc tac 595
Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu Pro Leu Asp Arg Tyr
      150                      155                      160                      165

cgc agc atg ctc acc gtc gac aac gag gaa gaa tcc ctc cgc gca ctg 643
Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu Ser Leu Arg Ala Leu
      170                      175                      180

ttt acc acc tgg atc acc atc ccc atc ggt aaa cga cac gaa ctc atc 691
Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys Arg His Glu Leu Ile
      185                      190                      195

gat gcc ctc atc agc aac gcc cac acc tac ctt gag gca agc gat cgt 739
Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu Glu Ala Ser Asp Arg
      200                      205                      210

gac gag gac atc gca ttc gtg ctc tca cac atc atc gag ctc aac gaa 787
Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile Ile Glu Leu Asn Glu
      215                      220                      225

cag tac ccc ggc gat gtc ggc 808
Gln Tyr Pro Gly Asp Val Gly
      230                      235

```

&lt;210&gt; 358

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 358

Met Glu Leu Leu Glu Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg

```

1           5           10           15
Thr Leu Ile Ala Asp Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro
                20                25                30
Glu Ala Glu Val Trp Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile
                35                40                45
Gly Gly Asn Ala Leu Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala
                50                55                60
Leu Gly Thr Arg Val Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu
                65                70                75                80
Leu Lys Ile Leu Ala Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro
                85                90                95
Ser Leu Glu Gln Ala Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly
                100                105                110
Ile Asp Leu Gly Ala Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys
                115                120                125
Pro Glu Leu Ile Val Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe
                130                135                140
Arg Pro Leu Arg Asn Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu
                145                150                155                160
Pro Leu Asp Arg Tyr Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu
                165                170                175
Ser Leu Arg Ala Leu Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys
                180                185                190
Arg His Glu Leu Ile Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu
                195                200                205
Glu Ala Ser Asp Arg Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile
                210                215                220
Ile Glu Leu Asn Glu Gln Tyr Pro Gly Asp Val Gly
                225                230                235

```

```

<210> 359
<211> 1775
<212> DNA
<213> Corynebacterium glutamicum

```

```

<220>
<221> CDS
<222> (1)..(1752)
<223> RXA02611

```

```

<400> 359
gat gcg tgg tcg gat cct atg gct acg tgg cgt cat gcg att acc act 48
Asp Ala Trp Ser Asp Pro Met Ala Thr Trp Arg His Ala Ile Thr Thr
1           5           10           15
aag att gag gcc ggc cag ggt tcg gat gag ttg tat aac gac ttt gag 96

```



Lys	Ile	Glu	Ala	Gly	Gln	Gly	Ser	Asp	Glu	Leu	Tyr	Asn	Asp	Phe	Glu		
			20					25					30				
cac	ggg	gct	cag	ctg	ttt	gag	cgt	gct	gcg	gag	aat	ttg	tct	aaa	gag	144	
His	Gly	Ala	Gln	Leu	Phe	Glu	Arg	Ala	Ala	Glu	Asn	Leu	Ser	Lys	Glu		
			35				40					45					
gat	agg	act	gcg	ctt	ttc	gac	gtc	gcc	tcc	tct	ctg	cgg	cgc	ggc	ggc	192	
Asp	Arg	Thr	Ala	Leu	Phe	Asp	Val	Ala	Ser	Ser	Leu	Arg	Arg	Gly	Gly		
			50			55					60						
gat	gta	cgc	gca	cgt	ctc	gcc	cca	gcg	ctc	acc	gcg	agt	gtc	act	cat	240	
Asp	Val	Arg	Ala	Arg	Leu	Ala	Pro	Ala	Leu	Thr	Ala	Ser	Val	Thr	His		
			65		70					75					80		
ctt	tta	gaa	ctt	aac	ccg	ttg	cgt	gag	ttg	gtc	acg	atg	ggt	gaa	aac	288	
Leu	Leu	Glu	Leu	Asn	Pro	Leu	Arg	Glu	Leu	Val	Thr	Met	Gly	Glu	Asn		
				85				90					95				
ctg	cag	gtt	cgt	gtc	gag	cgt	cgt	gcc	gct	ttg	gtc	aac	tct	tgg	tat	336	
Leu	Gln	Val	Arg	Val	Glu	Arg	Arg	Ala	Ala	Leu	Val	Asn	Ser	Trp	Tyr		
			100					105					110				
gag	ctt	ttc	cct	cgt	tcc	aca	ggg	ggg	tgg	gat	gag	tcc	ggc	acc	ccc	384	
Glu	Leu	Phe	Pro	Arg	Ser	Thr	Gly	Gly	Trp	Asp	Glu	Ser	Gly	Thr	Pro		
			115				120					125					
gtt	cat	ggc	act	ttc	gct	acc	act	gct	cag	gcg	ttg	gag	cgt	gtc	gcg	432	
Val	His	Gly	Thr	Phe	Ala	Thr	Thr	Ala	Gln	Ala	Leu	Glu	Arg	Val	Ala		
			130			135					140						
aag	atg	ggc	ttc	gat	act	gtt	tac	ttc	ccg	ccg	atc	cat	ccg	att	ggc	480	
Lys	Met	Gly	Phe	Asp	Thr	Val	Tyr	Phe	Pro	Pro	Ile	His	Pro	Ile	Gly		
					150				155						160		
gag	gtc	aac	cgc	aag	ggc	cgc	aat	aat	acg	ctg	acc	ccg	gaa	cct	cat	528	
Glu	Val	Asn	Arg	Lys	Gly	Arg	Asn	Asn	Thr	Leu	Thr	Pro	Glu	Pro	His		
				165				170						175			
gat	gtg	ggt	tcg	ccg	tgg	gct	att	ggg	tct	aaa	gat	ggt	ggg	cat	gat	576	
Asp	Val	Gly	Ser	Pro	Trp	Ala	Ile	Gly	Ser	Lys	Asp	Gly	Gly	His	Asp		
			180					185					190				
gca	acg	cat	ccg	cgg	ttg	ggc	acc	att	gaa	gat	ttc	cag	gcg	ttg	ttg	624	
Ala	Thr	His	Pro	Arg	Leu	Gly	Thr	Ile	Glu	Asp	Phe	Gln	Ala	Leu	Leu		
			195			200						205					
gct	cgc	gca	cgg	gaa	ctc	aat	ttg	gaa	gtt	gca	ctc	gat	cta	gct	ctg	672	
Ala	Arg	Ala	Arg	Glu	Leu	Asn	Leu	Glu	Val	Ala	Leu	Asp	Leu	Ala	Leu		
			210			215					220						
cag	gct	gcc	cct	gat	cat	cca	tgg	gcg	cag	gaa	cac	cgc	gag	ttt	ttc	720	
Gln	Ala	Ala	Pro	Asp	His	Pro	Trp	Ala	Gln	Glu	His	Arg	Glu	Phe	Phe		
			225		230				235					240			
acg	gtg	ttg	gct	gat	ggc	acc	att	gcg	tat	gca	gaa	aac	cca	ccg	aag	768	
Thr	Val	Leu	Ala	Asp	Gly	Thr	Ile	Ala	Tyr	Ala	Glu	Asn	Pro	Pro	Lys		
				245				250					255				
aag	tac	cag	gat	att	tat	ccc	atc	aac	ttt	gat	aat	gat	gct	ccg	aag	816	
Lys	Tyr	Gln	Asp	Ile	Tyr	Pro	Ile	Asn	Phe	Asp	Asn	Asp	Ala	Pro	Lys		

260	265	270	
atc tac gaa gag gtc tat cgt gtg gtg aag ttc tgg gtg gat ttg ggt Ile Tyr Glu Glu Val Tyr Arg Val Val Lys Phe Trp Val Asp Leu Gly 275 280 285			864
gtg acc aca ttc cgc gtg gat aac ccg cac act aag ccc gct aat ttc Val Thr Thr Phe Arg Val Asp Asn Pro His Thr Lys Pro Ala Asn Phe 290 295 300			912
tgg cag tgg ctt att tct gcc atc cat aaa tca aac cct gag gtc att Trp Gln Trp Leu Ile Ser Ala Ile His Lys Ser Asn Pro Glu Val Ile 305 310 315 320			960
ttc cta gcg gag gcg tct act cgc ccg gca cgt ctg tat ttc ttg tcc Phe Leu Ala Glu Ala Ser Thr Arg Pro Ala Arg Leu Tyr Phe Leu Ser 325 330 335			1008
aag att ggt ttc tcc cag tct tac acc tac ttc acc tgg aag gtc acc Lys Ile Gly Phe Ser Gln Ser Tyr Thr Tyr Phe Thr Trp Lys Val Thr 340 345 350			1056
aac gag gag ctc acc gag ttc gct act gag atc gcc ccc atg gcg gat Asn Glu Glu Leu Thr Glu Phe Ala Thr Glu Ile Ala Pro Met Ala Asp 355 360 365			1104
att tct cgt ccg aac ctg ttt gtg aac act ccc gac att ttg cat gcg Ile Ser Arg Pro Asn Leu Phe Val Asn Thr Pro Asp Ile Leu His Ala 370 375 380			1152
tct ctg cag cat ggt gga cgc gcc atg ttc gct atc cgc gcc gca ttg Ser Leu Gln His Gly Gly Arg Ala Met Phe Ala Ile Arg Ala Ala Leu 385 390 395 400			1200
gcc gcc acg atg tct cct gtg tgg ggc gta tat tcc gga tat gag ctc Ala Ala Thr Met Ser Pro Val Trp Gly Val Tyr Ser Gly Tyr Glu Leu 405 410 415			1248
ttt gag cac gag gcc gtc aag cct ggt tgc gaa gag tac ttg gat tct Phe Glu His Glu Ala Val Lys Pro Gly Ser Glu Glu Tyr Leu Asp Ser 420 425 430			1296
gag aag tac gag ctg cgt ccc cgc gat ttc gag ggt gct ctg gaa cgt Glu Lys Tyr Glu Leu Arg Pro Arg Asp Phe Glu Gly Ala Leu Glu Arg 435 440 445			1344
ggc gat tct ctc gag gat tac atc gct ctg ctc aac cag atc cgt cgc Gly Asp Ser Leu Glu Asp Tyr Ile Ala Leu Leu Asn Gln Ile Arg Arg 450 455 460			1392
gcg aac cct gcc ttg cag caa cta cgc aac atc cac ttc cac gaa gcg Ala Asn Pro Ala Leu Gln Gln Leu Arg Asn Ile His Phe His Glu Ala 465 470 475 480			1440
gac aat gat cag atc atc gcc tac tcc aag gtt gat gct ttg acc gga Asp Asn Asp Gln Ile Ile Ala Tyr Ser Lys Val Asp Ala Leu Thr Gly 485 490 495			1488
aat acc gtg ttg att gtg gtc aac ttg gat cca cgt agt gct cgt gag Asn Thr Val Leu Ile Val Val Asn Leu Asp Pro Arg Ser Ala Arg Glu 500 505 510			1536

gct act gtt cgc ctt gat ctt gga gcg ctt ggc tta gaa gcg ggt gca 1584  
 Ala Thr Val Arg Leu Asp Leu Gly Ala Leu Gly Leu Glu Ala Gly Ala  
           515                          520                          525

cag ttt gag gtg cgc gat gcg atc acc ggc tcc cgt tac ctg tgg tca 1632  
 Gln Phe Glu Val Arg Asp Ala Ile Thr Gly Ser Arg Tyr Leu Trp Ser  
           530                          535                          540

gag acg aac ttt gtc cgc ctc gag ccc cta cgc gat gtc gcc cac atc 1680  
 Glu Thr Asn Phe Val Arg Leu Glu Pro Leu Arg Asp Val Ala His Ile  
           545                          550                          555                          560

ttt gtt ctt cct gaa ctt cca gcg tct cgc cgt gag cgt ctc gcg tgg 1728  
 Phe Val Leu Pro Glu Leu Pro Ala Ser Arg Arg Glu Arg Leu Ala Trp  
                           565                          570                          575

cgc gaa atc aag acc tac cgc gcg taatttccca tctctgtacc ttc 1775  
 Arg Glu Ile Lys Thr Tyr Arg Ala  
                           580

<210> 360  
 <211> 584  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 360  
 Asp Ala Trp Ser Asp Pro Met Ala Thr Trp Arg His Ala Ile Thr Thr  
   1                          5                          10                          15

Lys Ile Glu Ala Gly Gln Gly Ser Asp Glu Leu Tyr Asn Asp Phe Glu  
                           20                          25                          30

His Gly Ala Gln Leu Phe Glu Arg Ala Ala Glu Asn Leu Ser Lys Glu  
           35                          40                          45

Asp Arg Thr Ala Leu Phe Asp Val Ala Ser Ser Leu Arg Arg Gly Gly  
   50                          55                          60

Asp Val Arg Ala Arg Leu Ala Pro Ala Leu Thr Ala Ser Val Thr His  
   65                          70                          75                          80

Leu Leu Glu Leu Asn Pro Leu Arg Glu Leu Val Thr Met Gly Glu Asn  
                           85                          90                          95

Leu Gln Val Arg Val Glu Arg Arg Ala Ala Leu Val Asn Ser Trp Tyr  
           100                          105                          110

Glu Leu Phe Pro Arg Ser Thr Gly Gly Trp Asp Glu Ser Gly Thr Pro  
   115                          120                          125

Val His Gly Thr Phe Ala Thr Thr Ala Gln Ala Leu Glu Arg Val Ala  
   130                          135                          140

Lys Met Gly Phe Asp Thr Val Tyr Phe Pro Pro Ile His Pro Ile Gly  
   145                          150                          155                          160

Glu Val Asn Arg Lys Gly Arg Asn Asn Thr Leu Thr Pro Glu Pro His  
                           165                          170                          175

Asp Val Gly Ser Pro Trp Ala Ile Gly Ser Lys Asp Gly Gly His Asp  
 180 185 190  
 Ala Thr His Pro Arg Leu Gly Thr Ile Glu Asp Phe Gln Ala Leu Leu  
 195 200 205  
 Ala Arg Ala Arg Glu Leu Asn Leu Glu Val Ala Leu Asp Leu Ala Leu  
 210 215 220  
 Gln Ala Ala Pro Asp His Pro Trp Ala Gln Glu His Arg Glu Phe Phe  
 225 230 235 240  
 Thr Val Leu Ala Asp Gly Thr Ile Ala Tyr Ala Glu Asn Pro Pro Lys  
 245 250 255  
 Lys Tyr Gln Asp Ile Tyr Pro Ile Asn Phe Asp Asn Asp Ala Pro Lys  
 260 265 270  
 Ile Tyr Glu Glu Val Tyr Arg Val Val Lys Phe Trp Val Asp Leu Gly  
 275 280 285  
 Val Thr Thr Phe Arg Val Asp Asn Pro His Thr Lys Pro Ala Asn Phe  
 290 295 300  
 Trp Gln Trp Leu Ile Ser Ala Ile His Lys Ser Asn Pro Glu Val Ile  
 305 310 315 320  
 Phe Leu Ala Glu Ala Ser Thr Arg Pro Ala Arg Leu Tyr Phe Leu Ser  
 325 330 335  
 Lys Ile Gly Phe Ser Gln Ser Tyr Thr Tyr Phe Thr Trp Lys Val Thr  
 340 345 350  
 Asn Glu Glu Leu Thr Glu Phe Ala Thr Glu Ile Ala Pro Met Ala Asp  
 355 360 365  
 Ile Ser Arg Pro Asn Leu Phe Val Asn Thr Pro Asp Ile Leu His Ala  
 370 375 380  
 Ser Leu Gln His Gly Gly Arg Ala Met Phe Ala Ile Arg Ala Ala Leu  
 385 390 395 400  
 Ala Ala Thr Met Ser Pro Val Trp Gly Val Tyr Ser Gly Tyr Glu Leu  
 405 410 415  
 Phe Glu His Glu Ala Val Lys Pro Gly Ser Glu Glu Tyr Leu Asp Ser  
 420 425 430  
 Glu Lys Tyr Glu Leu Arg Pro Arg Asp Phe Glu Gly Ala Leu Glu Arg  
 435 440 445  
 Gly Asp Ser Leu Glu Asp Tyr Ile Ala Leu Leu Asn Gln Ile Arg Arg  
 450 455 460  
 Ala Asn Pro Ala Leu Gln Gln Leu Arg Asn Ile His Phe His Glu Ala  
 465 470 475 480  
 Asp Asn Asp Gln Ile Ile Ala Tyr Ser Lys Val Asp Ala Leu Thr Gly  
 485 490 495  
 Asn Thr Val Leu Ile Val Val Asn Leu Asp Pro Arg Ser Ala Arg Glu

500 505 510

Ala Thr Val Arg Leu Asp Leu Gly Ala Leu Gly Leu Glu Ala Gly Ala  
515 520 525

Gln Phe Glu Val Arg Asp Ala Ile Thr Gly Ser Arg Tyr Leu Trp Ser  
530 535 540

Glu Thr Asn Phe Val Arg Leu Glu Pro Leu Arg Asp Val Ala His Ile  
545 550 555 560

Phe Val Leu Pro Glu Leu Pro Ala Ser Arg Arg Glu Arg Leu Ala Trp  
565 570 575

Arg Glu Ile Lys Thr Tyr Arg Ala  
580

<210> 361  
<211> 2316  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(2293)  
<223> RXA02612

<400> 361  
gaacttccag cgtctcgccg tgagcgtctc gcgtggcgcg aatcaagac ctaccgcgcg 60

taatttccca tctctgtacc ttctatcaag gattatcatc atg acc gtt gac ccc 115  
Met Thr Val Asp Pro  
1 5

gcg agc cac atc acc atc cct gaa gca gat ctg gcc cgc ctg cgc cac 163  
Ala Ser His Ile Thr Ile Pro Glu Ala Asp Leu Ala Arg Leu Arg His  
10 15 20

tgc aac cat cac gat cct cat gga ttt tat ggt tgg cat gag acc gaa 211  
Cys Asn His His Asp Pro His Gly Phe Tyr Gly Trp His Glu Thr Glu  
25 30 35

gct ggt tcg gtt atc cgc acg cgc cag gtc ggc gcg acg cag gtt aat 259  
Ala Gly Ser Val Ile Arg Thr Arg Gln Val Gly Ala Thr Gln Val Asn  
40 45 50

ttg ctt atc gac gac acc tcc cac gtc atg acc cct atc ggc gac gac 307  
Leu Leu Ile Asp Asp Thr Ser His Val Met Thr Pro Ile Gly Asp Asp  
55 60 65

att ttc gca att gac tta ggt cac cgc gag cgc gct gac tat cgc ttg 355  
Ile Phe Ala Ile Asp Leu Gly His Arg Glu Arg Ala Asp Tyr Arg Leu  
70 75 80 85

gaa gtc acc tgg cct gat caa gaa ccg cag gtc aag gct gat cca tac 403  
Glu Val Thr Trp Pro Asp Gln Glu Pro Gln Val Lys Ala Asp Pro Tyr  
90 95 100

tac ttc ctc ccc acc gta ggc gag atg gat att tac ctc ttc tct gag 451  
Tyr Phe Leu Pro Thr Val Gly Glu Met Asp Ile Tyr Leu Phe Ser Glu

105	110	115	
gga cgc cat gag cgt ttg tgg gag att ctc ggt gcc aac atc aag acc Gly Arg His Glu Arg Leu Trp Glu Ile Leu Gly Ala Asn Ile Lys Thr 120 125 130			499
tac caa act gcg ctc gga aca gtt cgt ggc acc gca ttt act gtg tgg Tyr Gln Thr Ala Leu Gly Thr Val Arg Gly Thr Ala Phe Thr Val Trp 135 140 145			547
gct cca aac gca att ggc tgc gca gtg gtc ggt ggc ttc aac ggt tgg Ala Pro Asn Ala Ile Gly Cys Ala Val Val Gly Gly Phe Asn Gly Trp 150 155 160 165			595
aat gca tcc cag cat ccg atg cgt tct atg ggt ggt tcg ggt ctg tgg Asn Ala Ser Gln His Pro Met Arg Ser Met Gly Gly Ser Gly Leu Trp 170 175 180			643
gag ctg ttc atc cca ggc ata gag gaa ggc gaa gtg tac aaa ttc gcc Glu Leu Phe Ile Pro Gly Ile Glu Glu Gly Glu Val Tyr Lys Phe Ala 185 190 195			691
gtc caa acc agg gaa ggc caa cgt cgt gat aag gcc gat ccg atg gct Val Gln Thr Arg Glu Gly Gln Arg Arg Asp Lys Ala Asp Pro Met Ala 200 205 210			739
cgt cgc gca gaa ctg gcg ccg gca acc gga tct att gtc gct tcc tct Arg Arg Ala Glu Leu Ala Pro Ala Thr Gly Ser Ile Val Ala Ser Ser 215 220 225			787
gag tac cag tgg cag gat tcc gag tgg ctg cgc gag cgt tcc caa act Glu Tyr Gln Trp Gln Asp Ser Glu Trp Leu Arg Glu Arg Ser Gln Thr 230 235 240 245			835
gat ctc gca tcc aag cca atg agt gtc tac gag gtc cac ctc ggt tct Asp Leu Ala Ser Lys Pro Met Ser Val Tyr Glu Val His Leu Gly Ser 250 255 260			883
tgg cgc tgg ggt aag aac tat gag gat ttg gct act gag ctg gtt gat Trp Arg Trp Gly Lys Asn Tyr Glu Asp Leu Ala Thr Glu Leu Val Asp 265 270 275			931
tac gtc gca gat ctt ggc tac acc cac gtg gaa ttc ctc cct gtc gca Tyr Val Ala Asp Leu Gly Tyr Thr His Val Glu Phe Leu Pro Val Ala 280 285 290			979
gag cac ccc ttc ggt ggt tcc tgg ggt tac cag gtc acc ggc tac tac Glu His Pro Phe Gly Gly Ser Trp Gly Tyr Gln Val Thr Gly Tyr Tyr 295 300 305			1027
gca ccg acc tct cgt tgg ggt act cca gat cag ttc cgt gcg cta gtc Ala Pro Thr Ser Arg Trp Gly Thr Pro Asp Gln Phe Arg Ala Leu Val 310 315 320 325			1075
gac gct ttc cac gcc cgc ggt att ggc gtg atc atg gac tgg gtt cct Asp Ala Phe His Ala Arg Gly Ile Gly Val Ile Met Asp Trp Val Pro 330 335 340			1123
gcc cac ttc cct aag gat gat tgg gct ctt gcc cgc ttt gat ggc gaa Ala His Phe Pro Lys Asp Asp Trp Ala Leu Ala Arg Phe Asp Gly Glu 345 350 355			1171

gcc ctc tat gaa cac cct gac tgg agg cgc ggc gaa caa aag gat tgg	1219
Ala Leu Tyr Glu His Pro Asp Trp Arg Arg Gly Glu Gln Lys Asp Trp	
360 365 370	
ggc acc ctg gtc ttt gac ttc ggt cgc aac gaa gtc cgc aac ttc ctc	1267
Gly Thr Leu Val Phe Asp Phe Gly Arg Asn Glu Val Arg Asn Phe Leu	
375 380 385	
gtc gct aat gcg ttg tac tgg att gaa gaa ttc cac atc gat ggt ctg	1315
Val Ala Asn Ala Leu Tyr Trp Ile Glu Glu Phe His Ile Asp Gly Leu	
390 395 400 405	
cgc gtc gac gcc gtg gcc tcc atg ctg tac ctc gat tac tcc cgt gag	1363
Arg Val Asp Ala Val Ala Ser Met Leu Tyr Leu Asp Tyr Ser Arg Glu	
410 415 420	
cac ggc gaa tgg gaa cca aac atc tac ggt ggt cgc gag aac ctc gag	1411
His Gly Glu Trp Glu Pro Asn Ile Tyr Gly Gly Arg Glu Asn Leu Glu	
425 430 435	
gca gtg cag ttc ctg cag gaa atg aac gcc acg gtg ctg cga ctg cac	1459
Ala Val Gln Phe Leu Gln Glu Met Asn Ala Thr Val Leu Arg Leu His	
440 445 450	
cct ggt gcg ctc acc atc gct gag gaa tca act tca tgg cct ggc gtg	1507
Pro Gly Ala Leu Thr Ile Ala Glu Glu Ser Thr Ser Trp Pro Gly Val	
455 460 465	
acc gca cca acg tgg gac ggc ggc ttg gga ttc tcc ctc aag tgg aac	1555
Thr Ala Pro Thr Trp Asp Gly Gly Leu Gly Phe Ser Leu Lys Trp Asn	
470 475 480 485	
atg ggc tgg atg cac gac acc tta gag tac ttc tcc aaa aac cct gtg	1603
Met Gly Trp Met His Asp Thr Leu Glu Tyr Phe Ser Lys Asn Pro Val	
490 495 500	
cac cgc gca ttc cac cac agt gag ctc act ttc tcc ttg gtg tac gca	1651
His Arg Ala Phe His His Ser Glu Leu Thr Phe Ser Leu Val Tyr Ala	
505 510 515	
ttc tct gag cgt ttt gta ctt ccg atc tct cac gat gaa gtc gtc cac	1699
Phe Ser Glu Arg Phe Val Leu Pro Ile Ser His Asp Glu Val Val His	
520 525 530	
ggc aag ggt tcc ctg tgg gac cgt atg cct ggc gat acg tgg aac aag	1747
Gly Lys Gly Ser Leu Trp Asp Arg Met Pro Gly Asp Thr Trp Asn Lys	
535 540 545	
gcc gct ggt ctt cgc acc ttc ctt gcg tac atg tgg tca cac cca ggc	1795
Ala Ala Gly Leu Arg Thr Phe Leu Ala Tyr Met Trp Ser His Pro Gly	
550 555 560 565	
aag aag ctg ctt ttc atg ggt cag gag ttt ggt cag cgt gaa gag tgg	1843
Lys Lys Leu Leu Phe Met Gly Gln Glu Phe Gly Gln Arg Glu Glu Trp	
570 575 580	
gct gaa ggc cag gga ctg cca tgg gat att gtc gac ggc tgg caa ggc	1891
Ala Glu Gly Gln Gly Leu Pro Trp Asp Ile Val Asp Gly Trp Gln Gly	
585 590 595	

gag tac cac gaa gcc atc cgc act ctg acc cgc tcc ctc aac ggt gtc 1939  
 Glu Tyr His Glu Ala Ile Arg Thr Leu Thr Arg Ser Leu Asn Gly Val  
 600 605 610  
 tac tca gac tcc cct gcg ctg cac act cag gat ttc acc gga gaa ggc 1987  
 Tyr Ser Asp Ser Pro Ala Leu His Thr Gln Asp Phe Thr Gly Glu Gly  
 615 620 625  
 ttc aca tgg aat aag ggc gac gac gcc acc aac aac att ttg gcg ttc 2035  
 Phe Thr Trp Asn Lys Gly Asp Asp Ala Thr Asn Asn Ile Leu Ala Phe  
 630 635 640 645  
 act cgt ttc ggc agc gac ggc tcc cag atg ctg tgt gta ttc aac ctg 2083  
 Thr Arg Phe Gly Ser Asp Gly Ser Gln Met Leu Cys Val Phe Asn Leu  
 650 655 660  
 tct gga acc tcc cag cct gag tac cag ctc ggt gtt gca gcg ggt ggc 2131  
 Ser Gly Thr Ser Gln Pro Glu Tyr Gln Leu Gly Val Ala Ala Gly Gly  
 665 670 675  
 gaa tgg aag ctc gtt ctc aac act gat gat gct gaa ttc ctc ggt gca 2179  
 Glu Trp Lys Leu Val Leu Asn Thr Asp Asp Ala Glu Phe Leu Gly Ala  
 680 685 690  
 gaa aac gat atc gct act tcc gtt caa gca gca gcg aca cca cgc gat 2227  
 Glu Asn Asp Ile Ala Thr Ser Val Gln Ala Ala Thr Pro Arg Asp  
 695 700 705  
 aat ttc gcc tac tca ctc tca ctg cat gtc cca gcg atg agt gct cag 2275  
 Asn Phe Ala Tyr Ser Leu Ser Leu His Val Pro Ala Met Ser Ala Gln  
 710 715 720 725  
 ttc tac tca ctg cag aag taggacacag gaaaatgcat cct 2316  
 Phe Tyr Ser Leu Gln Lys  
 730

&lt;210&gt; 362

&lt;211&gt; 731

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 362

Met Thr Val Asp Pro Ala Ser His Ile Thr Ile Pro Glu Ala Asp Leu  
 1 5 10 15  
 Ala Arg Leu Arg His Cys Asn His His Asp Pro His Gly Phe Tyr Gly  
 20 25 30  
 Trp His Glu Thr Glu Ala Gly Ser Val Ile Arg Thr Arg Gln Val Gly  
 35 40 45  
 Ala Thr Gln Val Asn Leu Leu Ile Asp Asp Thr Ser His Val Met Thr  
 50 55 60  
 Pro Ile Gly Asp Asp Ile Phe Ala Ile Asp Leu Gly His Arg Glu Arg  
 65 70 75 80  
 Ala Asp Tyr Arg Leu Glu Val Thr Trp Pro Asp Gln Glu Pro Gln Val  
 85 90 95



Lys Ala Asp Pro Tyr Tyr Phe Leu Pro Thr Val Gly Glu Met Asp Ile  
 100 105 110  
 Tyr Leu Phe Ser Glu Gly Arg His Glu Arg Leu Trp Glu Ile Leu Gly  
 115 120 125  
 Ala Asn Ile Lys Thr Tyr Gln Thr Ala Leu Gly Thr Val Arg Gly Thr  
 130 135 140  
 Ala Phe Thr Val Trp Ala Pro Asn Ala Ile Gly Cys Ala Val Val Gly  
 145 150 155 160  
 Gly Phe Asn Gly Trp Asn Ala Ser Gln His Pro Met Arg Ser Met Gly  
 165 170 175  
 Gly Ser Gly Leu Trp Glu Leu Phe Ile Pro Gly Ile Glu Glu Gly Glu  
 180 185 190  
 Val Tyr Lys Phe Ala Val Gln Thr Arg Glu Gly Gln Arg Arg Asp Lys  
 195 200 205  
 Ala Asp Pro Met Ala Arg Arg Ala Glu Leu Ala Pro Ala Thr Gly Ser  
 210 215 220  
 Ile Val Ala Ser Ser Glu Tyr Gln Trp Gln Asp Ser Glu Trp Leu Arg  
 225 230 235 240  
 Glu Arg Ser Gln Thr Asp Leu Ala Ser Lys Pro Met Ser Val Tyr Glu  
 245 250 255  
 Val His Leu Gly Ser Trp Arg Trp Gly Lys Asn Tyr Glu Asp Leu Ala  
 260 265 270  
 Thr Glu Leu Val Asp Tyr Val Ala Asp Leu Gly Tyr Thr His Val Glu  
 275 280 285  
 Phe Leu Pro Val Ala Glu His Pro Phe Gly Gly Ser Trp Gly Tyr Gln  
 290 295 300  
 Val Thr Gly Tyr Tyr Ala Pro Thr Ser Arg Trp Gly Thr Pro Asp Gln  
 305 310 315 320  
 Phe Arg Ala Leu Val Asp Ala Phe His Ala Arg Gly Ile Gly Val Ile  
 325 330 335  
 Met Asp Trp Val Pro Ala His Phe Pro Lys Asp Asp Trp Ala Leu Ala  
 340 345 350  
 Arg Phe Asp Gly Glu Ala Leu Tyr Glu His Pro Asp Trp Arg Arg Gly  
 355 360 365  
 Glu Gln Lys Asp Trp Gly Thr Leu Val Phe Asp Phe Gly Arg Asn Glu  
 370 375 380  
 Val Arg Asn Phe Leu Val Ala Asn Ala Leu Tyr Trp Ile Glu Glu Phe  
 385 390 395 400  
 His Ile Asp Gly Leu Arg Val Asp Ala Val Ala Ser Met Leu Tyr Leu  
 405 410 415  
 Asp Tyr Ser Arg Glu His Gly Glu Trp Glu Pro Asn Ile Tyr Gly Gly

420										425					430				
Arg	Glu	Asn	Leu	Glu	Ala	Val	Gln	Phe	Leu	Gln	Glu	Met	Asn	Ala	Thr				
		435					440					445							
Val	Leu	Arg	Leu	His	Pro	Gly	Ala	Leu	Thr	Ile	Ala	Glu	Glu	Ser	Thr				
		450				455					460								
Ser	Trp	Pro	Gly	Val	Thr	Ala	Pro	Thr	Trp	Asp	Gly	Gly	Leu	Gly	Phe				
465					470					475					480				
Ser	Leu	Lys	Trp	Asn	Met	Gly	Trp	Met	His	Asp	Thr	Leu	Glu	Tyr	Phe				
				485					490					495					
Ser	Lys	Asn	Pro	Val	His	Arg	Ala	Phe	His	His	Ser	Glu	Leu	Thr	Phe				
			500					505					510						
Ser	Leu	Val	Tyr	Ala	Phe	Ser	Glu	Arg	Phe	Val	Leu	Pro	Ile	Ser	His				
		515					520				525								
Asp	Glu	Val	Val	His	Gly	Lys	Gly	Ser	Leu	Trp	Asp	Arg	Met	Pro	Gly				
	530					535				540									
Asp	Thr	Trp	Asn	Lys	Ala	Ala	Gly	Leu	Arg	Thr	Phe	Leu	Ala	Tyr	Met				
545					550					555					560				
Trp	Ser	His	Pro	Gly	Lys	Lys	Leu	Leu	Phe	Met	Gly	Gln	Glu	Phe	Gly				
				565					570					575					
Gln	Arg	Glu	Glu	Trp	Ala	Glu	Gly	Gln	Gly	Leu	Pro	Trp	Asp	Ile	Val				
			580					585					590						
Asp	Gly	Trp	Gln	Gly	Glu	Tyr	His	Glu	Ala	Ile	Arg	Thr	Leu	Thr	Arg				
		595					600					605							
Ser	Leu	Asn	Gly	Val	Tyr	Ser	Asp	Ser	Pro	Ala	Leu	His	Thr	Gln	Asp				
		610				615					620								
Phe	Thr	Gly	Glu	Gly	Phe	Thr	Trp	Asn	Lys	Gly	Asp	Asp	Ala	Thr	Asn				
625					630					635					640				
Asn	Ile	Leu	Ala	Phe	Thr	Arg	Phe	Gly	Ser	Asp	Gly	Ser	Gln	Met	Leu				
				645					650					655					
Cys	Val	Phe	Asn	Leu	Ser	Gly	Thr	Ser	Gln	Pro	Glu	Tyr	Gln	Leu	Gly				
			660					665					670						
Val	Ala	Ala	Gly	Gly	Glu	Trp	Lys	Leu	Val	Leu	Asn	Thr	Asp	Asp	Ala				
		675					680					685							
Glu	Phe	Leu	Gly	Ala	Glu	Asn	Asp	Ile	Ala	Thr	Ser	Val	Gln	Ala	Ala				
		690				695					700								
Ala	Thr	Pro	Arg	Asp	Asn	Phe	Ala	Tyr	Ser	Leu	Ser	Leu	His	Val	Pro				
705					710					715					720				
Ala	Met	Ser	Ala	Gln	Phe	Tyr	Ser	Leu	Gln	Lys									
				725					730										

&lt;210&gt; 363

<211> 1913  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1890)  
 <223> RXN01884

<400> 363  
 gtg act gcc att gaa ttg atg ccg gtc cac cag ttc ctg cag gat gat 48  
 Val Thr Ala Ile Glu Leu Met Pro Val His Gln Phe Leu Gln Asp Asp  
 1 5 10 15  
 cgt ctc cgc gac cta gga atg cgc aac tac tgg ggc tac aac tct ttc 96  
 Arg Leu Arg Asp Leu Gly Met Arg Asn Tyr Trp Gly Tyr Asn Ser Phe  
 20 25 30  
 ggc ttc ttt gcg ccc tac aac gat tac gct gcc aac aag aac ccc ggt 144  
 Gly Phe Phe Ala Pro Tyr Asn Asp Tyr Ala Ala Asn Lys Asn Pro Gly  
 35 40 45  
 ggc gcc gtg gcc gag ttc aaa ggc ttg gtg cgc agc tac cac gaa gcg 192  
 Gly Ala Val Ala Glu Phe Lys Gly Leu Val Arg Ser Tyr His Glu Ala  
 50 55 60  
 ggc ctc gaa gta att ttg gat gtg gtc tac aac cac acc gcc gag ggc 240  
 Gly Leu Glu Val Ile Leu Asp Val Val Tyr Asn His Thr Ala Glu Gly  
 65 70 75 80  
 aac cac atg ggc ccc acc atc gcg ttc cga ggc att gac aac gag gcg 288  
 Asn His Met Gly Pro Thr Ile Ala Phe Arg Gly Ile Asp Asn Glu Ala  
 85 90 95  
 tac tac cga ctg gtt gag ggc gat cgc cgt cat tac atg gac tac acc 336  
 Tyr Tyr Arg Leu Val Glu Gly Asp Arg Arg His Tyr Met Asp Tyr Thr  
 100 105 110  
 ggt act ggt aac tcc ctc aat gtc cgc gac ccg cac tca ctg cag ctg 384  
 Gly Thr Gly Asn Ser Leu Asn Val Arg Asp Pro His Ser Leu Gln Leu  
 115 120 125  
 att atg gat tcg ctg cgc tac tgg gtc acc gag atg cat gtc gac ggc 432  
 Ile Met Asp Ser Leu Arg Tyr Trp Val Thr Glu Met His Val Asp Gly  
 130 135 140  
 ttc cgc ttc gac ctt gcc tct acc ctt gct cgt gaa ttt gat gat gtt 480  
 Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg Glu Phe Asp Asp Val  
 145 150 155 160  
 gac cgc ctg gca acc ttc ttc gac ctg gtc caa caa gac ccg gtg gtc 528  
 Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln Gln Asp Pro Val Val  
 165 170 175  
 tcc cag gtc aag ctc att gct gag ccg tgg gat gtt ggc gaa ggc gga 576  
 Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp Val Gly Glu Gly Gly  
 180 185 190  
 tac caa gtg ggt aac ttc cca cca ctg tgg act gag tgg aac ggt aaa 624  
 Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr Glu Trp Asn Gly Lys  
 195 200 205

tac cgc gac act gtc cgt gat ttc tgg cgt ggt gag cca gca acc ttg	672
Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly Glu Pro Ala Thr Leu	
210 215 220	
ggt gaa ttc gct tcc cga cta act ggt tcc tct gat ttg tat gca aac	720
Gly Glu Phe Ala Ser Arg Leu Thr Gly Ser Ser Asp Leu Tyr Ala Asn	
225 230 235 240	
aac ggc cgt cgc ccc act gca tcg atc aac ttt gtg act gct cac gac	768
Asn Gly Arg Arg Pro Thr Ala Ser Ile Asn Phe Val Thr Ala His Asp	
245 250 255	
ggc ttc acc ctc aat gac ttg gtc agt tac aac gag aag cac aac atg	816
Gly Phe Thr Leu Asn Asp Leu Val Ser Tyr Asn Glu Lys His Asn Met	
260 265 270	
gcc aac ggt gaa gac ggt cgg gac ggt gaa tca cac aac cgt tcc tgg	864
Ala Asn Gly Glu Asp Gly Arg Asp Gly Glu Ser His Asn Arg Ser Trp	
275 280 285	
aac tgt ggc gtc gaa gga cca act gac gat cct gag att atg cag ctg	912
Asn Cys Gly Val Glu Gly Pro Thr Asp Asp Pro Glu Ile Met Gln Leu	
290 295 300	
cgt gct cag caa cga cgc aac ttc ctc acc acc ttg ttg ctg tcc cag	960
Arg Ala Gln Gln Arg Arg Asn Phe Leu Thr Thr Leu Leu Leu Ser Gln	
305 310 315 320	
ggc acc cct atg ttg tcc cac ggt gat gaa atg gcc cgt acc caa aac	1008
Gly Thr Pro Met Leu Ser His Gly Asp Glu Met Ala Arg Thr Gln Asn	
325 330 335	
ggc aac aac aac gtc tac tgc caa gac aat gaa ctg gcg tgg gtg aat	1056
Gly Asn Asn Asn Val Tyr Cys Gln Asp Asn Glu Leu Ala Trp Val Asn	
340 345 350	
tgg gat cag gct gaa gaa aac gct gac ttg gtg agc ttc acc agg cgt	1104
Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val Ser Phe Thr Arg Arg	
355 360 365	
ttg ctg cgt atc cga gca aac cac cca gta ttt agg cgc agg cag ttc	1152
Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe Arg Arg Arg Gln Phe	
370 375 380	
ctt gcc ggt ggc cct ttg ggc gcc gat gtt cgt gac cgc gat atc gca	1200
Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg Asp Arg Asp Ile Ala	
385 390 395 400	
tgg ctg gta cca aat gga acc ttg atg act caa gat gac tgg gac ttc	1248
Trp Leu Val Pro Asn Gly Thr Leu Met Thr Gln Asp Asp Trp Asp Phe	
405 410 415	
gct ttc ggt aaa tca ctg cag gtg ttc ttc aac ggc gat gcc atc gaa	1296
Ala Phe Gly Lys Ser Leu Gln Val Phe Phe Asn Gly Asp Ala Ile Glu	
420 425 430	
gag cct gat tat cga gga cag aaa atc cac gat gac tcc ttc atc ttg	1344
Glu Pro Asp Tyr Arg Gly Gln Lys Ile His Asp Asp Ser Phe Ile Leu	
435 440 445	

atg ttc aac gct cac ttc gaa cct atc gat ttc aat ctc cct cct gag 1392  
 Met Phe Asn Ala His Phe Glu Pro Ile Asp Phe Asn Leu Pro Pro Glu  
 450 455 460

cat ttc ggt atg aag tgg aag ctt ttg gtc gat acc acc gaa gcg gtg 1440  
 His Phe Gly Met Lys Trp Lys Leu Leu Val Asp Thr Thr Glu Ala Val  
 465 470 475 480

ggc cac ccg ctg gag gat ctc acc atc gaa gct ggc gga acc atc act 1488  
 Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala Gly Gly Thr Ile Thr  
 485 490 495

gtt cct gcc cgt tcc acg atg ctg ctg cgc cag gtg gag gct ccg gac 1536  
 Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln Val Glu Ala Pro Asp  
 500 505 510

tac acc aag ctt gag gaa aag atc gct gct gaa aag cgt gag caa gaa 1584  
 Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu Lys Arg Glu Gln Glu  
 515 520 525

ctt gcg gca gag aag gaa gct gct gag aag cgc gaa ttg gaa ctg gcg 1632  
 Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg Glu Leu Glu Leu Ala  
 530 535 540

gca gca aag gaa gct gaa gat gct gct gag gct ctc cac ctt gcg gca 1680  
 Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala Leu His Leu Ala Ala  
 545 550 555 560

gaa cgt gct tcg act cag gaa gct gaa ttg gcc cat caa cac ggt gct 1728  
 Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala His Gln His Gly Ala  
 565 570 575

gat gcg att gcc gat gag gta gcg gaa gaa cca caa gag ctg cca caa 1776  
 Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro Gln Glu Leu Pro Gln  
 580 585 590

gat gaa gta gcg gca gag gtc gag act gag ccc gac acc gag cct gac 1824  
 Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro Asp Thr Glu Pro Asp  
 595 600 605

act gaa tct gac tcc gag cag gct gag gta gct tca gag gag cct gaa 1872  
 Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala Ser Glu Glu Pro Glu  
 610 615 620

gcg gac gaa gaa gag aag tagtacaccg aaagtggcgt cgc 1913  
 Ala Asp Glu Glu Glu Lys  
 625 630

&lt;210&gt; 364

&lt;211&gt; 630

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 364

Val Thr Ala Ile Glu Leu Met Pro Val His Gln Phe Leu Gln Asp Asp  
 1 5 10 15

Arg Leu Arg Asp Leu Gly Met Arg Asn Tyr Trp Gly Tyr Asn Ser Phe  
 20 25 30

Gly	Phe	Ala	Pro	Tyr	Asn	Asp	Tyr	Ala	Ala	Asn	Lys	Asn	Pro	Gly	
35						40			45						
Gly	Ala	Val	Ala	Glu	Phe	Lys	Gly	Leu	Val	Arg	Ser	Tyr	His	Glu	Ala
50						55			60						
Gly	Leu	Glu	Val	Ile	Leu	Asp	Val	Val	Tyr	Asn	His	Thr	Ala	Glu	Gly
65						70			75			80			
Asn	His	Met	Gly	Pro	Thr	Ile	Ala	Phe	Arg	Gly	Ile	Asp	Asn	Glu	Ala
			85						90			95			
Tyr	Tyr	Arg	Leu	Val	Glu	Gly	Asp	Arg	Arg	His	Tyr	Met	Asp	Tyr	Thr
			100			105						110			
Gly	Thr	Gly	Asn	Ser	Leu	Asn	Val	Arg	Asp	Pro	His	Ser	Leu	Gln	Leu
115						120						125			
Ile	Met	Asp	Ser	Leu	Arg	Tyr	Trp	Val	Thr	Glu	Met	His	Val	Asp	Gly
130						135			140						
Phe	Arg	Phe	Asp	Leu	Ala	Ser	Thr	Leu	Ala	Arg	Glu	Phe	Asp	Asp	Val
145			150			155			160						
Asp	Arg	Leu	Ala	Thr	Phe	Phe	Asp	Leu	Val	Gln	Gln	Asp	Pro	Val	Val
			165			170			175						
Ser	Gln	Val	Lys	Leu	Ile	Ala	Glu	Pro	Trp	Asp	Val	Gly	Glu	Gly	Gly
180						185			190						
Tyr	Gln	Val	Gly	Asn	Phe	Pro	Pro	Leu	Trp	Thr	Glu	Trp	Asn	Gly	Lys
195						200			205						
Tyr	Arg	Asp	Thr	Val	Arg	Asp	Phe	Trp	Arg	Gly	Glu	Pro	Ala	Thr	Leu
210			215			220			225						
Gly	Glu	Phe	Ala	Ser	Arg	Leu	Thr	Gly	Ser	Ser	Asp	Leu	Tyr	Ala	Asn
225			230			235			240						
Asn	Gly	Arg	Arg	Pro	Thr	Ala	Ser	Ile	Asn	Phe	Val	Thr	Ala	His	Asp
			245			250			255						
Gly	Phe	Thr	Leu	Asn	Asp	Leu	Val	Ser	Tyr	Asn	Glu	Lys	His	Asn	Met
260						265			270						
Ala	Asn	Gly	Glu	Asp	Gly	Arg	Asp	Gly	Glu	Ser	His	Asn	Arg	Ser	Trp
275			280			285			290						
Asn	Cys	Gly	Val	Glu	Gly	Pro	Thr	Asp	Asp	Pro	Glu	Ile	Met	Gln	Leu
290			295			300			305						
Arg	Ala	Gln	Gln	Arg	Arg	Asn	Phe	Leu	Thr	Thr	Leu	Leu	Leu	Ser	Gln
305			310			315			320						
Gly	Thr	Pro	Met	Leu	Ser	His	Gly	Asp	Glu	Met	Ala	Arg	Thr	Gln	Asn
			325			330			335						
Gly	Asn	Asn	Asn	Val	Tyr	Cys	Gln	Asp	Asn	Glu	Leu	Ala	Trp	Val	Asn
340			345			350			355						
Trp	Asp	Gln	Ala	Glu	Glu	Asn	Ala	Asp	Leu	Val	Ser	Phe	Thr	Arg	Arg

355	360	365
Leu Leu Arg Ile Arg Ala	Asn His Pro Val Phe Arg	Arg Arg Gln Phe
370	375	380
Leu Ala Gly Gly Pro Leu	Gly Ala Asp Val Arg Asp	Arg Asp Ile Ala
385	390	395
Trp Leu Val Pro Asn Gly	Thr Leu Met Thr Gln Asp	Asp Trp Asp Phe
	405	410
Ala Phe Gly Lys Ser Leu	Gln Val Phe Phe Asn Gly	Asp Ala Ile Glu
	420	425
Glu Pro Asp Tyr Arg Gly	Gln Lys Ile His Asp	Asp Ser Phe Ile Leu
	435	440
Met Phe Asn Ala His Phe	Glu Pro Ile Asp Phe	Asn Leu Pro Pro Glu
	450	455
His Phe Gly Met Lys Trp	Lys Leu Leu Val Asp	Thr Thr Glu Ala Val
	465	470
Gly His Pro Leu Glu Asp	Leu Thr Ile Glu Ala	Gly Gly Thr Ile Thr
	485	490
Val Pro Ala Arg Ser Thr	Met Leu Leu Arg Gln	Val Glu Ala Pro Asp
	500	505
Tyr Thr Lys Leu Glu Glu	Lys Ile Ala Ala Glu	Lys Arg Glu Gln Glu
	515	520
Leu Ala Ala Glu Lys Glu	Ala Ala Glu Lys Arg	Glu Leu Glu Leu Ala
	530	535
Ala Ala Lys Glu Ala Glu	Asp Ala Ala Glu Ala	Leu His Leu Ala Ala
	545	550
Glu Arg Ala Ser Thr Gln	Glu Ala Glu Leu Ala	His Gln His Gly Ala
	565	570
Asp Ala Ile Ala Asp Glu	Val Ala Glu Glu Pro	Gln Glu Leu Pro Gln
	580	585
Asp Glu Val Ala Ala Glu	Val Glu Thr Glu Pro	Asp Thr Glu Pro Asp
	595	600
Thr Glu Ser Asp Ser Glu	Gln Ala Glu Val Ala	Ser Glu Glu Pro Glu
	610	615
Ala Asp Glu Glu Glu Lys		
625	630	

&lt;210&gt; 365

&lt;211&gt; 1496

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1473)

&lt;223&gt; FRXA01884

&lt;400&gt; 365

atg cat gtc gac ggc ttc cgc ttc gac ctt gcc tct acc ctt gct cgt	48
Met His Val Asp Gly Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg	
1 5 10 15	
gaa ttt gat gat gtt gac cgc ctg gca acc ttc ttc gac ctg gtc caa	96
Glu Phe Asp Asp Val Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln	
20 25 30	
caa gac ccg gtg gtc tcc cag gtc aag ctc att gct gag ccg tgg gat	144
Gln Asp Pro Val Val Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp	
35 40 45	
gtt ggc gaa ggc gga tac caa gtg ggt aac ttc cca cca ctg tgg act	192
Val Gly Glu Gly Gly Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr	
50 55 60	
gag tgg aac ggt aaa tac cgc gac act gtc cgt gat ttc tgg cgt ggt	240
Glu Trp Asn Gly Lys Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly	
65 70 75 80	
gag cca gca acc ttg ggt gaa ttc gct tcc cga cta act ggt tcc tct	288
Glu Pro Ala Thr Leu Gly Glu Phe Ala Ser Arg Leu Thr Gly Ser Ser	
85 90 95	
gat ttg tat gca aac aac ggc cgt cgc ccc act gca tcg atc aac ttt	336
Asp Leu Tyr Ala Asn Asn Gly Arg Arg Pro Thr Ala Ser Ile Asn Phe	
100 105 110	
gtg act gct cac gac ggc ttc acc ctc aat gac ttg gtc agt tac aac	384
Val Thr Ala His Asp Gly Phe Thr Leu Asn Asp Leu Val Ser Tyr Asn	
115 120 125	
gag aag cac aac atg gcc aac ggt gaa gac ggt cgg gac ggt gaa tca	432
Glu Lys His Asn Met Ala Asn Gly Glu Asp Gly Arg Asp Gly Glu Ser	
130 135 140	
cac aac cgt tcc tgg aac tgt ggc gtc gaa gga cca act gac gat cct	480
His Asn Arg Ser Trp Asn Cys Gly Val Glu Gly Pro Thr Asp Asp Pro	
145 150 155 160	
gag att atg cag ctg cgt gct cag caa cga cgc aac ttc ctc acc acc	528
Glu Ile Met Gln Leu Arg Ala Gln Gln Arg Arg Asn Phe Leu Thr Thr	
165 170 175	
ttg ttg ctg tcc cag ggc acc cct atg ttg tcc cac ggt gat gaa atg	576
Leu Leu Leu Ser Gln Gly Thr Pro Met Leu Ser His Gly Asp Glu Met	
180 185 190	
gcc cgt acc caa aac ggc aac aac aac gtc tac tgc caa gac aat gaa	624
Ala Arg Thr Gln Asn Gly Asn Asn Asn Val Tyr Cys Gln Asp Asn Glu	
195 200 205	
ctg gcg tgg gtg aat tgg gat cag gct gaa gaa aac gct gac ttg gtg	672
Leu Ala Trp Val Asn Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val	
210 215 220	
agc ttc acc agg cgt ttg ctg cgt atc cga gca aac cac cca gta ttt	720



Ser Phe Thr Arg Arg Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe	
225 230 235 240	
agg cgc agg cag ttc ctt gcc ggt ggc cct ttg ggc gcc gat gtt cgt	768
Arg Arg Arg Gln Phe Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg	
245 250 255	
gac cgc gat atc gca tgg ctg gta cca aat gga acc ttg atg act caa	816
Asp Arg Asp Ile Ala Trp Leu Val Pro Asn Gly Thr Leu Met Thr Gln	
260 265 270	
gat gac tgg gac ttc gct ttc ggt aaa tca ctg cag gtg ttc ttc aac	864
Asp Asp Trp Asp Phe Ala Phe Gly Lys Ser Leu Gln Val Phe Phe Asn	
275 280 285	
ggc gat gcc atc gaa gag cct gat tat cga gga cag aaa atc cac gat	912
Gly Asp Ala Ile Glu Glu Pro Asp Tyr Arg Gly Gln Lys Ile His Asp	
290 295 300	
gac tcc ttc atc ttg atg ttc aac gct cac ttc gaa cct atc gat ttc	960
Asp Ser Phe Ile Leu Met Phe Asn Ala His Phe Glu Pro Ile Asp Phe	
305 310 315 320	
aat ctc cct cct gag cat ttc ggt atg aag tgg aag ctt ttg gtc gat	1008
Asn Leu Pro Pro Glu His Phe Gly Met Lys Trp Lys Leu Leu Val Asp	
325 330 335	
acc acc gaa gcg gtg ggc cac ccg ctg gag gat ctc acc atc gaa gct	1056
Thr Thr Glu Ala Val Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala	
340 345 350	
ggc gga acc atc act gtt cct gcc cgt tcc acg atg ctg ctg cgc cag	1104
Gly Gly Thr Ile Thr Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln	
355 360 365	
gtg gag gct ccg gac tac acc aag ctt gag gaa aag atc gct gct gaa	1152
Val Glu Ala Pro Asp Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu	
370 375 380	
aag cgt gag caa gaa ctt gcg gca gag aag gaa gct gct gag aag cgc	1200
Lys Arg Glu Gln Glu Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg	
385 390 395 400	
gaa ttg gaa ctg gcg gca gca aag gaa gct gaa gat gct gct gag gct	1248
Glu Leu Glu Leu Ala Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala	
405 410 415	
ctc cac ctt gcg gca gaa cgt gct tcg act cag gaa gct gaa ttg gcc	1296
Leu His Leu Ala Ala Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala	
420 425 430	
cat caa cac ggt gct gat gcg att gcc gat gag gta gcg gaa gaa cca	1344
His Gln His Gly Ala Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro	
435 440 445	
caa gag ctg cca caa gat gaa gta gcg gca gag gtc gag act gag ccc	1392
Gln Glu Leu Pro Gln Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro	
450 455 460	
gac acc gag cct gac act gaa tct gac tcc gag cag gct gag gta gct	1440
Asp Thr Glu Pro Asp Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala	

```

465              470              475              480
tca gag gag cct gaa gcg gac gaa gaa gag aag tagtacaccg aaagtggcgt 1493
Ser Glu Glu Pro Glu Ala Asp Glu Glu Lys
              485              490

```

cqc 1496

```
<210> 366
<211> 491
<212> PRT
<213> Corynebacterium glutamicum
```

```
<400> 366
Met His Val Asp Gly Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg
  1             5             10            15
```

Glu Phe Asp Asp Val Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln  
20 25 30

Gln Asp Pro Val Val Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp  
35 40 45

Val Gly Glu Gly Gly Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr  
50 55 60

Glu Trp Asn Gly Lys Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly  
65 70 75 80

Glu Pro Ala Thr Leu Gly Glu Phe Ala Ser Arg Leu Thr Gly Ser Ser  
85 90 95

Asp Leu Tyr Ala Asn Asn Gly Arg Arg Pro Thr Ala Ser Ile Asn Phe  
100 105 110

Val Thr Ala His Asp Gly Phe Thr Leu Asn Asp Leu Val Ser Tyr Asn  
115 120 125

Glu Lys His Asn Met Ala Asn Gly Glu Asp Gly Arg Asp Gly Glu Ser  
130 135 140

His Asn Arg Ser Trp Asn Cys Gly Val Glu Gly Pro Thr Asp Asp Pro  
145 150 155 160

Glu Ile Met Gln Leu Arg Ala Gln Gln Arg Arg Asn Phe Leu Thr Thr  
165 170 175

Leu Leu Leu Ser Gln Gly Thr Pro Met Leu Ser His Gly Asp Glu Met  
180 185 190

Ala Arg Thr Gln Asn Gly Asn Asn Val Tyr Cys Gln Asp Asn Glu  
195 200 205

Leu Ala Trp Val Asn Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val  
210 215 220

Ser Phe Thr Arg Arg Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe  
225 230 235 240

Arg Arg Arg Gln Phe Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg

<400> 367  
agaaaaccct gccgatgcaa actttgagga gagattcaat caaggaatag aaatcattct 60

ggtgggtcta gacgcgcttg ggcataataag atgacgttcc															atg	aca	tca	acg	att	115
															Met	Thr	Ser	Thr	Ile	
															1				5	
gag cac tcg tac caa gtt tgg cct gga cat gct tat cct ctg ggt tca															163					
Glu His Ser Tyr Gln Val Trp Pro Gly His Ala Tyr Pro Leu Gly Ser																				
															10				20	
acc tat gac ggt gct gga acg aac ttc gca ctc ttc tcc gac gtt gca															211					
Thr Tyr Asp Gly Ala Gly Thr Asn Phe Ala Leu Phe Ser Asp Val Ala																				
															25				35	
gag cgt gtt gag ctg tgt cta tta gat gca gat aac aac gag act cga															259					
Glu Arg Val Glu Leu Cys Leu Leu Asp Ala Asp Asn Asn Glu Thr Arg																				
															40				50	
att cca ctc gaa gag cgc gat gcc cac att tgg cat tgc tac ctt cct															307					
Ile Pro Leu Glu Glu Arg Asp Ala His Ile Trp His Cys Tyr Leu Pro																				
															55				65	
ggc gtt caa cct gga cag cgc tac gga ttc cga gtt cat ggc ccg tgg															355					
Gly Val Gln Pro Gly Gln Arg Tyr Gly Phe Arg Val His Gly Pro Trp																				
															70				85	
aac cca gat gag ggt aag cgg tgc gac gcg aac aaa ctt cta gtt gat															403					
Asn Pro Asp Glu Gly Lys Arg Cys Asp Ala Asn Lys Leu Leu Val Asp																				
															90				100	
ccc tat gct cgt gct ttc gat gga gat ttt gat gga cat ccg tca cta															451					
Pro Tyr Ala Arg Ala Phe Asp Gly Asp Phe Asp Gly His Pro Ser Leu																				
															105				115	
ttt tct tac gac atc acc aat cca aat gac ccc aac ggt cgc aat acc															499					
Phe Ser Tyr Asp Ile Thr Asn Pro Asn Asp Pro Asn Gly Arg Asn Thr																				
															120				130	
gaa gac agc att gat cac aca atg aag tct gtc gtg gtg aac cca ttc															547					
Glu Asp Ser Ile Asp His Thr Met Lys Ser Val Val Val Asn Pro Phe																				
															135				145	

<210> 368

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 368

Met Thr Ser Thr Ile Glu His Ser Tyr Gln Val Trp Pro Gly His Ala  
1 5 10 15

Tyr Pro Leu Gly Ser Thr Tyr Asp Gly Ala Gly Thr Asn Phe Ala Leu  
20 25 30

Phe Ser Asp Val Ala Glu Arg Val Glu Leu Cys Leu Leu Asp Ala Asp  
35 40 45

Asn Asn Glu Thr Arg Ile Pro Leu Glu Glu Arg Asp Ala His Ile Trp  
50 55 60

His Cys Tyr Leu Pro Gly Val Gln Pro Gly Gln Arg Tyr Gly Phe Arg  
65 70 75 80

[illegible]

```
<210> 369
<211> 1635
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1612)  
<223> RXN01550
```

<400> 369																			
ttc	gcc	cag	ca	gt	act	tct	ctt	c	cct	gc	cagg	cc	atg	att	cag	ggccac	ctg	g	60
cgc	cacc	acaa	gg	acct	cagc	aact	ttg	ccg	ag	tt	cact	cc	gtg	cag	ctc	aat	gac		115
												Val	Gln	Leu	Asn	Asp	5		
																1			
act	cac	cca	gtg	ttg	gct	atc	cct	gag	ctt	atg	cgt	ctg	ctc	atg	gac				163
Thr	His	Pro	Val	Leu	Ala	Ile	Pro	Glu	Leu	Met	Arg	Leu	Leu	Met	Asp				
				10				15				20							
gag	cat	gac	atg	ggc	tgg	gaa	gaa	tcc	tgg	gca	atc	gtg	ttc	aag	acc				211
Glu	His	Asp	Met	Gly	Trp	Glu	Glu	Ser	Trp	Ala	Ile	Val	Phe	Lys	Thr				
				25		30				35									
ttc	gca	tac	acc	aac	cac	acc	gtg	ctc	acc	gaa	gct	ctt	gag	cag	tgg				259
Phe	Ala	Tyr	Thr	Asn	His	Thr	Val	Leu	Thr	Glu	Ala	Leu	Glu	Gln	Trp				
			40			45			50										
gat	cag	cag	atc	ttc	caa	cag	ctg	ttc	tgg	cgc	gtg	tgg	gaa	atc	atc				307
Asp	Gln	Gln	Ile	Phe	Gln	Gln	Leu	Phe	Trp	Arg	Val	Trp	Glu	Ile	Ile				
			55			60			65										
aca	gag	atc	gat	cgc	cgc	ttc	cgt	ttg	gag	cgc	gca	gcc	gat	gga	ctg				355
Thr	Glu	Ile	Asp	Arg	Arg	Phe	Arg	Leu	Glu	Arg	Ala	Ala	Asp	Gly	Leu				
		70		75		80		85											
gat	gaa	gag	acc	atc	gac	cgc	atg	gct	cca	atc	cag	cac	ggc	act	gtt				403
Asp	Glu	Glu	Thr	Ile	Asp	Arg	Met	Ala	Pro	Ile	Gln	His	Gly	Thr	Val				
				90				95				100							
cat	atg	gca	tgg	att	gcc	tgt	tac	gcg	gca	tat	tcc	atc	aat	ggc	gtg				451
His	Met	Ala	Trp	Ile	Ala	Cys	Tyr	Ala	Ala	Tyr	Ser	Ile	Asn	Gly	Val				
			105			110			115										

gca gcg ctg cac acc gag atc atc aag gcc gag acc ttg gct gac tgg	499
Ala Ala Leu His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp	
120 125 130	
tac gca ctg tgg cca gag aag ttc aac aac aag act aac ggt gtt acc	547
Tyr Ala Leu Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr	
135 140 145	
cca cgc cgt tgg ctg cgc atg atc aac cca ggt ctg tct gac ctg ctc	595
Pro Arg Arg Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu	
150 155 160 165	
act cga ctt tcc ggt tcc gat gat tgg gta acc gat ctg gat gag ctg	643
Thr Arg Leu Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu	
170 175 180	
aag aag ctg cgc tcc tat gcc gac gat aag tcc gtg ctt gaa gaa ctc	691
Lys Lys Leu Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu	
185 190 195	
cgc gct atc aag gct gct aat aag caa gac ttc gcc gag tgg atc ctc	739
Arg Ala Ile Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu	
200 205 210	
gag cgc cag ggc att gag att gat cca gaa tcc atc ttt gac gtg cag	787
Glu Arg Gln Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln	
215 220 225	
att aag cgc ctc cac gag tac aag cgc cag ctc atg aac gcg ctc tac	835
Ile Lys Arg Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr	
230 235 240 245	
gta cta gac ctt tac ttc cgt att aag gaa gat ggc ctc acc gac atc	883
Val Leu Asp Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile	
250 255 260	
cca gca cgc act gtc atc ttt ggc gcc aag gcc gcg ccg ggt tat gtc	931
Pro Ala Arg Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val	
265 270 275	
cgc gcc aag gcg att atc aag ctc atc aac tct att gct gac ttg gta	979
Arg Ala Lys Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val	
280 285 290	
aac aac gat cct gag gtc tcc ccg ctg ctc aag gtg gtc ttt gta gag	1027
Asn Asn Asp Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu	
295 300 305	
aac tac aac gtc tcc cct gct gag cac atc ttg cct gcg tct gat gtc	1075
Asn Tyr Asn Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val	
310 315 320 325	
tcc gaa cag att tcc acc gcc ggc aag gaa gcc agc ggt acc tcc aac	1123
Ser Glu Gln Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn	
330 335 340	
atg aag ttc atg atg aac ggc gcc ctc acc ctg ggc acc atg gac ggc	1171
Met Lys Phe Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly	
345 350 355	

gcc aac gta gag atc gtg gat tct gtg ggc gag gaa aac gcc tat atc 1219  
 Ala Asn Val Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile  
 360 365 370

ttc ggt gct cgc gtg gaa gaa ttg cca gcc ctg cgc gaa agc tac gag 1267  
 Phe Gly Ala Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu  
 375 380 385

cca tat gag ctc tat gag acc gtc cct ggc ctc aag cgc gca ttg gac 1315  
 Pro Tyr Glu Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp  
 390 395 400 405

gcc ctg gat aac ggc acc ctc aac gac aac aac agt ggt ttg ttc tac 1363  
 Ala Leu Asp Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr  
 410 415 420

gac ctc aag cat tcc ttg atc cac ggt tat gga aaa gac gcc agc gac 1411  
 Asp Leu Lys His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp  
 425 430 435

acc tac tac gtg ctt ggc gat ttc gca gat tac cgc gag acc cgc gac 1459  
 Thr Tyr Tyr Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp  
 440 445 450

cgt atg gcc gcc gac tac gcc tcc gat ccc ctg ggt tgg gca cgc atg 1507  
 Arg Met Ala Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met  
 455 460 465

gcc tgg atc aac att tgc gag tcc ggc cgt ttc tcc tcc gac cgc acc 1555  
 Ala Trp Ile Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr  
 470 475 480 485

atc cgc gat tat gcc acc gag atc tgg aag ctc gag cca act cct gct 1603  
 Ile Arg Asp Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala  
 490 495 500

gtt aag aag taggttttaa cctccgcttc taa 1635  
 Val Lys Lys

&lt;210&gt; 370

&lt;211&gt; 504

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 370

Val Gln Leu Asn Asp Thr His Pro Val Leu Ala Ile Pro Glu Leu Met  
 1 5 10 15

Arg Leu Leu Met Asp Glu His Asp Met Gly Trp Glu Glu Ser Trp Ala  
 20 25 30

Ile Val Phe Lys Thr Phe Ala Tyr Thr Asn His Thr Val Leu Thr Glu  
 35 40 45

Ala Leu Glu Gln Trp Asp Gln Gln Ile Phe Gln Gln Leu Phe Trp Arg  
 50 55 60

Val Trp Glu Ile Ile Thr Glu Ile Asp Arg Arg Phe Arg Leu Glu Arg  
 65 70 75 80

Ala Ala Asp Gly Leu Asp Glu Glu Thr Ile Asp Arg Met Ala Pro Ile  
                             85                            90                            95  
 Gln His Gly Thr Val His Met Ala Trp Ile Ala Cys Tyr Ala Ala Tyr  
                             100                            105                            110  
 Ser Ile Asn Gly Val Ala Ala Leu His Thr Glu Ile Ile Lys Ala Glu  
                             115                            120                            125  
 Thr Leu Ala Asp Trp Tyr Ala Leu Trp Pro Glu Lys Phe Asn Asn Lys  
                             130                            135                            140  
 Thr Asn Gly Val Thr Pro Arg Arg Trp Leu Arg Met Ile Asn Pro Gly  
                             145                            150                            155                            160  
 Leu Ser Asp Leu Leu Thr Arg Leu Ser Gly Ser Asp Asp Trp Val Thr  
                             165                            170                            175  
 Asp Leu Asp Glu Leu Lys Lys Leu Arg Ser Tyr Ala Asp Asp Lys Ser  
                             180                            185                            190  
 Val Leu Glu Glu Leu Arg Ala Ile Lys Ala Ala Asn Lys Gln Asp Phe  
                             195                            200                            205  
 Ala Glu Trp Ile Leu Glu Arg Gln Gly Ile Glu Ile Asp Pro Glu Ser  
                             210                            215                            220  
 Ile Phe Asp Val Gln Ile Lys Arg Leu His Glu Tyr Lys Arg Gln Leu  
                             225                            230                            235                            240  
 Met Asn Ala Leu Tyr Val Leu Asp Leu Tyr Phe Arg Ile Lys Glu Asp  
                             245                            250                            255  
 Gly Leu Thr Asp Ile Pro Ala Arg Thr Val Ile Phe Gly Ala Lys Ala  
                             260                            265                            270  
 Ala Pro Gly Tyr Val Arg Ala Lys Ala Ile Ile Lys Leu Ile Asn Ser  
                             275                            280                            285  
 Ile Ala Asp Leu Val Asn Asn Asp Pro Glu Val Ser Pro Leu Leu Lys  
                             290                            295                            300  
 Val Val Phe Val Glu Asn Tyr Asn Val Ser Pro Ala Glu His Ile Leu  
                             305                            310                            315                            320  
 Pro Ala Ser Asp Val Ser Glu Gln Ile Ser Thr Ala Gly Lys Glu Ala  
                             325                            330                            335  
 Ser Gly Thr Ser Asn Met Lys Phe Met Met Asn Gly Ala Leu Thr Leu  
                             340                            345                            350  
 Gly Thr Met Asp Gly Ala Asn Val Glu Ile Val Asp Ser Val Gly Glu  
                             355                            360                            365  
 Glu Asn Ala Tyr Ile Phe Gly Ala Arg Val Glu Glu Leu Pro Ala Leu  
                             370                            375                            380  
 Arg Glu Ser Tyr Glu Pro Tyr Glu Leu Tyr Glu Thr Val Pro Gly Leu  
                             385                            390                            395                            400



Lys Arg Ala Leu Asp Ala Leu Asp Asn Gly Thr Leu Asn Asp Asn Asn  
                     405                    410                    415  
 Ser Gly Leu Phe Tyr Asp Leu Lys His Ser Leu Ile His Gly Tyr Gly  
                     420                    425                    430  
 Lys Asp Ala Ser Asp Thr Tyr Tyr Val Leu Gly Asp Phe Ala Asp Tyr  
                     435                    440                    445  
 Arg Glu Thr Arg Asp Arg Met Ala Ala Asp Tyr Ala Ser Asp Pro Leu  
                     450                    455                    460  
 Gly Trp Ala Arg Met Ala Trp Ile Asn Ile Cys Glu Ser Gly Arg Phe  
                     465                    470                    475                    480  
 Ser Ser Asp Arg Thr Ile Arg Asp Tyr Ala Thr Glu Ile Trp Lys Leu  
                     485                    490                    495  
 Glu Pro Thr Pro Ala Val Lys Lys  
                     500

<210> 371  
 <211> 1367  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1344)  
 <223> FRXA01550

<400> 371  
 atc ttc caa cag ctg ttc tgg cgc gtg tgg gaa atc atc aca gag atc 48  
 Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu Ile  
   1                    5                    10                    15  
 gat cgc cgc ttc cgt ttg gag cgc gca gcc gat gga ctg gat gaa gag 96  
 Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu Glu  
                     20                    25                    30  
 acc atc gac cgc atg gct cca atc cag cgc ggc act gtt cat atg gca 144  
 Thr Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met Ala  
                     35                    40                    45  
 tgg att gcc tgt tac gcg gca tat tcc atc aat ggc gtg gca gcg ctg 192  
 Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Leu  
   50                    55                    60  
 cac acc gag atc atc aag gcc gag acc ttg gct gac tgg tac gca ctg 240  
 His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp Tyr Ala Leu  
   65                    70                    75                    80  
 tgg cca gag aag ttc aac aac aag act aac ggt gtt acc cca cgc cgt 288  
 Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr Pro Arg Arg  
                     85                    90                    95  
 tgg ctg cgc atg atc aac cca ggt ctg tct gac ctg ctc act cga ctt 336  
 Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu Thr Arg Leu  
                     100                    105                    110

tcc ggt tcc gat gat tgg gta acc gat ctg gat gag ctg aag aag ctg	384
Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu Lys Lys Leu	
115 120 125	
cgc tcc tat gcc gac gat aag tcc gtg ctt gaa gaa ctc cgc gct atc	432
Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu Arg Ala Ile	
130 135 140	
aag gct gct aat aag caa gac ttc gcc gag tgg atc ctc gag cgc cag	480
Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu Glu Arg Gln	
145 150 155 160	
ggc att gag att gat cca gaa tcc atc ttt gac gtg cag att aag cgc	528
Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln Ile Lys Arg	
165 170 175	
ctc cac gag tac aag cgc cag ctc atg aac gcg ctc tac gta cta gac	576
Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr Val Leu Asp	
180 185 190	
ctt tac ttc cgt att aag gaa gat ggc ctc acc gac atc cca gca cgc	624
Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile Pro Ala Arg	
195 200 205	
act gtc atc ttt ggc gcc aag gcc gcg ccg ggt tat gtc cgc gcc aag	672
Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val Arg Ala Lys	
210 215 220	
gcg att atc aag ctc atc aac tct att gct gac ttg gta aac aac gat	720
Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val Asn Asn Asp	
225 230 235 240	
cct gag gtc tcc ccg ctg ctc aag gtg gtc ttt gta gag aac tac aac	768
Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu Asn Tyr Asn	
245 250 255	
gtc tcc cct gct gag cac atc ttg cct gcg tct gat gtc tcc gaa cag	816
Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val Ser Glu Gln	
260 265 270	
att tcc acc gcc ggc aag gaa gcc agc ggt acc tcc aac atg aag ttc	864
Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn Met Lys Phe	
275 280 285	
atg atg aac ggc gcc ctc acc ctg ggc acc atg gac ggc gcc aac gta	912
Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly Ala Asn Val	
290 295 300	
gag atc gtg gat tct gtg ggc gag gaa aac gcc tat atc ttc ggt gct	960
Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile Phe Gly Ala	
305 310 315 320	
cgc gtg gaa gaa ttg cca gcc ctg cgc gaa agc tac gag cca tat gag	1008
Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu Pro Tyr Glu	
325 330 335	
ctc tat gag acc gtc cct ggc ctc aag cgc gca ttg gac gcc ctg gat	1056
Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp Ala Leu Asp	
340 345 350	
aac ggc acc ctc aac gac aac aac agt ggt ttg ttc tac gac ctc aag	1104

Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr Asp Leu Lys  
 355 360 365  
 cat tcc ttg atc cac ggt tat gga aaa gac gcc agc gac acc tac tac 1152  
 His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp Thr Tyr Tyr  
 370 375 380  
 gtg ctt ggc gat ttc gca gat tac cgc gag acc cgc gac cgt atg gcc 1200  
 Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp Arg Met Ala  
 385 390 395 400  
 gcc gac tac gcc tcc gat ccc ctg ggt tgg gca cgc atg gcc tgg atc 1248  
 Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met Ala Trp Ile  
 405 410 415  
 aac att tgc gag tcc ggc cgt ttc tcc tcc gac cgc acc atc cgc gat 1296  
 Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr Ile Arg Asp  
 420 425 430  
 tat gcc acc gag atc tgg aag ctg gag cca act cct gct gtt aag aag 1344  
 Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala Val Lys Lys  
 435 440 445  
 taggttttaa cctccgcttc taa 1367

&lt;210&gt; 372

&lt;211&gt; 448

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 372

Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu Ile  
 1 5 10 15

Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu Glu  
 20 25 30

Thr Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met Ala  
 35 40 45

Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Leu  
 50 55 60

His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp Tyr Ala Leu  
 65 70 75 80

Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr Pro Arg Arg  
 85 90 95

Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu Thr Arg Leu  
 100 105 110

Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu Lys Lys Leu  
 115 120 125

Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu Arg Ala Ile  
 130 135 140

Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu Glu Arg Gln  
 145 150 155 160

Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln Ile Lys Arg  
 165 170 175  
 Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr Val Leu Asp  
 180 185 190  
 Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile Pro Ala Arg  
 195 200 205  
 Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val Arg Ala Lys  
 210 215 220  
 Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val Asn Asn Asp  
 225 230 235 240  
 Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu Asn Tyr Asn  
 245 250 255  
 Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val Ser Glu Gln  
 260 265 270  
 Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn Met Lys Phe  
 275 280 285  
 Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly Ala Asn Val  
 290 295 300  
 Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile Phe Gly Ala  
 305 310 315 320  
 Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu Pro Tyr Glu  
 325 330 335  
 Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp Ala Leu Asp  
 340 345 350  
 Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr Asp Leu Lys  
 355 360 365  
 His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp Thr Tyr Tyr  
 370 375 380  
 Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp Arg Met Ala  
 385 390 395 400  
 Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met Ala Trp Ile  
 405 410 415  
 Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr Ile Arg Asp  
 420 425 430  
 Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala Val Lys Lys  
 435 440 445

&lt;210&gt; 373

&lt;211&gt; 2348

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2325)

&lt;223&gt; RXN02100

&lt;400&gt; 373

cta ggt cga atc aac gcc gag gag caa aac ctc agc gaa tac ctc agc	48
Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser	
1 5 10 15	
gac aag ctg tgg tac cag gac acc gca gat gca acc gat gct gtc gga	96
Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly	
20 25 30	
gat cca ctc gtt gcg tac ttc tcc atg gag ttt ggc att cac cca agc	144
Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser	
35 40 45	
ctg cca atc tac tct ggc gga ctt ggt gtg ctt gcg ggc gag aac atg	192
Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met	
50 55 60	
aag tct gca tct gac ttg ggt gtg cca ctg atc ggt gtt ggt ttg ctc	240
Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu	
65 70 75 80	
tac acc cac ggc tac ttc acc cag tca ctg tcc ggt gac ggt tgg cag	288
Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln	
85 90 95	
cag gaa gag tac aag tac cac gat cca gca gaa ctg ccg att gag gca	336
Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala	
100 105 110	
gtt aaa gat aag aac ggc gag cag gtc act gtt tct gtc acc tac cca	384
Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro	
115 120 125	
ggt gcg cag gaa gta aag att gca ctg tgg gta gca aac gtt ggc cgc	432
Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg	
130 135 140	
atc cca ttg ctg ctg ctt gat acc aac atc gag gca aac cca gaa gag	480
Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu	
145 150 155 160	
ctc cgc aac gtt act gac cgc ctg tac ggt ggc gac aat gag cac cgc	528
Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg	
165 170 175	
atc aag cag gaa ctc gtt ctc ggt gtt ggt ggc gtc cgc gct gtc aac	576
Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn	
180 185 190	
gca ttc tgc gaa gct cgt ggt ctg aag cgc tca tct gtt gca cac ctc	624
Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu	
195 200 205	

aac gaa ggc cac gca ggt ttc ctg acc ctg gag cgt atc cgc gag cgc	672
Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg	
210 215 220	
atc gca gag ggc atg gag tac cca gca gca ttc gag cag gtt cgt gcg	720
Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala	
225 230 235 240	
tcc aac atc ttc acc acc cac acc cca gtc cca gca ggc atc gac cgc	768
Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg	
245 250 255	
ttc gac atg gag atg gtg cgt cgt tat ctc ggt ggc ggt cag cca gaa	816
Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu	
260 265 270	
gat cag cag ctg tgc gtt ggt gtt cca att gag aag gca ctt gag ctt	864
Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu	
275 280 285	
ggt caa gag tcc gat cca cac cgc ttc aac atg gct cat atg ggc ctt	912
Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu	
290 295 300	
cgc gcg agc caa cat gct aat ggc gtc gca aag ctt cat ggt gaa gta	960
Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val	
305 310 315 320	
agc cgt gac atg ttc gcc ggc ctg tac ccc gga tat gag cct cgt gaa	1008
Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu	
325 330 335	
gtg ccc atc ggg cac gtc acc aac ggt gtt cac ctg ccg acg tgg gtc	1056
Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val	
340 345 350	
aag cca gag atg aag gaa ctc atc gat cgc gtc act ggc ggc gct gat	1104
Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp	
355 360 365	
ctt gcg gtt gct gat tct tgg tca aac cca cag gct gtc gag tct gag	1152
Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu	
370 375 380	
aag atc tgg aag gtg cgc aac aag ttc cgt gct gac cta gtg gag gtt	1200
Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val	
385 390 395 400	
gct cgc gct gca act gca aag tcc tgg tct cac cgt gga cac acc gaa	1248
Ala Arg Ala Ala Thr Ala Lys Ser Trp Ser His Arg Gly His Thr Glu	
405 410 415	
gca gaa ctt gcg tgg acc tcc cgc gtt ctg gat cca aac gtg ctg acc	1296
Ala Glu Leu Ala Trp Thr Ser Arg Val Leu Asp Pro Asn Val Leu Thr	
420 425 430	
att ggt ttc gca cgt cgc gta tcc acc tac aag cgc ttg acc ttg atg	1344
Ile Gly Phe Ala Arg Arg Val Ser Thr Tyr Lys Arg Leu Thr Leu Met	
435 440 445	
ctg cgc aac cct gaa cgc ctg cgt tcc atc ttg ctt aat gag gaa cgc	1392

Leu Arg Asn Pro Glu Arg Leu Arg Ser Ile Leu Leu Asn Glu Glu Arg	
450 455 460	
cca gtt cag ttc gtt att gct ggt aag gca cac cca cat gac atg ggt	1440
Pro Val Gln Phe Val Ile Ala Gly Lys Ala His Pro His Asp Met Gly	
465 470 475 480	
ggc aag aag ctc atg cag gaa atc gtc cac ttc gct gat caa gct ggt	1488
Gly Lys Lys Leu Met Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly	
485 490 495	
gtc cgt gac cgt ttc ctc ttc ctg cct gat tac gac atc aac ctg gcc	1536
Val Arg Asp Arg Phe Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala	
500 505 510	
agc tac ctg atc tct ggt gct gac gtg tgg ctg aac aac cca gtg cgc	1584
Ser Tyr Leu Ile Ser Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg	
515 520 525	
cct cag gaa gca tcg gga acc tcc ggt atg aag gcc gtc atg aat ggt	1632
Pro Gln Glu Ala Ser Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly	
530 535 540	
ggc ctg acc ctg tcc atc tct gat ggt tgg tgg gat gaa atg cct aag	1680
Gly Leu Thr Leu Ser Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys	
545 550 555 560	
gag acc acc ggc tgg acc atc cca acc gtt gag tcc cag gac ttg gaa	1728
Glu Thr Thr Gly Trp Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu	
565 570 575	
tgc cgc gac cac ctg gaa tcc cag gcg ctg tac gac ctg ctg gaa aac	1776
Cys Arg Asp His Leu Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn	
580 585 590	
gaa gtt gca ccg ctg ttt tac aag cgc gac aag aac ggc atc cca cag	1824
Glu Val Ala Pro Leu Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln	
595 600 605	
gac tgg ctg gac ctg gtt cgc gaa tcc tgg acc acc ctg tca cca atg	1872
Asp Trp Leu Asp Leu Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met	
610 615 620	
gtc acc tcc acc cgc atg gtg cgc gac tac acc acc cag tac tac cgc	1920
Val Thr Ser Thr Arg Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg	
625 630 635 640	
cca acc aaa cac cag gca gag ctc att gcg cag cct gca gaa gca gcg	1968
Pro Thr Lys His Gln Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala	
645 650 655	
gat tac gcg gca tgg ctt gag cac atc aaa gca gag tgg gct ggc gtc	2016
Asp Tyr Ala Ala Trp Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val	
660 665 670	
aag gtc tca gac ctg aag atc agc gag agc gcc atc acg gcg cag gag	2064
Lys Val Ser Asp Leu Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu	
675 680 685	
ctt gaa gtc agc gtt cgc gtt gat tcc ggt tcg ctt aac gac gac gag	2112
Leu Glu Val Ser Val Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu	

690	695	700	
ttc caa gct cag gca ctc ttt ggt gcg ctc gga cac aac ggt gac atc			2160
Phe Gln Ala Gln Ala Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile			
705	710	715	720
gaa gat cca gaa atc acc gtt ttg acc cca cgc ggc gat ggc gcc tac			2208
Glu Asp Pro Glu Ile Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr			
725	730		735
gcg gca aag gtc agc act gac ctg cca ggc aac tac ggc atc act gcc			2256
Ala Ala Lys Val Ser Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala			
740	745		750
cgc gtt gtt cca aac aac agg atg ctg gtc agc cca gcg gaa acc cgc			2304
Arg Val Val Pro Asn Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg			
755	760		765
ctg atc acc tac ttg gag aac tagggcgaaa ctagctttac caa			2348
Leu Ile Thr Tyr Leu Glu Asn			
770	775		
<210> 374			
<211> 775			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 374			
Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser			
1	5	10	15
Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly			
20	25		30
Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser			
35	40		45
Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met			
50	55		60
Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu			
65	70	75	80
Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln			
85	90		95
Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala			
100	105		110
Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro			
115	120		125
Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg			
130	135		140
Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu			
145	150	155	160
Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg			
165	170		175



Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn  
 180 185 190  
 Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu  
 195 200 205  
 Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg  
 210 215 220  
 Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala  
 225 230 235 240  
 Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg  
 245 250 255  
 Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu  
 260 265 270  
 Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu  
 275 280 285  
 Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu  
 290 295 300  
 Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val  
 305 310 315 320  
 Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu  
 325 330 335  
 Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val  
 340 345 350  
 Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp  
 355 360 365  
 Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu  
 370 375 380  
 Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val  
 385 390 395 400  
 Ala Arg Ala Ala Thr Ala Lys Ser Trp Ser His Arg Gly His Thr Glu  
 405 410 415  
 Ala Glu Leu Ala Trp Thr Ser Arg Val Leu Asp Pro Asn Val Leu Thr  
 420 425 430  
 Ile Gly Phe Ala Arg Arg Val Ser Thr Tyr Lys Arg Leu Thr Leu Met  
 435 440 445  
 Leu Arg Asn Pro Glu Arg Leu Arg Ser Ile Leu Leu Asn Glu Glu Arg  
 450 455 460  
 Pro Val Gln Phe Val Ile Ala Gly Lys Ala His Pro His Asp Met Gly  
 465 470 475 480  
 Gly Lys Lys Leu Met Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly  
 485 490 495

Val Arg Asp Arg Phe Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala  
 500 505 510  
 Ser Tyr Leu Ile Ser Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg  
 515 520 525  
 Pro Gln Glu Ala Ser Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly  
 530 535 540  
 Gly Leu Thr Leu Ser Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys  
 545 550 555 560  
 Glu Thr Thr Gly Trp Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu  
 565 570 575  
 Cys Arg Asp His Leu Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn  
 580 585 590  
 Glu Val Ala Pro Leu Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln  
 595 600 605  
 Asp Trp Leu Asp Leu Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met  
 610 615 620  
 Val Thr Ser Thr Arg Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg  
 625 630 635 640  
 Pro Thr Lys His Gln Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala  
 645 650 655  
 Asp Tyr Ala Ala Trp Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val  
 660 665 670  
 Lys Val Ser Asp Leu Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu  
 675 680 685  
 Leu Glu Val Ser Val Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu  
 690 695 700  
 Phe Gln Ala Gln Ala Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile  
 705 710 715 720  
 Glu Asp Pro Glu Ile Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr  
 725 730 735  
 Ala Ala Lys Val Ser Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala  
 740 745 750  
 Arg Val Val Pro Asn Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg  
 755 760 765  
 Leu Ile Thr Tyr Leu Glu Asn  
 770 775

&lt;210&gt; 375

&lt;211&gt; 941

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(918)

&lt;223&gt; FRXA02100

&lt;400&gt; 375

att gct ggt aag gca cac cca cat gac atg ggt ggc aag aag ctc atg	48
Ile Ala Gly Lys Ala His Pro His Asp Met Gly Gly Lys Lys Leu Met	
1 5 10 15	
cag gaa atc gtc cac ttc gct gat caa gct ggt gtc cgt gac cgt ttc	96
Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly Val Arg Asp Arg Phe	
20 25 30	
ctc ttc ctg cct gat tac gac atc aac ctg gcc agc tac ctg atc tct	144
Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala Ser Tyr Leu Ile Ser	
35 40 45	
ggt gct gac gtg tgg ctg aac aac cca gtg cgc cct cag gaa gca tcg	192
Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg Pro Gln Glu Ala Ser	
50 55 60	
gga acc tcc ggt atg aag gcc gtc atg aat ggt ggc ctg acc ctg tcc	240
Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly Gly Leu Thr Leu Ser	
65 70 75 80	
atc tct gat ggt tgg tgg gat gaa atg cct aag gag acc acc ggc tgg	288
Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys Glu Thr Thr Gly Trp	
85 90 95	
acc atc cca acc gtt gag tcc cag gac ttg gaa tgc cgc gac cac ctg	336
Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu Cys Arg Asp His Leu	
100 105 110	
gaa tcc cag gcg ctg tac gac ctg ctg gaa aac gaa gtt gca ccg ctg	384
Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn Glu Val Ala Pro Leu	
115 120 125	
ttt tac aag cgc gac aag aac ggc atc cca cag gac tgg ctg gac ctg	432
Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln Asp Trp Leu Asp Leu	
130 135 140	
gtt cgc gaa tcc tgg acc acc ctg tca cca atg gtc acc tcc acc cgc	480
Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met Val Thr Ser Thr Arg	
145 150 155 160	
atg gtg cgc gac tac acc acc cag tac tac cgc cca acc aaa cac cag	528
Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg Pro Thr Lys His Gln	
165 170 175	
gca gag ctc att gcg cag cct gca gaa gca gcg gat tac gcg gca tgg	576
Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala Asp Tyr Ala Ala Trp	
180 185 190	
ctt gag cac atc aaa gca gag tgg gct ggc gtc aag gtc tca gac ctg	624
Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val Lys Val Ser Asp Leu	
195 200 205	
aag atc agc gag agc gcc atc acg gcg cag gag ctt gaa gtc agc gtt	672
Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu Leu Glu Val Ser Val	
210 215 220	

cgc gtt gat tcc ggt tcg ctt aac gac gac gag ttc caa gct cag gca 720  
 Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu Phe Gln Ala Gln Ala  
 225 230 235 240

ctc ttt ggt gcg ctc gga cac aac ggt gac atc gaa gat cca gaa atc 768  
 Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile Glu Asp Pro Glu Ile  
 245 250 255

acc gtt ttg acc cca cgc ggc gat ggc gcc tac gcg gca aag gtc agc 816  
 Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr Ala Ala Lys Val Ser  
 260 265 270

act gac ctg cca ggc aac tac ggc atc act gcc cgc gtt gtt cca aac 864  
 Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala Arg Val Val Pro Asn  
 275 280 285

aac agg atg ctg gtc agc cca gcg gaa acc cgc ctg atc acc tac ttg 912  
 Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg Leu Ile Thr Tyr Leu  
 290 295 300

gag aac tagggcgaaa ctagctttac caa 941  
 Glu Asn  
 305

<210> 376  
 <211> 306  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 376  
 Ile Ala Gly Lys Ala His Pro His Asp Met Gly Gly Lys Lys Leu Met  
 1 5 10 15

Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly Val Arg Asp Arg Phe  
 20 25 30

Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala Ser Tyr Leu Ile Ser  
 35 40 45

Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg Pro Gln Glu Ala Ser  
 50 55 60

Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly Gly Leu Thr Leu Ser  
 65 70 75 80

Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys Glu Thr Thr Gly Trp  
 85 90 95

Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu Cys Arg Asp His Leu  
 100 105 110

Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn Glu Val Ala Pro Leu  
 115 120 125

Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln Asp Trp Leu Asp Leu  
 130 135 140

Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met Val Thr Ser Thr Arg  
 145 150 155 160

Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg Pro Thr Lys His Gln  
 165 170 175

Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala Asp Tyr Ala Ala Trp  
 180 185 190

Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val Lys Val Ser Asp Leu  
 195 200 205

Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu Leu Glu Val Ser Val  
 210 215 220

Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu Phe Gln Ala Gln Ala  
 225 230 235 240

Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile Glu Asp Pro Glu Ile  
 245 250 255

Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr Ala Ala Lys Val Ser  
 260 265 270

Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala Arg Val Val Pro Asn  
 275 280 285

Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg Leu Ile Thr Tyr Leu  
 290 295 300

Glu Asn  
 305

<210> 377  
 <211> 1206  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1206)  
 <223> FRXA02113

<400> 377  
 cta ggt cga atc aac gcc gag gag caa aac ctc agc gaa tac ctc agc 48  
 Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser  
 1 5 10 15

gac aag ctg tgg tac cag gac acc gca gat gca acc gat gct gtc gga 96  
 Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly  
 20 25 30

gat cca ctc gtt gcg tac ttc tcc atg gag ttt ggc att cac cca agc 144  
 Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser  
 35 40 45

ctg cca atc tac tct ggc gga ctt ggt gtg ctt gcg ggc gag aac atg 192  
 Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met  
 50 55 60

aag tct gca tct gac ttg ggt gtg cca ctg atc ggt gtt ggt ttg ctc 240  
 Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu  
 65 70 75 80

tac acc cac ggc tac ttc acc cag tca ctg tcc ggt gac ggt tgg cag	288
Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln	
85 90 95	
cag gaa gag tac aag tac cac gat cca gca gaa ctg ccg att gag gca	336
Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala	
100 105 110	
gtt aaa gat aag aac ggc gag cag gtc act gtt tct gtc acc tac cca	384
Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro	
115 120 125	
ggt gcg cag gaa gta aag att gca ctg tgg gta gca aac gtt ggc cgc	432
Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg	
130 135 140	
atc cca ttg ctg ctg ctt gat acc aac atc gag gca aac cca gaa gag	480
Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu	
145 150 155 160	
ctc cgc aac gtt act gac cgc ctg tac ggt ggc gac aat gag cac cgc	528
Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg	
165 170 175	
atc aag cag gaa ctc gtt ctc ggt gtt ggt ggc gtc cgc gct gtc aac	576
Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn	
180 185 190	
gca ttc tgc gaa gct cgt ggt ctg aag cgc tca tct gtt gca cac ctc	624
Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu	
195 200 205	
aac gaa ggc cac gca ggt ttc ctg acc ctg gag cgt atc cgc gag cgc	672
Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg	
210 215 220	
atc gca gag ggc atg gag tac cca gca gca ttc gag cag gtt cgt gcg	720
Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala	
225 230 235 240	
tcc aac atc ttc acc acc cac acc cca gtc cca gca ggc atc gac cgc	768
Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg	
245 250 255	
ttc gac atg gag atg gtg cgt cgt tat ctc ggt ggc ggt cag cca gaa	816
Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu	
260 265 270	
gat cag cag ctg tgc gtt ggt gtt cca att gag aag gca ctt gag ctt	864
Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu	
275 280 285	
ggt caa gag tcc gat cca cac cgc ttc aac atg gct cat atg ggc ctt	912
Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu	
290 295 300	
cgc gcg agc caa cat gct aat ggc gtc gca aag ctt cat ggt gaa gta	960
Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val	
305 310 315 320	

```

agc cgt gac atg ttc gcc ggc ctg tac ccc gga tat gag cct cgt gaa 1008
Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu
                325                      330                      335

gtg ccc atc ggg cac gtc acc aac ggt gtt cac ctg ccg acg tgg gtc 1056
Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val
                340                      345                      350

aag cca gag atg aag gaa ctc atc gat cgc gtc act ggc ggc gct gat 1104
Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp
                355                      360                      365

ctt gcg gtt gct gat tct tgg tca aac cca cag gct gtc gag tct gag 1152
Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu
                370                      375                      380

aag atc tgg aag gtg cgc aac aag ttc cgt gct gac cta gtg gag gtt 1200
Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val
385                      390                      395                      400

gct cgc
Ala Arg
206

```

&lt;210&gt; 378

&lt;211&gt; 402

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 378

```

Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser
 1                      5                      10                      15

Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly
20                      25                      30

Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser
35                      40                      45

Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met
50                      55                      60

Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu
65                      70                      75                      80

Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln
85                      90                      95

Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala
100                      105                      110

Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro
115                      120                      125

Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg
130                      135                      140

Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu
145                      150                      155                      160

```

Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg  
 165 170 175  
 Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn  
 180 185 190  
 Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu  
 195 200 205  
 Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg  
 210 215 220  
 Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala  
 225 230 235 240  
 Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg  
 245 250 255  
 Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu  
 260 265 270  
 Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu  
 275 280 285  
 Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu  
 290 295 300  
 Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val  
 305 310 315 320  
 Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu  
 325 330 335  
 Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val  
 340 345 350  
 Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp  
 355 360 365  
 Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu  
 370 375 380  
 Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val  
 385 390 395 400

Ala Arg

<210> 379  
 <211> 1140  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1117)  
 <223> RXA02147

<400> 379  
 aaaagttag agcggcttg cttcttttcc tggctaggct tttgtaatcg ggtagagta 60



gtggagttgc ttgaatgagg ttgatagggg atttttgaag atg ttt ggt cgc cgt	115
Met Phe Gly Arg Arg	
1 5	
tgg gtg agc gtt gtg gcg tca tgt gtt atc gca agc acg ctg att ctg	163
Trp Val Ser Val Val Ala Ser Cys Val Ile Ala Ser Thr Leu Ile Leu	
10 15 20	
gtg cct tcg cat tcc ggt gcg gag gaa gtc gat caa ctg att gct gat	211
Val Pro Ser His Ser Gly Ala Glu Glu Val Asp Gln Leu Ile Ala Asp	
25 30 35	
atc gag cat gtc tct cag gaa acg tct gcc cag aat gag gaa gtc aaa	259
Ile Glu His Val Ser Gln Glu Thr Ser Ala Gln Asn Glu Glu Val Lys	
40 45 50	
cag ctt gag att gat att gag gct cgt gag gtc acg atc aag gaa gtt	307
Gln Leu Glu Ile Asp Ile Glu Ala Arg Glu Val Thr Ile Lys Glu Val	
55 60 65	
cag gag cag tcg gta agc tac cgt gag gcg gct gat caa gca tcg gag	355
Gln Glu Gln Ser Val Ser Tyr Arg Glu Ala Ala Asp Gln Ala Ser Glu	
70 75 80 85	
aat gtc gaa gct tat cgt tcg gag atc aat cgg atc gct cag gcg aag	403
Asn Val Glu Ala Tyr Arg Ser Glu Ile Asn Arg Ile Ala Gln Ala Lys	
90 95 100	
tat cgt ggc aca gtc acg gat cct ttg agc att gcg gtg tct gca gaa	451
Tyr Arg Gly Thr Val Thr Asp Pro Leu Ser Ile Ala Val Ser Ala Glu	
105 110 115	
gat cca caa aac gtg att gat cgg atg agc tac ctt tca acg ttg act	499
Asp Pro Gln Asn Val Ile Asp Arg Met Ser Tyr Leu Ser Thr Leu Thr	
120 125 130	
aag tcc act agt gat gtg gtt gaa tcc ctc aac gcg gag act gag aag	547
Lys Ser Thr Ser Asp Val Val Glu Ser Leu Asn Ala Glu Thr Glu Lys	
135 140 145	
tcc gca gaa gct gtg tat caa gca aac cgt act aag gcg gaa gcg gag	595
Ser Ala Glu Ala Val Tyr Gln Ala Asn Arg Thr Lys Ala Glu Ala Glu	
150 155 160 165	
ttc cag ttg ggg cag ctg aag gta cgc cag gcg gag ctt gaa tct gaa	643
Phe Gln Leu Gly Gln Leu Lys Val Arg Gln Ala Glu Leu Glu Ser Glu	
170 175 180	
aag gaa gca ttg gat ggt cga aaa tcg gag atc cga gac cgg gtg gat	691
Lys Glu Ala Leu Asp Gly Arg Lys Ser Glu Ile Arg Asp Arg Val Asp	
185 190 195	
gcc ctg acg cca cag gag cgg gaa atg tgg gtt gct aag aat ggt cca	739
Ala Leu Thr Pro Gln Glu Arg Glu Met Trp Val Ala Lys Asn Gly Pro	
200 205 210	
ttg gac att gat ctg act gat ttg ctt ggt ctt tcc gct gcg act tcg	787
Leu Asp Ile Asp Leu Thr Asp Leu Leu Gly Leu Ser Ala Ala Thr Ser	
215 220 225	

ggt gcg gtg gat gct gcc ttg tct aag ttg gga agc cct tat ggt tgg 835  
 Gly Ala Val Asp Ala Ala Leu Ser Lys Leu Gly Ser Pro Tyr Gly Trp  
 230 235 240 245  
 ggt ggc att ggc cca aat gag ttt gat tgc tca ggt ttg atc tat tgg 883  
 Gly Gly Ile Gly Pro Asn Glu Phe Asp Cys Ser Gly Leu Ile Tyr Trp  
 250 255 260  
 gcg tat cag cag atg ggt aag act ttg cca cgt acg tct caa gct cag 931  
 Ala Tyr Gln Gln Met Gly Lys Thr Leu Pro Arg Thr Ser Gln Ala Gln  
 265 270 275  
 atg gct ggc gga acg ccg gtg agc aga gat gag ctg cag cct ggc gat 979  
 Met Ala Gly Gly Thr Pro Val Ser Arg Asp Glu Leu Gln Pro Gly Asp  
 280 285 290  
 gtc att gga tat tac cca ggt gct act cac gtg gga ctg tat att ggg 1027  
 Val Ile Gly Tyr Tyr Pro Gly Ala Thr His Val Gly Leu Tyr Ile Gly  
 295 300 305  
 gac gga aag att gtg cac gcc tca gac tac gga atc cct gtg cag gtg 1075  
 Asp Gly Lys Ile Val His Ala Ser Asp Tyr Gly Ile Pro Val Gln Val  
 310 315 320 325  
 gta tct gtt gat tca gca ccg ttt tat ggt gcg cgt cgc tac 1117  
 Val Ser Val Asp Ser Ala Pro Phe Tyr Gly Ala Arg Arg Tyr  
 330 335  
 taagaaatag ttcgtcagga gaa 1140

&lt;210&gt; 380

&lt;211&gt; 339

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 380

Met Phe Gly Arg Arg Trp Val Ser Val Val Ala Ser Cys Val Ile Ala  
 1 5 10 15  
 Ser Thr Leu Ile Leu Val Pro Ser His Ser Gly Ala Glu Glu Val Asp  
 20 25 30  
 Gln Leu Ile Ala Asp Ile Glu His Val Ser Gln Glu Thr Ser Ala Gln  
 35 40 45  
 Asn Glu Glu Val Lys Gln Leu Glu Ile Asp Ile Glu Ala Arg Glu Val  
 50 55 60  
 Thr Ile Lys Glu Val Gln Glu Gln Ser Val Ser Tyr Arg Glu Ala Ala  
 65 70 75 80  
 Asp Gln Ala Ser Glu Asn Val Glu Ala Tyr Arg Ser Glu Ile Asn Arg  
 85 90 95  
 Ile Ala Gln Ala Lys Tyr Arg Gly Thr Val Thr Asp Pro Leu Ser Ile  
 100 105 110  
 Ala Val Ser Ala Glu Asp Pro Gln Asn Val Ile Asp Arg Met Ser Tyr  
 115 120 125

Leu Ser Thr Leu Thr Lys Ser Thr Ser Asp Val Val Glu Ser Leu Asn  
 130 135 140  
 Ala Glu Thr Glu Lys Ser Ala Glu Ala Val Tyr Gln Ala Asn Arg Thr  
 145 150 155 160  
 Lys Ala Glu Ala Glu Phe Gln Leu Gly Gln Leu Lys Val Arg Gln Ala  
 165 170 175  
 Glu Leu Glu Ser Glu Lys Glu Ala Leu Asp Gly Arg Lys Ser Glu Ile  
 180 185 190  
 Arg Asp Arg Val Asp Ala Leu Thr Pro Gln Glu Arg Glu Met Trp Val  
 195 200 205  
 Ala Lys Asn Gly Pro Leu Asp Ile Asp Leu Thr Asp Leu Leu Gly Leu  
 210 215 220  
 Ser Ala Ala Thr Ser Gly Ala Val Asp Ala Ala Leu Ser Lys Leu Gly  
 225 230 235 240  
 Ser Pro Tyr Gly Trp Gly Gly Ile Gly Pro Asn Glu Phe Asp Cys Ser  
 245 250 255  
 Gly Leu Ile Tyr Trp Ala Tyr Gln Gln Met Gly Lys Thr Leu Pro Arg  
 260 265 270  
 Thr Ser Gln Ala Gln Met Ala Gly Gly Thr Pro Val Ser Arg Asp Glu  
 275 280 285  
 Leu Gln Pro Gly Asp Val Ile Gly Tyr Tyr Pro Gly Ala Thr His Val  
 290 295 300  
 Gly Leu Tyr Ile Gly Asp Gly Lys Ile Val His Ala Ser Asp Tyr Gly  
 305 310 315 320  
 Ile Pro Val Gln Val Val Ser Val Asp Ser Ala Pro Phe Tyr Gly Ala  
 325 330 335  
 Arg Arg Tyr

<210> 381  
 <211> 1959  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1936)  
 <223> RXA01478

<400> 381  
 gcggggttttg ttgtggaggg gcgcgtcgaa aagcaatddd tttccaaga tagctcactt 60  
 tattggagtc acctggcctg aaatcctcta ctctgggcgc atg acc att cca gga 115  
 Met Thr Ile Pro Gly  
 1 5  
 gct tcc aca cag act gat atc cct ctg gac aca ctt ctt gag gat tac 163

Ala	Ser	Thr	Gln	Thr	Asp	Ile	Pro	Leu	Asp	Thr	Leu	Leu	Glu	Asp	Tyr	
				10					15					20		
gcg	cta	ctg	tca	gac	act	cac	acc	ggc	gct	ctg	ctg	tcc	aac	atg	ggc	211
Ala	Leu	Leu	Ser	Asp	Thr	His	Thr	Gly	Ala	Leu	Leu	Ser	Asn	Met	Gly	
			25					30					35			
agt	ttg	gac	tgg	ttg	tgc	ctg	cct	cgt	ttt	gat	tcc	caa	gcc	atg	ttc	259
Ser	Leu	Asp	Trp	Leu	Cys	Leu	Pro	Arg	Phe	Asp	Ser	Gln	Ala	Met	Phe	
		40					45					50				
acc	agg	ctg	ctt	ggg	gat	cgc	gag	cac	gga	cac	tgg	agt	ttg	cgt	gtc	307
Thr	Arg	Leu	Leu	Gly	Asp	Arg	Glu	His	Gly	His	Trp	Ser	Leu	Arg	Val	
	55					60					65					
cca	ggg	ggg	gag	gtg	atc	agc	caa	aac	tac	ctc	ggc	gat	tcc	ttc	gtg	355
Pro	Gly	Gly	Glu	Val	Ile	Ser	Gln	Asn	Tyr	Leu	Gly	Asp	Ser	Phe	Val	
	70				75					80					85	
gtg	cag	acc	gtg	tgg	cgt	tca	gag	acc	ggg	act	gcc	cgg	gtt	gtt	gat	403
Val	Gln	Thr	Val	Trp	Arg	Ser	Glu	Thr	Gly	Thr	Ala	Arg	Val	Val	Asp	
				90					95					100		
ttc	atg	cca	att	cac	ggg	caa	gaa	caa	ccc	gat	atc	acc	gac	ctg	gtg	451
Phe	Met	Pro	Ile	His	Gly	Gln	Glu	Gln	Pro	Asp	Ile	Thr	Asp	Leu	Val	
			105					110					115			
cgc	tct	gtg	cac	tgc	gtg	gaa	ggc	gaa	gtg	gat	gtg	gaa	tcg	atc	ctg	499
Arg	Ser	Val	His	Cys	Val	Glu	Gly	Glu	Val	Asp	Val	Glu	Ser	Ile	Leu	
		120					125					130				
cgc	ctg	cgt	ttt	gat	tat	ggc	gag	tcc	act	ccg	tat	ttc	cgc	acc	agc	547
Arg	Leu	Arg	Phe	Asp	Tyr	Gly	Glu	Ser	Thr	Pro	Tyr	Phe	Arg	Thr	Ser	
	135					140					145					
act	gtc	gac	ggc	atc	agc	atc	gtg	cag	gct	gtc	gcc	ggc	ccc	aat	gcg	595
Thr	Val	Asp	Gly	Ile	Ser	Ile	Val	Gln	Ala	Val	Ala	Gly	Pro	Asn	Ala	
	150				155					160					165	
gta	tat	gtt	cgt	gga	cct	gag	atg	cca	cac	cgc	cct	gca	aag	gat	tgt	643
Val	Tyr	Val	Arg	Gly	Pro	Glu	Met	Pro	His	Arg	Pro	Ala	Lys	Asp	Cys	
				170					175					180		
cac	agt	ggc	acc	ttc	cac	ctg	acg	gcc	ggc	gaa	tcc	gtg	gaa	tgg	gtt	691
His	Ser	Gly	Thr	Phe	His	Leu	Thr	Ala	Gly	Glu	Ser	Val	Glu	Trp	Val	
			185					190					195			
ctc	acc	tgg	gca	ccg	tcg	ttc	gaa	ccg	cat	ccc	ccc	atg	ccg	gat	tac	739
Leu	Thr	Trp	Ala	Pro	Ser	Phe	Glu	Pro	His	Pro	Pro	Met	Pro	Asp	Tyr	
		200					205					210				
acc	cgc	tct	ttg	gag	agc	acc	ttg	agc	ttc	tgg	gca	tca	tgg	gtt	gaa	787
Thr	Arg	Ser	Leu	Glu	Ser	Thr	Leu	Ser	Phe	Trp	Ala	Ser	Trp	Val	Glu	
	215					220					225					
gag	ctc	ccc	cac	cag	cgc	ctc	tac	gac	gct	gaa	gtc	cgc	cgc	tcc	atg	835
Glu	Leu	Pro	His	Gln	Arg	Leu	Tyr	Asp	Ala	Glu	Val	Arg	Arg	Ser	Met	
	230				235					240					245	
ctc	gta	ctg	cgc	gcc	ttg	acc	gat	cta	caa	acc	ggg	ggc	atc	gtg	gcc	883
Leu	Val	Leu	Arg	Ala	Leu	Thr	Asp	Leu	Gln	Thr	Gly	Gly	Ile	Val	Ala	

250								255				260					
gca Ala	ccg Pro	acc Thr	acc Thr	tca Ser	cta Leu	cca Pro	gag Glu	gat Asp	ttc Phe	gga Gly	ggc Gly	atc Ile	cgt Arg	aac Asn	tgg Trp	931	
265								270				275					
gac Asp	tac Tyr	cgc Arg	tac Tyr	gtg Val	tgg Trp	ctg Leu	cgc Arg	gac Asp	tcc Ser	gca Ala	ctc Leu	acc Thr	att Ile	gaa Glu	gcc Ala	979	
280								285				290					
ctc Leu	gtg Val	gaa Glu	tac Tyr	gga Gly	ttc Phe	tcc Ser	caa Gln	gca Ala	gcc Ala	ctc Leu	caa Gln	tgg Trp	cgc Arg	acc Thr	tgg Trp	1027	
295								300				305					
ctg Leu	ctg Leu	cgc Arg	gcc Ala	atc Ile	gca Ala	ggc Gly	gac Asp	ccg Pro	gaa Glu	aac Asn	ctc Leu	cgc Arg	atc Ile	atg Met	tat Tyr	1075	
310								315				320				325	
ggc Gly	ctc Leu	ggc Gly	ggc Gly	gaa Glu	cga Arg	cac His	ctc Leu	cct Pro	gaa Glu	cgc Arg	gaa Glu	ctc Leu	caa Gln	cac His	ctg Leu	1123	
330								335				340					
cgc Arg	gga Gly	tac Tyr	gaa Glu	aac Asn	tcc Ser	gtg Val	cct Pro	gtt Val	cgc Arg	gtt Val	ggc Gly	aat Asn	gga Gly	gcc Ala	gcc Ala	1171	
345								350				355					
gaa Glu	caa Gln	tac Tyr	caa Gln	gca Ala	gat Asp	gtc Val	gtc Val	ggc Gly	gaa Glu	gta Val	atg Met	gtc Val	gcg Ala	ctt Leu	gaa Glu	1219	
360								365				370					
acc Thr	atc Ile	cgc Arg	cgc Arg	gcc Ala	ggg Gly	tgc Cys	ctc Leu	gag Glu	gac Asp	gaa Glu	ttc Phe	tcc Ser	tgg Trp	ggc Gly	atg Met	1267	
375								380				385					
caa Gln	aaa Lys	gcc Ala	atc Ile	ctc Leu	gat Asp	ttc Phe	caa Gln	gaa Glu	gcc Ala	aac Asn	ttc Phe	gac Asp	cgc Arg	aag Lys	gat Asp	1315	
390								395				400				405	
caa Gln	ggc Gly	atc Ile	tgg Trp	gaa Glu	atg Met	cgc Arg	tcc Ser	gaa Glu	ccg Pro	caa Gln	tat Tyr	ttc Phe	acc Thr	cac His	ggc Gly	1363	
410								415				420					
cgc Arg	gcc Ala	atg Met	atg Met	tgg Trp	gcc Ala	ggc Gly	ttc Phe	gac Asp	cgc Arg	ggc Gly	atc Ile	aaa Lys	gcc Ala	atc Ile	gaa Glu	1411	
425								430				435					
gaa Glu	ttc Phe	aac Asn	ctc Leu	gac Asp	ggc Gly	ccc Pro	atc Ile	gag Glu	cgc Arg	tgg Trp	cgt Arg	gaa Glu	ctc Leu	cgc Arg	gcc Ala	1459	
440								445				450					
aaa Lys	ctc Leu	cgc Arg	gaa Glu	gaa Glu	atc Ile	atg Met	acc Thr	aac Asn	ggc Gly	ttc Phe	aac Asn	gaa Glu	gag Glu	atc Ile	caa Gln	1507	
455								460				465					
tcc Ser	ttc Phe	acc Thr	cag Gln	tgc Cys	tac Tyr	gac Asp	aac Asn	acc Thr	caa Gln	gtc Val	gac Asp	gcc Ala	tgc Ser	ctg Leu	ctt Leu	1555	
470								475				480				485	
cag Gln	ctc Leu	gcc Ala	caa Gln	ata Ile	ggc Gly	ttc Phe	atc Ile	ggc Gly	ttc Phe	gac Asp	gat Asp	cca Pro	aaa Lys	atg Met	ctc Leu	1603	
490								495				500					

agc acc gta gcg cgc att gag caa gag ctt ctc gac gcc cac ggc ttt 1651  
 Ser Thr Val Ala Arg Ile Glu Gln Glu Leu Leu Asp Ala His Gly Phe  
                   505                                  510                                  515  
  
 ctt cac agg tac cac acc gac ggg tct gac ggc ctt gcc ggc gac gaa 1699  
 Leu His Arg Tyr His Thr Asp Gly Ser Asp Gly Leu Ala Gly Asp Glu  
                   520                                  525                                  530  
  
 tac ccc ttc ctc atc tgt tca ttc tgg ctg gta gaa caa tac gca agc 1747  
 Tyr Pro Phe Leu Ile Cys Ser Phe Trp Leu Val Glu Gln Tyr Ala Ser  
                   535                                  540                                  545  
  
 tcc aac cgc ctc gac gag gcc aaa gaa aag atg aac cgc atc ctt gcc 1795  
 Ser Asn Arg Leu Asp Glu Ala Lys Glu Lys Met Asn Arg Ile Leu Ala  
                   550                                  555                                  560                                  565  
  
 gtc caa agc cca ctt ggc cta ctg gct gag gaa tac tcc acc cac cat 1843  
 Val Gln Ser Pro Leu Gly Leu Leu Ala Glu Glu Tyr Ser Thr His His  
                                   570                                  575                                  580  
  
 ggc agg ctc gct gga aac tac cct cag gcc ttt tcc cac att ggt ctg 1891  
 Gly Arg Leu Ala Gly Asn Tyr Pro Gln Ala Phe Ser His Ile Gly Leu  
                   585                                  590                                  595  
  
 atc agc gct gcc cgt gcc ata aat ttc gaa gaa gcg cga aac agg 1936  
 Ile Ser Ala Ala Arg Ala Ile Asn Phe Glu Glu Ala Arg Asn Arg  
                   600                                  605                                  610  
  
 tagagtctaa ggtgtcattc ttg 1959

&lt;210&gt; 382

&lt;211&gt; 612

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 382

Met Thr Ile Pro Gly Ala Ser Thr Gln Thr Asp Ile Pro Leu Asp Thr  
   1                                  5                                  10                                  15  
  
 Leu Leu Glu Asp Tyr Ala Leu Leu Ser Asp Thr His Thr Gly Ala Leu  
                   20                                  25                                  30  
  
 Leu Ser Asn Met Gly Ser Leu Asp Trp Leu Cys Leu Pro Arg Phe Asp  
                   35                                  40                                  45  
  
 Ser Gln Ala Met Phe Thr Arg Leu Leu Gly Asp Arg Glu His Gly His  
                   50                                  55                                  60  
  
 Trp Ser Leu Arg Val Pro Gly Gly Glu Val Ile Ser Gln Asn Tyr Leu  
                   65                                  70                                  75                                  80  
  
 Gly Asp Ser Phe Val Val Gln Thr Val Trp Arg Ser Glu Thr Gly Thr  
                   85                                  90                                  95  
  
 Ala Arg Val Val Asp Phe Met Pro Ile His Gly Gln Glu Gln Pro Asp  
                   100                                  105                                  110  
  
 Ile Thr Asp Leu Val Arg Ser Val His Cys Val Glu Gly Glu Val Asp  
                   115                                  120                                  125

Val Glu Ser Ile Leu Arg Leu Arg Phe Asp Tyr Gly Glu Ser Thr Pro  
 130 135 140  
 Tyr Phe Arg Thr Ser Thr Val Asp Gly Ile Ser Ile Val Gln Ala Val  
 145 150 155 160  
 Ala Gly Pro Asn Ala Val Tyr Val Arg Gly Pro Glu Met Pro His Arg  
 165 170 175  
 Pro Ala Lys Asp Cys His Ser Gly Thr Phe His Leu Thr Ala Gly Glu  
 180 185 190  
 Ser Val Glu Trp Val Leu Thr Trp Ala Pro Ser Phe Glu Pro His Pro  
 195 200 205  
 Pro Met Pro Asp Tyr Thr Arg Ser Leu Glu Ser Thr Leu Ser Phe Trp  
 210 215 220  
 Ala Ser Trp Val Glu Glu Leu Pro His Gln Arg Leu Tyr Asp Ala Glu  
 225 230 235 240  
 Val Arg Arg Ser Met Leu Val Leu Arg Ala Leu Thr Asp Leu Gln Thr  
 245 250 255  
 Gly Gly Ile Val Ala Ala Pro Thr Thr Ser Leu Pro Glu Asp Phe Gly  
 260 265 270  
 Gly Ile Arg Asn Trp Asp Tyr Arg Tyr Val Trp Leu Arg Asp Ser Ala  
 275 280 285  
 Leu Thr Ile Glu Ala Leu Val Glu Tyr Gly Phe Ser Gln Ala Ala Leu  
 290 295 300  
 Gln Trp Arg Thr Trp Leu Leu Arg Ala Ile Ala Gly Asp Pro Glu Asn  
 305 310 315 320  
 Leu Arg Ile Met Tyr Gly Leu Gly Gly Glu Arg His Leu Pro Glu Arg  
 325 330 335  
 Glu Leu Gln His Leu Arg Gly Tyr Glu Asn Ser Val Pro Val Arg Val  
 340 345 350  
 Gly Asn Gly Ala Ala Glu Gln Tyr Gln Ala Asp Val Val Gly Glu Val  
 355 360 365  
 Met Val Ala Leu Glu Thr Ile Arg Arg Ala Gly Cys Leu Glu Asp Glu  
 370 375 380  
 Phe Ser Trp Gly Met Gln Lys Ala Ile Leu Asp Phe Gln Glu Ala Asn  
 385 390 395 400  
 Phe Asp Arg Lys Asp Gln Gly Ile Trp Glu Met Arg Ser Glu Pro Gln  
 405 410 415  
 Tyr Phe Thr His Gly Arg Ala Met Met Trp Ala Gly Phe Asp Arg Gly  
 420 425 430  
 Ile Lys Ala Ile Glu Glu Phe Asn Leu Asp Gly Pro Ile Glu Arg Trp  
 435 440 445

Arg Glu Leu Arg Ala Lys Leu Arg Glu Glu Ile Met Thr Asn Gly Phe  
 450 455 460  
 Asn Glu Glu Ile Gln Ser Phe Thr Gln Cys Tyr Asp Asn Thr Gln Val  
 465 470 475 480  
 Asp Ala Ser Leu Leu Gln Leu Ala Gln Ile Gly Phe Ile Gly Phe Asp  
 485 490 495  
 Asp Pro Lys Met Leu Ser Thr Val Ala Arg Ile Glu Gln Glu Leu Leu  
 500 505 510  
 Asp Ala His Gly Phe Leu His Arg Tyr His Thr Asp Gly Ser Asp Gly  
 515 520 525  
 Leu Ala Gly Asp Glu Tyr Pro Phe Leu Ile Cys Ser Phe Trp Leu Val  
 530 535 540  
 Glu Gln Tyr Ala Ser Ser Asn Arg Leu Asp Glu Ala Lys Glu Lys Met  
 545 550 555 560  
 Asn Arg Ile Leu Ala Val Gln Ser Pro Leu Gly Leu Leu Ala Glu Glu  
 565 570 575  
 Tyr Ser Thr His His Gly Arg Leu Ala Gly Asn Tyr Pro Gln Ala Phe  
 580 585 590  
 Ser His Ile Gly Leu Ile Ser Ala Ala Arg Ala Ile Asn Phe Glu Glu  
 595 600 605  
 Ala Arg Asn Arg  
 610

<210> 383  
 <211> 658  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(658)  
 <223> RXA01888

<400> 383  
 agtagatact agataccacc cattgatgcc gtcaaggggt ttcctgtaaa gatgtaagag 60  
 attaagaaaa gaggtagata tggcgtcaaa gcgaccgaca atg gct gat gtg gca 115  
 Met Ala Asp Val Ala  
 1 5  
 aaa gct gct gga gta tcc act gcg ctg gtc tcc atc gtg ttt cgc gat 163  
 Lys Ala Ala Gly Val Ser Thr Ala Leu Val Ser Ile Val Phe Arg Asp  
 10 15 20  
 gcc ccc gga gca agt gaa tcc acc cgc aac cat gtg aaa gaa aaa gcc 211  
 Ala Pro Gly Ala Ser Glu Ser Thr Arg Asn His Val Lys Glu Lys Ala  
 25 30 35  
 gcc gaa ctc gga tac att cct gat cga cga gcc caa aaa ctt cgc caa 259  
 Ala Glu Leu Gly Tyr Ile Pro Asp Arg Arg Ala Gln Lys Leu Arg Gln



40	45	50	
aac cgc tcc gga ctc atc ggt gtg gca ttc gaa atg cac caa gca ttc			307
Asn Arg Ser Gly Leu Ile Gly Val Ala Phe Glu Met His Gln Ala Phe			
55	60	65	
cac ggc gat atc gtc gaa cac ctc tat ccc acc gcc cga aaa cat ggc			355
His Gly Asp Ile Val Glu His Leu Tyr Pro Thr Ala Arg Lys His Gly			
70	75	80	85
ttc gac ctg tac ctt agc gcg atc aca ccg act cgc act gaa aaa gat			403
Phe Asp Leu Tyr Leu Ser Ala Ile Thr Pro Thr Arg Thr Glu Lys Asp			
90	95	100	
gcc gtc aac gcc ctg atc agg gaa cga tgc gaa gca gta att ctt cta			451
Ala Val Asn Ala Leu Ile Arg Glu Arg Cys Glu Ala Val Ile Leu Leu			
105	110	115	
gga tct cgc atg tca cct agt gat ttg gaa aca atc gca cag caa ctt			499
Gly Ser Arg Met Ser Pro Ser Asp Leu Glu Thr Ile Ala Gln Gln Leu			
120	125	130	
ccc gtc caa gta att gcc cgc ggt tcc gga acc ccc aaa gtc agt tcc			547
Pro Val Gln Val Ile Ala Arg Gly Ser Gly Thr Pro Lys Val Ser Ser			
135	140	145	
gtc cat gtc gac gac gca gtt ggc gcc caa tta gcc ctc aac cac ctc			595
Val His Val Asp Asp Ala Val Gly Ala Gln Leu Ala Leu Asn His Leu			
150	155	160	165
atc gaa tta ggc cac gaa cac atc atc tac atc gat ggt ggc gac gcc			643
Ile Glu Leu Gly His Glu His Ile Ile Tyr Ile Asp Gly Gly Asp Ala			
170	175	180	
cct ggc acc cag gaa			658
Pro Gly Thr Gln Glu			
185			

&lt;210&gt; 384

&lt;211&gt; 186

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 384

Met Ala Asp Val Ala Lys Ala Ala Gly Val Ser Thr Ala Leu Val Ser			
1	5	10	15
Ile Val Phe Arg Asp Ala Pro Gly Ala Ser Glu Ser Thr Arg Asn His			
20	25	30	
Val Lys Glu Lys Ala Ala Glu Leu Gly Tyr Ile Pro Asp Arg Arg Ala			
35	40	45	
Gln Lys Leu Arg Gln Asn Arg Ser Gly Leu Ile Gly Val Ala Phe Glu			
50	55	60	
Met His Gln Ala Phe His Gly Asp Ile Val Glu His Leu Tyr Pro Thr			
65	70	75	80
Ala Arg Lys His Gly Phe Asp Leu Tyr Leu Ser Ala Ile Thr Pro Thr			

85	90	95
Arg Thr Glu Lys Asp Ala Val Asn Ala Leu Ile Arg Glu Arg Cys Glu 100 105 110		
Ala Val Ile Leu Leu Gly Ser Arg Met Ser Pro Ser Asp Leu Glu Thr 115 120 125		
Ile Ala Gln Gln Leu Pro Val Gln Val Ile Ala Arg Gly Ser Gly Thr 130 135 140		
Pro Lys Val Ser Ser Val His Val Asp Asp Ala Val Gly Ala Gln Leu 145 150 155 160		
Ala Leu Asn His Leu Ile Glu Leu Gly His Glu His Ile Ile Tyr Ile 165 170 175		
Asp Gly Gly Asp Ala Pro Gly Thr Gln Glu 180 185		
 <210> 385 <211> 1503 <212> DNA <213> Corynebacterium glutamicum		
 <220> <221> CDS <222> (101)..(1480) <223> RXN01927		
 <400> 385 gagcagcggg atcttttgcg taattcgcgc gcgcagatcc atgtgattga ccacaatggg 60		
gatgaaattt tggatacccc aacggaagag gatttttaag atg gct ttg gtt ctt 115 Met Ala Leu Val Leu 1 5		
gga atc gat agt tcc acc caa tcc tgc aag gct ttg ctt gtc gac gcc 163 Gly Ile Asp Ser Ser Thr Gln Ser Cys Lys Ala Leu Leu Val Asp Ala 10 15 20		
gcc acc ggc cag gtt atc gac gaa ggc cgc gcg agt cac ccg agc ggg 211 Ala Thr Gly Gln Val Ile Asp Glu Gly Arg Ala Ser His Pro Ser Gly 25 30 35		
tcg gag gta gat cca cgt gcg tgg atc gct gcg ctg gat caa gct acc 259 Ser Glu Val Asp Pro Arg Ala Trp Ile Ala Ala Leu Asp Gln Ala Thr 40 45 50		
gag ggg ttg tta gaa cgc gcg gac gct gta tct att gca ggc cag cag 307 Glu Gly Leu Leu Glu Arg Ala Asp Ala Val Ser Ile Ala Gly Gln Gln 55 60 65		
cac ggc atg gtg gcg ttg gat gaa aac gat gaa atc gtt cgc ccg gcg 355 His Gly Met Val Ala Leu Asp Glu Asn Asp Glu Ile Val Arg Pro Ala 70 75 80 85		
ttg tta tgg aat gac act cgt tct gcc cag gct gcg ttg gat ctc aat 403 Leu Leu Trp Asn Asp Thr Arg Ser Ala Gln Ala Ala Leu Asp Leu Asn 90 95 100		

gag gag atc ggc ggc gat cag gct gcg gta gat gcc acg gga agt gtg	451
Glu Glu Ile Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val	
105 110 115	
tat gtt gct tct tta act gcc acc aaa atg cgg tgg atg cgt gat cat	499
Tyr Val Ala Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His	
120 125 130	
gaa cca gaa aat gca gcg cgc acg gcg tcg gtg atg ttg cct cat gat	547
Glu Pro Glu Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp	
135 140 145	
ttc ctc acc tgg cat ttg atg gga cgc gga cgc aaa gtc acc gac cat	595
Phe Leu Thr Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His	
150 155 160 165	
ggt gat gct tct gga acg ggc tac tac agc acg cgt gat cgt gcg tgg	643
Gly Asp Ala Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp	
170 175 180	
cgc acc gat cta gct gcc ttg gcg ctg ggc cat gag gtg gaa ctt cct	691
Arg Thr Asp Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro	
185 190 195	
gaa ctc ctg gcc cca aat gcg att gcg gga aca act cca ggt gga gtg	739
Glu Leu Leu Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val	
200 205 210	
aaa gtt gct gca ggc acg gga gat aat gct gcg gct gcg ctt ggc ctt	787
Lys Val Ala Ala Gly Thr Gly Asp Asn Ala Ala Ala Ala Leu Gly Leu	
215 220 225	
gat ttg cag cct ggt gat gtc agc gtg tcg atc gcc acc tct ggc gtt	835
Asp Leu Gln Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val	
230 235 240 245	
gcc ggc atg acc gtt caa cat agc gtc cac gat cca tct ggt ttg gtc	883
Ala Gly Met Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val	
250 255 260	
act ggt ttc gcc gat gcc acg ggt gcg tat ttc ccg ctg gcc tgc acg	931
Thr Gly Phe Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr	
265 270 275	
ctt aat ggc gca ccg gtg ttg gaa ttc ggc cgc cgc att ctg ggc gtg	979
Leu Asn Gly Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val	
280 285 290	
gaa tgg gaa gag ttc gat gcg ctt gca ctg gct gct caa ccc ggt tca	1027
Glu Trp Glu Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser	
295 300 305	
ggt ggc gtg acg ctc cag cct tat ttg gag ggc gag cgt acg ccg aat	1075
Gly Gly Val Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn	
310 315 320 325	
cgt ccc gca gca cgt ggc gtt ttg gct gga cta aac tgt gca acg acc	1123
Arg Pro Ala Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr	
330 335 340	

cgc gag gac ttt gcc cga gca act gtt gaa ggc ttg ttg ttg gca ttg 1171  
 Arg Glu Asp Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Leu Ala Leu  
 345 350 355  
 gat gat gct gta acg gcg ctg gtt gag gcc acg gga gtg ccc gtt cag 1219  
 Asp Asp Ala Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln  
 360 365 370  
 cgc atc cag ctc atc ggt ggc ggc gcg cgt tca cag gcg gtt cgt gag 1267  
 Arg Ile Gln Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu  
 375 380 385  
 att gcc cct gag att ttc ggc cat gag att gtg gtt cca gaa ccc gct 1315  
 Ile Ala Pro Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala  
 390 395 400 405  
 gaa tat gtg gcg ttg ggt gca gct cgt cag gcg gca tgg gcg ctg tcg 1363  
 Glu Tyr Val Ala Leu Gly Ala Ala Arg Gln Ala Ala Trp Ala Leu Ser  
 410 415 420  
 ggt gag gcc acg cca ccg cag tgg cca act ccc ggt tcc gat ccg cac 1411  
 Gly Glu Ala Thr Pro Pro Gln Trp Pro Thr Pro Gly Ser Asp Pro His  
 425 430 435  
 cgc gca cct aaa aac act gag ctg agc acg cgt tat gcg aag ctg cgt 1459  
 Arg Ala Pro Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg  
 440 445 450  
 gct gca acg cag ggt tgg tac tagagctcga tattgtcgat caa 1503  
 Ala Ala Thr Gln Gly Trp Tyr  
 455 460

&lt;210&gt; 386

&lt;211&gt; 460

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 386

Met Ala Leu Val Leu Gly Ile Asp Ser Ser Thr Gln Ser Cys Lys Ala  
 1 5 10 15  
 Leu Leu Val Asp Ala Ala Thr Gly Gln Val Ile Asp Glu Gly Arg Ala  
 20 25 30  
 Ser His Pro Ser Gly Ser Glu Val Asp Pro Arg Ala Trp Ile Ala Ala  
 35 40 45  
 Leu Asp Gln Ala Thr Glu Gly Leu Leu Glu Arg Ala Asp Ala Val Ser  
 50 55 60  
 Ile Ala Gly Gln Gln His Gly Met Val Ala Leu Asp Glu Asn Asp Glu  
 65 70 75 80  
 Ile Val Arg Pro Ala Leu Leu Trp Asn Asp Thr Arg Ser Ala Gln Ala  
 85 90 95  
 Ala Leu Asp Leu Asn Glu Glu Ile Gly Gly Asp Gln Ala Ala Val Asp  
 100 105 110  
 Ala Thr Gly Ser Val Tyr Val Ala Ser Leu Thr Ala Thr Lys Met Arg

115					120					125						
Trp	Met	Arg	Asp	His	Glu	Pro	Glu	Asn	Ala	Ala	Arg	Thr	Ala	Ser	Val	
130					135					140						
Met	Leu	Pro	His	Asp	Phe	Leu	Thr	Trp	His	Leu	Met	Gly	Arg	Gly	Arg	
145					150					155					160	
Lys	Val	Thr	Asp	His	Gly	Asp	Ala	Ser	Gly	Thr	Gly	Tyr	Tyr	Ser	Thr	
165					170					175						
Arg	Asp	Arg	Ala	Trp	Arg	Thr	Asp	Leu	Ala	Ala	Leu	Ala	Leu	Gly	His	
180					185					190						
Glu	Val	Glu	Leu	Pro	Glu	Leu	Leu	Ala	Pro	Asn	Ala	Ile	Ala	Gly	Thr	
195					200					205						
Thr	Pro	Gly	Gly	Val	Lys	Val	Ala	Ala	Gly	Thr	Gly	Asp	Asn	Ala	Ala	
210					215					220						
Ala	Ala	Leu	Gly	Leu	Asp	Leu	Gln	Pro	Gly	Asp	Val	Ser	Val	Ser	Ile	
225					230					235					240	
Gly	Thr	Ser	Gly	Val	Ala	Gly	Met	Thr	Val	Gln	His	Ser	Val	His	Asp	
245					250					255						
Pro	Ser	Gly	Leu	Val	Thr	Gly	Phe	Ala	Asp	Ala	Thr	Gly	Ala	Tyr	Phe	
260					265					270						
Pro	Leu	Ala	Cys	Thr	Leu	Asn	Gly	Ala	Pro	Val	Leu	Glu	Phe	Gly	Arg	
275					280					285						
Arg	Ile	Leu	Gly	Val	Glu	Trp	Glu	Glu	Phe	Asp	Ala	Leu	Ala	Leu	Ala	
290					295					300						
Ala	Gln	Pro	Gly	Ser	Gly	Gly	Val	Thr	Leu	Gln	Pro	Tyr	Leu	Glu	Gly	
305					310					315					320	
Glu	Arg	Thr	Pro	Asn	Arg	Pro	Ala	Ala	Arg	Gly	Val	Leu	Ala	Gly	Leu	
325					330					335						
Asn	Cys	Ala	Thr	Thr	Arg	Glu	Asp	Phe	Ala	Arg	Ala	Thr	Val	Glu	Gly	
340					345					350						
Leu	Leu	Leu	Ala	Leu	Asp	Asp	Ala	Val	Thr	Ala	Leu	Val	Glu	Ala	Thr	
355					360					365						
Gly	Val	Pro	Val	Gln	Arg	Ile	Gln	Leu	Ile	Gly	Gly	Gly	Ala	Arg	Ser	
370					375					380						
Gln	Ala	Val	Arg	Glu	Ile	Ala	Pro	Glu	Ile	Phe	Gly	His	Glu	Ile	Val	
385					390					395					400	
Val	Pro	Glu	Pro	Ala	Glu	Tyr	Val	Ala	Leu	Gly	Ala	Ala	Arg	Gln	Ala	
405					410					415						
Ala	Trp	Ala	Leu	Ser	Gly	Glu	Ala	Thr	Pro	Pro	Gln	Trp	Pro	Thr	Pro	
420					425					430						
Gly	Ser	Asp	Pro	His	Arg	Ala	Pro	Lys	Asn	Thr	Glu	Leu	Ser	Thr	Arg	
435					440					445						

Tyr Ala Lys Leu Arg Ala Ala Thr Gln Gly Trp Tyr  
 450 455 460

<210> 387  
 <211> 1139  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1116)  
 <223> FRXA01927

<400> 387  
 aat gac act cgt tct gcc cag gct gcg ttg gat ctc aat gag gag atc 48  
 Asn Asp Thr Arg Ser Ala Gln Ala Ala Leu Asp Leu Asn Glu Glu Ile  
 1 5 10 15  
 ggc ggc gat cag gct gcg gta gat gcc acg gga agt gtg tat gtt gct 96  
 Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val Tyr Val Ala  
 20 25 30  
 tct tta act gcc acc aaa atg cgg tgg atg cgt gat cat gaa cca gaa 144  
 Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His Glu Pro Glu  
 35 40 45  
 aat gca gcg cgc acg gcg tcg gtg atg ttg cct cat gat ttc ctc acc 192  
 Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp Phe Leu Thr  
 50 55 60  
 tgg cat ttg atg gga cgc gga cgc aaa gtc acc gac cat ggt gat gct 240  
 Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His Gly Asp Ala  
 65 70 75 80  
 tct gga acg ggc tac tac agc acg cgt gat cgt gcg tgg cgc acc gat 288  
 Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp Arg Thr Asp  
 85 90 95  
 cta gct gcc ttg gcg ctg ggc cat gag gtg gaa ctt cct gaa ctc ctg 336  
 Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro Glu Leu Leu  
 100 105 110  
 gcc cca aat gcg att gcg gga aca act cca ggt gga gtg aaa gtt gct 384  
 Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val Lys Val Ala  
 115 120 125  
 gca ggc acg gga gat aat gct gcg gct gcg ctt ggc ctt gat ttg cag 432  
 Ala Gly Thr Gly Asp Asn Ala Ala Ala Ala Leu Gly Leu Asp Leu Gln  
 130 135 140  
 cct ggt gat gtc agc gtg tcg atc ggc acc tct ggc gtt gcc ggc atg 480  
 Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val Ala Gly Met  
 145 150 155 160  
 acc gtt caa cat agc gtc cac gat cca tct ggt ttg gtc act ggt ttc 528  
 Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val Thr Gly Phe  
 165 170 175  
 gcc gat gcc acg ggt gcg tat ttc ccg ctg gcc tgc acg ctt aat ggc 576

Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr Leu Asn Gly  
180 185 190

gca ccg gtg ttg gaa ttc ggc cgc cgc att ctg ggc gtg gaa tgg gaa 624  
Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val Glu Trp Glu  
195 200 205

gag ttc gat gcg ctt gca ctg gct gct caa ccc ggt tca ggt ggc gtg 672  
Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser Gly Gly Val  
210 215 220

acg ctc cag cct tat ttg gag ggc gag cgt acg ccg aat cgt ccc gca 720  
Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn Arg Pro Ala  
225 230 235 240

gca cgt ggc gtt ttg gct gga cta aac tgt gca acg acc cgc gag gac 768  
Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr Arg Glu Asp  
245 250 255

ttt gcc cga gca act gtt gaa ggc ttg ttg ttg gca ttg gat gat gct 816  
Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Leu Ala Leu Asp Asp Ala  
260 265 270

gta acg gcg ctg gtt gag gcc acg gga gtg ccc gtt cag cgc atc cag 864  
Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln Arg Ile Gln  
275 280 285

ctc atc ggt ggc ggc gcg cgt tca cag gcg gtt cgt gag att gcc cct 912  
Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu Ile Ala Pro  
290 295 300

gag att ttc ggc cat gag att gtg gtt cca gaa ccc gct gaa tat gtg 960  
Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala Glu Tyr Val  
305 310 315 320

gcg ttg ggt gca gct cgt cag gcg gca tgg gcg ctg tcg ggt gag gcc 1008  
Ala Leu Gly Ala Ala Arg Gln Ala Ala Trp Ala Leu Ser Gly Glu Ala  
325 330 335

acg cca ccg cag tgg cca act ccc ggt tcc gat ccg cac cgc gca cct 1056  
Thr Pro Pro Gln Trp Pro Thr Pro Gly Ser Asp Pro His Arg Ala Pro  
340 345 350

aaa aac act gag ctg agc acg cgt tat gcg aag ctg cgt gct gca acg 1104  
Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg Ala Ala Thr  
355 360 365

cag ggt tgg tac tagagctcga tattgtcgat caa 1139  
Gln Gly Trp Tyr  
370

&lt;210&gt; 388

&lt;211&gt; 372

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 388

Asn Asp Thr Arg Ser Ala Gln Ala Ala Leu Asp Leu Asn Glu Glu Ile  
1 5 10 15

Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val Tyr Val Ala  
                   20                                  25                                  30  
 Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His Glu Pro Glu  
                   35                                  40                                  45  
 Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp Phe Leu Thr  
                   50                                  55                                  60  
 Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His Gly Asp Ala  
                   65                                  70                                  75                                  80  
 Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp Arg Thr Asp  
                   85                                  90                                  95  
 Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro Glu Leu Leu  
                   100                                  105                                  110  
 Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val Lys Val Ala  
                   115                                  120                                  125  
 Ala Gly Thr Gly Asp Asn Ala Ala Ala Ala Leu Gly Leu Asp Leu Gln  
                   130                                  135                                  140  
 Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val Ala Gly Met  
                   145                                  150                                  155                                  160  
 Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val Thr Gly Phe  
                   165                                  170                                  175  
 Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr Leu Asn Gly  
                   180                                  185                                  190  
 Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val Glu Trp Glu  
                   195                                  200                                  205  
 Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser Gly Gly Val  
                   210                                  215                                  220  
 Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn Arg Pro Ala  
                   225                                  230                                  235                                  240  
 Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr Arg Glu Asp  
                   245                                  250                                  255  
 Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Leu Ala Leu Asp Asp Ala  
                   260                                  265                                  270  
 Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln Arg Ile Gln  
                   275                                  280                                  285  
 Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu Ile Ala Pro  
                   290                                  295                                  300  
 Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala Glu Tyr Val  
                   305                                  310                                  315                                  320  
 Ala Leu Gly Ala Ala Arg Gln Ala Ala Trp Ala Leu Ser Gly Glu Ala  
                   325                                  330                                  335  
 Thr Pro Pro Gln Trp Pro Thr Pro Gly Ser Asp Pro His Arg Ala Pro



340 345 350  
 Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg Ala Ala Thr  
 355 360 365  
 Gln Gly Trp Tyr  
 370  
  
 <210> 389  
 <211> 844  
 <212> DNA  
 <213> Corynebacterium glutamicum  
  
 <220>  
 <221> CDS  
 <222> (101)..(844)  
 <223> RXA02729  
  
 <400> 389  
 gaattaattg caggcacggt acctagcgtg acgaaaacta cgatccccac tgcccttatt 60  
  
 catcgtgaat caatcatcaa ctccacttta aggaagaagg atg gac tcc cca atg 115  
 Met Asp Ser Pro Met  
 1 5  
  
 agt aac tca acc ggt acc gac att gtc gtt gtc gga tcc atc aat gcc 163  
 Ser Asn Ser Thr Gly Thr Asp Ile Val Val Val Gly Ser Ile Asn Ala  
 10 15 20  
  
 gat ctc acc gca aaa gtt caa cgc cac cct gaa cct gga gaa acc ctc 211  
 Asp Leu Thr Ala Lys Val Gln Arg His Pro Glu Pro Gly Glu Thr Leu  
 25 30 35  
  
 ctg ggt agc ggc ggc aca gtg agt gct ggt ggc aaa ggc gcc aac caa 259  
 Leu Gly Ser Gly Gly Thr Val Ser Ala Gly Gly Lys Gly Ala Asn Gln  
 40 45 50  
  
 gct gtg gcg gca gcg caa tta ggt gcc aaa gtc acc atg atc ggt gcg 307  
 Ala Val Ala Ala Ala Gln Leu Gly Ala Lys Val Thr Met Ile Gly Ala  
 55 60 65  
  
 gtc gga acc gat caa atg gct ggc gag gcg ctg aca cat ttg cgt caa 355  
 Val Gly Thr Asp Gln Met Ala Gly Glu Ala Leu Thr His Leu Arg Gln  
 70 75 80 85  
  
 tca gga gca gat atg tcc gcg att gcc act gtg gac ggt ccc act ggt 403  
 Ser Gly Ala Asp Met Ser Ala Ile Ala Thr Val Asp Gly Pro Thr Gly  
 90 95 100  
  
 ctt gcc atc atc act gtg tct gac gat ggg gaa aac acc atc atc gtt 451  
 Leu Ala Ile Ile Thr Val Ser Asp Asp Gly Glu Asn Thr Ile Ile Val  
 105 110 115  
  
 atc cct ggc gct aac gct tct gtc acc gcg gaa ttt gtt gat aaa cac 499  
 Ile Pro Gly Ala Asn Ala Ser Val Thr Ala Glu Phe Val Asp Lys His  
 120 125 130  
  
 tcc caa ctc att gag aac gcc ggc att gtg ttg ctt cag ggt gag atc 547  
 Ser Gln Leu Ile Glu Asn Ala Gly Ile Val Leu Leu Gln Gly Glu Ile  
 135 140 145

cct gcc gat ggt ttc gag cgt gcc gtt gat ctt tca caa gga cgt gtg 595  
 Pro Ala Asp Gly Phe Glu Arg Ala Val Asp Leu Ser Gln Gly Arg Val  
 150 155 160 165  
 gtg atc aat ctg gct cca gtt gtg ccc gtg gga cat gat cag ctg cgt 643  
 Val Ile Asn Leu Ala Pro Val Val Pro Val Gly His Asp Gln Leu Arg  
 170 175 180  
 cgt gcc gat cca ttg ctg gtc aac gaa cac gaa ggc gct ctg gtg ctg 691  
 Arg Ala Asp Pro Leu Leu Val Asn Glu His Glu Gly Ala Leu Val Leu  
 185 190 195  
 gac atg ctt gga act cca gcg acc acg tct gat ccc caa agt ttg gtc 739  
 Asp Met Leu Gly Thr Pro Ala Thr Thr Ser Asp Pro Gln Ser Leu Val  
 200 205 210  
 act gaa ttg ctg gag cag ggt ttt act tcc gtg gtg atg aca ctt ggt 787  
 Thr Glu Leu Leu Glu Gln Gly Phe Thr Ser Val Val Met Thr Leu Gly  
 215 220 225  
 gcc gaa ggt gct ctg gtt ggc acg ccg ggc caa ctc acg gca att cct 835  
 Ala Glu Gly Ala Leu Val Gly Thr Pro Gly Gln Leu Thr Ala Ile Pro  
 230 235 240 245  
 acc cca aag 844  
 Thr Pro Lys

<210> 390  
 <211> 248  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 390  
 Met Asp Ser Pro Met Ser Asn Ser Thr Gly Thr Asp Ile Val Val Val  
 1 5 10 15  
 Gly Ser Ile Asn Ala Asp Leu Thr Ala Lys Val Gln Arg His Pro Glu  
 20 25 30  
 Pro Gly Glu Thr Leu Leu Gly Ser Gly Gly Thr Val Ser Ala Gly Gly  
 35 40 45  
 Lys Gly Ala Asn Gln Ala Val Ala Ala Ala Gln Leu Gly Ala Lys Val  
 50 55 60  
 Thr Met Ile Gly Ala Val Gly Thr Asp Gln Met Ala Gly Glu Ala Leu  
 65 70 75 80  
 Thr His Leu Arg Gln Ser Gly Ala Asp Met Ser Ala Ile Ala Thr Val  
 85 90 95  
 Asp Gly Pro Thr Gly Leu Ala Ile Ile Thr Val Ser Asp Asp Gly Glu  
 100 105 110  
 Asn Thr Ile Ile Val Ile Pro Gly Ala Asn Ala Ser Val Thr Ala Glu  
 115 120 125  
 Phe Val Asp Lys His Ser Gln Leu Ile Glu Asn Ala Gly Ile Val Leu

130	135	140	
Leu Gln Gly Glu Ile Pro Ala Asp Gly Phe Glu Arg Ala Val Asp Leu 145 150 155 160			
Ser Gln Gly Arg Val Val Ile Asn Leu Ala Pro Val Val Pro Val Gly 165 170 175			
His Asp Gln Leu Arg Arg Ala Asp Pro Leu Leu Val Asn Glu His Glu 180 185 190			
Gly Ala Leu Val Leu Asp Met Leu Gly Thr Pro Ala Thr Thr Ser Asp 195 200 205			
Pro Gln Ser Leu Val Thr Glu Leu Leu Glu Gln Gly Phe Thr Ser Val 210 215 220			
Val Met Thr Leu Gly Ala Glu Gly Ala Leu Val Gly Thr Pro Gly Gln 225 230 235 240			
Leu Thr Ala Ile Pro Thr Pro Lys 245			
<210> 391			
<211> 1026			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(1003)			
<223> RXA02797			
<400> 391			
acagtctcat gaagccataa taaccacctt ctacaaagat cgacgtagaa tggaataacc 60			
ccttatgaaa acgtttgcat aactccgcta aggatgttcc atg aat aat cga att 115			
Met Asn Asn Arg Ile 5			
1			
gtc gta gtc ggc tcc atc aac gct gat ctt aat gtt ctc gtt gac cgc 163			
Val Val Val Gly Ser Ile Asn Ala Asp Leu Asn Val Leu Val Asp Arg 20			
10 15			
cac cca gca cct ggc gaa aca ctg ttg ggc agt ggt gga cac atc act 211			
His Pro Ala Pro Gly Glu Thr Leu Leu Gly Ser Gly Gly His Ile Thr 35			
25 30			
gca gga ggc aaa ggc gcc aac cag gca gta gct gcc gct ctt caa ggt 259			
Ala Gly Gly Lys Gly Ala Asn Gln Ala Val Ala Ala Ala Leu Gln Gly 50			
40 45 50			
gca gac gtc gcc ttt gtc ggc gct gtg ggc aag gat cct tac gct gcc 307			
Ala Asp Val Ala Phe Val Gly Ala Val Gly Lys Asp Pro Tyr Ala Ala 65			
55 60 65			
cca gcc tta gaa ttc ctt cgt tct tca ggc gtc gac ctt acg gca gta 355			
Pro Ala Leu Glu Phe Leu Arg Ser Ser Gly Val Asp Leu Thr Ala Val 85			
70 75 80 85			

```

tcc gaa gta gat gac acc acc ggg ctt gca gtt atc acc gtt gcc aaa 403
Ser Glu Val Asp Asp Thr Thr Gly Leu Ala Val Ile Thr Val Ala Lys
          90                      95                      100

gac ggc gag aac aat atc gtt gtc atc ccc ggc gcg aat tcc ctg gtc 451
Asp Gly Glu Asn Asn Ile Val Val Ile Pro Gly Ala Asn Ser Leu Val
          105                      110                      115

aat tgt gat tat gta agc agc caa tcc gct ctt tta gct gaa gct gga 499
Asn Cys Asp Tyr Val Ser Ser Gln Ser Ala Leu Leu Ala Glu Ala Gly
          120                      125                      130

atc ctg ttg ctg caa ggt gag atc cct gcg gat ggc ttc aaa gag gcc 547
Ile Leu Leu Leu Gln Gly Glu Ile Pro Ala Asp Gly Phe Lys Glu Ala
          135                      140                      145

att cac cac acc atg ggt cgc gtc gtg gtg aat cta gcg ccc gtc atc 595
Ile His His Thr Met Gly Arg Val Val Val Asn Leu Ala Pro Val Ile
          150                      155                      160                      165

gag gta gag aag tcc gcg tta ctt gag gct gat ccg atc atc gcc aat 643
Glu Val Glu Lys Ser Ala Leu Leu Glu Ala Asp Pro Ile Ile Ala Asn
          170                      175                      180

gag cac gag gcc ggc ctg att ctg gat caa ttc ggg gca ggc atc gat 691
Glu His Glu Ala Gly Leu Ile Leu Asp Gln Phe Gly Ala Gly Ile Asp
          185                      190                      195

tcc atg gat ccc cac gag ctc gcg caa gct ctc ctc gac gcc ggt ttc 739
Ser Met Asp Pro His Glu Leu Ala Gln Ala Leu Leu Asp Ala Gly Phe
          200                      205                      210

gcc tct gtt gtt tta acg ctt gga tcc gca ggc gcg ttg gtc gcc gat 787
Ala Ser Val Val Leu Thr Leu Gly Ser Ala Gly Ala Leu Val Ala Asp
          215                      220                      225

gcc acc ggt atc acg gac atc gcc aca cca acg gtg cag gca gtt gac 835
Ala Thr Gly Ile Thr Asp Ile Ala Thr Pro Thr Val Gln Ala Val Asp
          230                      235                      240                      245

acc acg gga gcc ggt gac gct ttt gcc gga gcc ttc tgc gca cga cta 883
Thr Thr Gly Ala Gly Asp Ala Phe Ala Gly Ala Phe Cys Ala Arg Leu
          250                      255                      260

att aaa ggc gat tcg ctt atc gac gcc gcc acc cac gca gca cgc gtc 931
Ile Lys Gly Asp Ser Leu Ile Asp Ala Ala Thr His Ala Ala Arg Val
          265                      270                      275

ggc gct tac tcg gtg caa acc gcc gga gcg caa gcg tcc tat ccg gac 979
Gly Ala Tyr Ser Val Gln Thr Ala Gly Ala Gln Ala Ser Tyr Pro Asp
          280                      285                      290

gcg agc gtt tca ctt ccc tct gtt taaaaaaaaact atttaagaag agg 1026
Ala Ser Val Ser Leu Pro Ser Val
          295                      300

```

&lt;210&gt; 392

&lt;211&gt; 301

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 392

```

Met Asn Asn Arg Ile Val Val Val Gly Ser Ile Asn Ala Asp Leu Asn
 1           5           10           15

Val Leu Val Asp Arg His Pro Ala Pro Gly Glu Thr Leu Leu Gly Ser
          20           25           30

Gly Gly His Ile Thr Ala Gly Gly Lys Gly Ala Asn Gln Ala Val Ala
          35           40           45

Ala Ala Leu Gln Gly Ala Asp Val Ala Phe Val Gly Ala Val Gly Lys
          50           55           60

Asp Pro Tyr Ala Ala Pro Ala Leu Glu Phe Leu Arg Ser Ser Gly Val
          65           70           75           80

Asp Leu Thr Ala Val Ser Glu Val Asp Asp Thr Thr Gly Leu Ala Val
          85           90           95

Ile Thr Val Ala Lys Asp Gly Glu Asn Asn Ile Val Val Ile Pro Gly
          100          105          110

Ala Asn Ser Leu Val Asn Cys Asp Tyr Val Ser Ser Gln Ser Ala Leu
          115          120          125

Leu Ala Glu Ala Gly Ile Leu Leu Leu Gln Gly Glu Ile Pro Ala Asp
          130          135          140

Gly Phe Lys Glu Ala Ile His His Thr Met Gly Arg Val Val Val Asn
          145          150          155          160

Leu Ala Pro Val Ile Glu Val Glu Lys Ser Ala Leu Leu Glu Ala Asp
          165          170          175

Pro Ile Ile Ala Asn Glu His Glu Ala Gly Leu Ile Leu Asp Gln Phe
          180          185          190

Gly Ala Gly Ile Asp Ser Met Asp Pro His Glu Leu Ala Gln Ala Leu
          195          200          205

Leu Asp Ala Gly Phe Ala Ser Val Val Leu Thr Leu Gly Ser Ala Gly
          210          215          220

Ala Leu Val Ala Asp Ala Thr Gly Ile Thr Asp Ile Ala Thr Pro Thr
          225          230          235          240

Val Gln Ala Val Asp Thr Thr Gly Ala Gly Asp Ala Phe Ala Gly Ala
          245          250          255

Phe Cys Ala Arg Leu Ile Lys Gly Asp Ser Leu Ile Asp Ala Ala Thr
          260          265          270

His Ala Ala Arg Val Gly Ala Tyr Ser Val Gln Thr Ala Gly Ala Gln
          275          280          285

Ala Ser Tyr Pro Asp Ala Ser Val Ser Leu Pro Ser Val
          290          295          300

```

&lt;210&gt; 393

```
<211> 1161
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1138)
<223> RXA02730
```

<400> 393																
ccaacatcgc	cttgcacgta	ataggttaaa	acacaagtga	atgtaatcgt	ttgcagcaat	60										
cgattacata aaggtagata atgagataaa gcgaggcgct						atg	gcg	acg	gaa	aaa	115					
						Met	Ala	Thr	Glu	Lys						
						1				5						
ttc	cga	ccg	act	ctt	aaa	gat	gtc	gct	cgt	caa	gca	ggc	gtc	tcc	atc	163
Phe	Arg	Pro	Thr	Leu	Lys	Asp	Val	Ala	Arg	Gln	Ala	Gly	Val	Ser	Ile	
				10					15					20		
gcc	aca	gca	tca	cga	gca	cta	gcg	gat	aat	ccg	gcg	ggt	gct	gca	tcg	211
Ala	Thr	Ala	Ser	Arg	Ala	Leu	Ala	Asp	Asn	Pro	Ala	Val	Ala	Ala	Ser	
				25					30					35		
act	cgt	gaa	aga	atc	caa	caa	tta	gcc	tct	gat	ctg	ggc	tac	cgg	gcc	259
Thr	Arg	Glu	Arg	Ile	Gln	Gln	Leu	Ala	Ser	Asp	Leu	Gly	Tyr	Arg	Ala	
				40					45					50		
aat	gct	caa	gct	cgt	gcg	ctt	cgc	agt	tct	cgc	agc	aac	acc	att	ggc	307
Asn	Ala	Gln	Ala	Arg	Ala	Leu	Arg	Ser	Ser	Arg	Ser	Asn	Thr	Ile	Gly	
		55					60					65				
gtg	att	ggt	ccc	agt	ttg	att	aac	cat	tac	ttc	gcc	gca	atg	ggt	act	355
Val	Ile	Val	Pro	Ser	Leu	Ile	Asn	His	Tyr	Phe	Ala	Ala	Met	Val	Thr	
70					75					80					85	
gaa	att	caa	agc	acc	gcc	agc	aaa	gct	gga	ctt	gcc	acg	att	atc	acc	403
Glu	Ile	Gln	Ser	Thr	Ala	Ser	Lys	Ala	Gly	Leu	Ala	Thr	Ile	Ile	Thr	
				90					95					100		
aac	agc	aat	gaa	gat	gcg	acc	act	atg	tct	ggg	tct	ttg	gag	ttt	ctc	451
Asn	Ser	Asn	Glu	Asp	Ala	Thr	Thr	Met	Ser	Gly	Ser	Leu	Glu	Phe	Leu	
				105					110					115		
acc	tcg	cat	ggc	gtc	gat	gga	atc	atc	tgc	gta	cct	aat	gag	gaa	tgc	499
Thr	Ser	His	Gly	Val	Asp	Gly	Ile	Ile	Cys	Val	Pro	Asn	Glu	Glu	Cys	
			120					125					130			
gcg	aat	caa	cta	gag	gac	ttg	cag	aag	caa	gga	atg	cca	gtg	gtg	ttg	547
Ala	Asn	Gln	Leu	Glu	Asp	Leu	Gln	Lys	Gln	Gly	Met	Pro	Val	Val	Leu	
			135					140					145			
ggt	gac	cga	gag	ctt	cca	gga	gac	tcc	acc	atc	cca	acg	gcg	acc	tct	595
Val	Asp	Arg	Glu	Leu	Pro	Gly	Asp	Ser	Thr	Ile	Pro	Thr	Ala	Thr	Ser	
150					155					160					165	
aac	ccc	caa	cca	gga	atc	gcc	gca	gca	gta	gaa	ctc	ctg	gct	cac	aac	643
Asn	Pro	Gln	Pro	Gly	Ile	Ala	Ala	Ala	Val	Glu	Leu	Leu	Ala	His	Asn	
				170					175					180		
aac	gcg	ttg	ccg	att	ggt	tac	ctc	tca	ggt	ccc	atg	gac	acc	tca	aca	691

Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro Met Asp Thr Ser Thr  
 185 190 195  
 ggt aga gag cga tta gag gat ttc aaa gca gcc tgc gcc aac tcc aaa 739  
 Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala Cys Ala Asn Ser Lys  
 200 205 210  
 att ggc gaa cag ctc gtt ttt ctg ggt ggg tac gaa caa agc gtt gga 787  
 Ile Gly Glu Gln Leu Val Phe Leu Gly Gly Tyr Glu Gln Ser Val Gly  
 215 220 225  
 ttt gaa ggc gct acg aaa ttg ctc gat caa gga gct aaa act ctt ttt 835  
 Phe Glu Gly Ala Thr Lys Leu Leu Asp Gln Gly Ala Lys Thr Leu Phe  
 230 235 240 245  
 gcc ggc gat tct atg atg acg atc ggt gtc att gaa gcc tgc cat aag 883  
 Ala Gly Asp Ser Met Met Thr Ile Gly Val Ile Glu Ala Cys His Lys  
 250 255 260  
 gct ggt ttg gtt atc ggc aag gat gtc agc gtg att ggt ttt gat aca 931  
 Ala Gly Leu Val Ile Gly Lys Asp Val Ser Val Ile Gly Phe Asp Thr  
 265 270 275  
 cat ccg ctt ttt gcc ctg caa cct cat ccg ttg aca gtg att gat caa 979  
 His Pro Leu Phe Ala Leu Gln Pro His Pro Leu Thr Val Ile Asp Gln  
 280 285 290  
 aat gta gaa caa cta gcc caa cga gca gtg tct atc ctc acc gaa tta 1027  
 Asn Val Glu Gln Leu Ala Gln Arg Ala Val Ser Ile Leu Thr Glu Leu  
 295 300 305  
 att gca ggc acg gta cct agc gtg acg aaa act acg atc ccc act gcc 1075  
 Ile Ala Gly Thr Val Pro Ser Val Thr Lys Thr Thr Ile Pro Thr Ala  
 310 315 320 325  
 ctt att cat cgt gaa tca atc atc aac tcc act tta agg aag aag gat 1123  
 Leu Ile His Arg Glu Ser Ile Ile Asn Ser Thr Leu Arg Lys Lys Asp  
 330 335 340  
 gga ctc ccc aat gag taactcaacc ggtaccgaca ttg 1161  
 Gly Leu Pro Asn Glu  
 345

&lt;210&gt; 394

&lt;211&gt; 346

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 394

Met Ala Thr Glu Lys Phe Arg Pro Thr Leu Lys Asp Val Ala Arg Gln  
 1 5 10 15  
 Ala Gly Val Ser Ile Ala Thr Ala Ser Arg Ala Leu Ala Asp Asn Pro  
 20 25 30  
 Ala Val Ala Ala Ser Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp  
 35 40 45  
 Leu Gly Tyr Arg Ala Asn Ala Gln Ala Arg Ala Leu Arg Ser Ser Arg  
 50 55 60

Ser Asn Thr Ile Gly Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe  
 65 70 75 80  
 Ala Ala Met Val Thr Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu  
 85 90 95  
 Ala Thr Ile Ile Thr Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly  
 100 105 110  
 Ser Leu Glu Phe Leu Thr Ser His Gly Val Asp Gly Ile Ile Cys Val  
 115 120 125  
 Pro Asn Glu Glu Cys Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly  
 130 135 140  
 Met Pro Val Val Leu Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile  
 145 150 155 160  
 Pro Thr Ala Thr Ser Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu  
 165 170 175  
 Leu Leu Ala His Asn Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro  
 180 185 190  
 Met Asp Thr Ser Thr Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala  
 195 200 205  
 Cys Ala Asn Ser Lys Ile Gly Glu Gln Leu Val Phe Leu Gly Gly Tyr  
 210 215 220  
 Glu Gln Ser Val Gly Phe Glu Gly Ala Thr Lys Leu Leu Asp Gln Gly  
 225 230 235 240  
 Ala Lys Thr Leu Phe Ala Gly Asp Ser Met Met Thr Ile Gly Val Ile  
 245 250 255  
 Glu Ala Cys His Lys Ala Gly Leu Val Ile Gly Lys Asp Val Ser Val  
 260 265 270  
 Ile Gly Phe Asp Thr His Pro Leu Phe Ala Leu Gln Pro His Pro Leu  
 275 280 285  
 Thr Val Ile Asp Gln Asn Val Glu Gln Leu Ala Gln Arg Ala Val Ser  
 290 295 300  
 Ile Leu Thr Glu Leu Ile Ala Gly Thr Val Pro Ser Val Thr Lys Thr  
 305 310 315 320  
 Thr Ile Pro Thr Ala Leu Ile His Arg Glu Ser Ile Ile Asn Ser Thr  
 325 330 335  
 Leu Arg Lys Lys Asp Gly Leu Pro Asn Glu  
 340 345

&lt;210&gt; 395

&lt;211&gt; 483

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(460)

&lt;223&gt; RXA02551

&lt;400&gt; 395

gctgcacaaa ttccgcgaaa gggatcacc atcgacatca cagatgaaga ccgtgagatc 60

ttaaaaaac accgtcgatt tcatttcctt ctctattac	atg tcc gta tgt gaa	115
	Met Ser Val Cys Glu	
	1 5	

gcc cac aac ccc gaa aac tac tca acc ggt ggc ggt aac atc atc ggc	163
Ala His Asn Pro Glu Asn Tyr Ser Thr Gly Gly Gly Asn Ile Ile Gly	
10 15 20	

gga gtg gtc agc ccc act ctc gcg gct tcc gaa tgg ggt tgg caa gtt	211
Gly Val Val Ser Pro Thr Leu Ala Ala Ser Glu Trp Gly Trp Gln Val	
25 30 35	

gat ccc ctc ggt ttg cgc atc gtc ctg aac aac tac tgg gag cgc tgg	259
Asp Pro Leu Gly Leu Arg Ile Val Leu Asn Asn Tyr Trp Glu Arg Trp	
40 45 50	

cag aag cca ctg ttc atc gtc gaa aac gga cta gga gca aag gac gtg	307
Gln Lys Pro Leu Phe Ile Val Glu Asn Gly Leu Gly Ala Lys Asp Val	
55 60 65	

ctt atc gac gga ccc tcc ggc cca aca gta aac gat gac tac cgc atc	355
Leu Ile Asp Gly Pro Ser Gly Pro Thr Val Asn Asp Asp Tyr Arg Ile	
70 75 80 85	

aaa tac ctc gac gac ggc ggc tca gga atc ttg aag cgc tac aag aag	403
Lys Tyr Leu Asp Asp Gly Gly Ser Gly Ile Leu Lys Arg Tyr Lys Lys	
90 95 100	

aag tcc ttt gat tgg tgc cgc gac atc atc gcc acc aat ggc gaa agc	451
Lys Ser Phe Asp Trp Cys Arg Asp Ile Ile Ala Thr Asn Gly Glu Ser	
105 110 115	

ctg gaa tcc taagaaataa aggtaggtgt cac	483
Leu Glu Ser	
120	

&lt;210&gt; 396

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 396

Met Ser Val Cys Glu Ala His Asn Pro Glu Asn Tyr Ser Thr Gly Gly	
1 5 10 15	

Gly Asn Ile Ile Gly Gly Val Val Ser Pro Thr Leu Ala Ala Ser Glu	
20 25 30	

Trp Gly Trp Gln Val Asp Pro Leu Gly Leu Arg Ile Val Leu Asn Asn	
35 40 45	

Tyr Trp Glu Arg Trp Gln Lys Pro Leu Phe Ile Val Glu Asn Gly Leu	
---	--

50	55	60	
Gly Ala Lys Asp Val Leu Ile Asp Gly Pro Ser Gly Pro Thr Val Asn 65 70 75 80			
Asp Asp Tyr Arg Ile Lys Tyr Leu Asp Asp Gly Gly Ser Gly Ile Leu 85 90 95			
Lys Arg Tyr Lys Lys Lys Ser Phe Asp Trp Cys Arg Asp Ile Ile Ala 100 105 110			
Thr Asn Gly Glu Ser Leu Glu Ser 115 120			
<210> 397			
<211> 795			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(772)			
<223> RXA01325			
<400> 397			
gcgcagcgcgt cggacgatta cgaacttcag gagaactcgg ggtcattcgt tgcattctac	60		
cctggaaatt ttccacact aagtcaggtc taagtagggg atg gat atg acg att	115		
	Met Asp Met Thr Ile		
	1 5		
tcc cgc tcc acc atg gcc caa atc ctt gac tac acc ctc ctc gga cca	163		
Ser Arg Ser Thr Met Ala Gln Ile Leu Asp Tyr Thr Leu Leu Gly Pro			
	10 15 20		
gaa gta acc aac tcc gaa ctg gcc gca ttt ata gat tcc gca att gag	211		
Glu Val Thr Asn Ser Glu Leu Ala Ala Phe Ile Asp Ser Ala Ile Glu			
	25 30 35		
ctg gga gtc ggc acg atc tgt gtc ccc aac agc atg gtc aac cta act	259		
Leu Gly Val Gly Thr Ile Cys Val Pro Asn Ser Met Val Asn Leu Thr			
	40 45 50		
gca aaa gcc caa gaa gct gga att cga gtg gcc acc gtc gca gga ttc	307		
Ala Lys Ala Ala Gln Glu Ala Gly Ile Arg Val Ala Thr Val Ala Gly Phe			
	55 60 65		
ccg cac ggc aaa acc ccc gcg ttg gtg aaa gcc gcc gaa gcg cgc ctt	355		
Pro His Gly Lys Thr Pro Ala Leu Val Lys Ala Ala Glu Ala Arg Leu			
	70 75 80 85		
gcc gta cag tcc gga gct tcc gaa gta gat gtt gtt ttg gat att gcg	403		
Ala Val Gln Ser Gly Ala Ser Glu Val Asp Val Val Leu Asp Ile Ala			
	90 95 100		
gta gtg aaa gag gga gat gcc aat agg ttg ctg cag gaa att gtg gca	451		
Val Val Lys Glu Gly Asp Ala Asn Arg Leu Leu Gln Glu Ile Val Ala			
	105 110 115		
atc agg gag gct gtt cca tct cct gtg qtg ctg aaa ttc atc ctc gaa	499		

Ile Arg Glu Ala Val Pro Ser Pro Val Val Leu Lys Phe Ile Leu Glu  
 120 125 130

aca gct gtt gtg agt gat gaa gca att gtg act gca gtg aat gcg ttg 547  
 Thr Ala Val Val Ser Asp Glu Ala Ile Val Thr Ala Val Asn Ala Leu  
 135 140 145

att gct gct ggt gct gac ttc gct aaa act tcc acg gga ttc cac cca 595  
 Ile Ala Ala Gly Ala Asp Phe Ala Lys Thr Ser Thr Gly Phe His Pro  
 150 155 160 165

gcg gga ggg gca act gtt gag gct gtt cgg gtg atg gct tcg gct tct 643  
 Ala Gly Gly Ala Thr Val Glu Ala Val Arg Val Met Ala Ser Ala Ser  
 170 175 180

cgg gga agg gtt gga att aag gct gcc ggt ggg gtg aaa act tgg gaa 691  
 Arg Gly Arg Val Gly Ile Lys Ala Ala Gly Gly Val Lys Thr Trp Glu  
 185 190 195

gat gcg gtg gcg ttt gtt gaa gca ggg gct act cgc att gga act tct 739  
 Asp Ala Val Ala Phe Val Glu Ala Gly Ala Thr Arg Ile Gly Thr Ser  
 200 205 210

aat gcg gga gcc att ttg gag ggt gcg ccg gag tagtttgccg ttctaatacgg 792  
 Asn Ala Gly Ala Ile Leu Glu Gly Ala Pro Glu  
 215 220

gac 795

&lt;210&gt; 398

&lt;211&gt; 224

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 398

Met Asp Met Thr Ile Ser Arg Ser Thr Met Ala Gln Ile Leu Asp Tyr  
 1 5 10 15

Thr Leu Leu Gly Pro Glu Val Thr Asn Ser Glu Leu Ala Ala Phe Ile  
 20 25 30

Asp Ser Ala Ile Glu Leu Gly Val Gly Thr Ile Cys Val Pro Asn Ser  
 35 40 45

Met Val Asn Leu Thr Ala Lys Ala Gln Glu Ala Gly Ile Arg Val Ala  
 50 55 60

Thr Val Ala Gly Phe Pro His Gly Lys Thr Pro Ala Leu Val Lys Ala  
 65 70 75 80

Ala Glu Ala Arg Leu Ala Val Gln Ser Gly Ala Ser Glu Val Asp Val  
 85 90 95

Val Leu Asp Ile Ala Val Val Lys Glu Gly Asp Ala Asn Arg Leu Leu  
 100 105 110

Gln Glu Ile Val Ala Ile Arg Glu Ala Val Pro Ser Pro Val Val Leu  
 115 120 125

Lys Phe Ile Leu Glu Thr Ala Val Val Ser Asp Glu Ala Ile Val Thr

130 135 140

Ala Val Asn Ala Leu Ile Ala Ala Gly Ala Asp Phe Ala Lys Thr Ser  
 145 150 155 160

Thr Gly Phe His Pro Ala Gly Gly Ala Thr Val Glu Ala Val Arg Val  
 165 170 175

Met Ala Ser Ala Ser Arg Gly Arg Val Gly Ile Lys Ala Ala Gly Gly  
 180 185 190

Val Lys Thr Trp Glu Asp Ala Val Ala Phe Val Glu Ala Gly Ala Thr  
 195 200 205

Arg Ile Gly Thr Ser Asn Ala Gly Ala Ile Leu Glu Gly Ala Pro Glu  
 210 215 220

<210> 399  
 <211> 684  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(661)  
 <223> RXA00195

<400> 399  
 tcgcagtcacat catgcaggca taacctgaaa cccatccggtt tggattgccc caaatgggtg 60

tagtgggtgc gtttacccaa caagtgaag aatgggagtc gtg act aaa aag atc 115  
 Val Thr Lys Lys Ile  
 1 5

ctt att ttg gga agc act ggt tcg att gga act cag gcg ctg gac gtt 163  
 Leu Ile Leu Gly Ser Thr Gly Ser Ile Gly Thr Gln Ala Leu Asp Val  
 10 15 20

att gct gat aat tca gac aag ttt gag gtg gtg ggt atc gct gcg ggc 211  
 Ile Ala Asp Asn Ser Asp Lys Phe Glu Val Val Gly Ile Ala Ala Gly  
 25 30 35

ggt tct cag cca gac ctc gtt att tcg cag gcg cag cag ttg ggg ctg 259  
 Gly Ser Gln Pro Asp Leu Val Ile Ser Gln Ala Gln Gln Leu Gly Leu  
 40 45 50

gct gca gac aag gtt gcg gtt gct gat gca cag gct gcc gca gta att 307  
 Ala Ala Asp Lys Val Ala Val Ala Asp Ala Gln Ala Ala Ala Val Ile  
 55 60 65

tcg aag gct ctc ggc ggc gag atc atc tct gga acc gat gct gcg aag 355  
 Ser Lys Ala Leu Gly Gly Glu Ile Ile Ser Gly Thr Asp Ala Ala Lys  
 70 75 80 85

att ctg gtg gaa acc aca aag gcc gac act gtg ctt aat gct ctg gtt 403  
 Ile Leu Val Glu Thr Thr Lys Ala Asp Thr Val Leu Asn Ala Leu Val  
 90 95 100

ggt tct ttg ggg ctt gcg gca acg ctg gcc act ctg gaa tct ggt gcg 451  
 Gly Ser Leu Gly Leu Ala Ala Thr Leu Ala Thr Leu Glu Ser Gly Ala  
 105 110 115  
 cat ctt gcc ttg gct aac aaa gaa tcg ctg gtt gcc ggt ggt gag ttt 499  
 His Leu Ala Leu Ala Asn Lys Glu Ser Leu Val Ala Gly Gly Glu Phe  
 120 125 130  
 gtt acc tca aag gca aag ctg ggg cag atc att ccg gtc gat tcg gag 547  
 Val Thr Ser Lys Ala Lys Leu Gly Gln Ile Ile Pro Val Asp Ser Glu  
 135 140 145  
 cac tct gcc atg gcg cag tgt ttg cgt tcg ggt act cgt gat gag gtt 595  
 His Ser Ala Met Ala Gln Cys Leu Arg Ser Gly Thr Arg Asp Glu Val  
 150 155 160 165  
 gcg cgg att gtg ctg aca gct tcg ggc gga cct ttc agg gct gga cca 643  
 Ala Arg Ile Val Leu Thr Ala Ser Gly Gly Pro Phe Arg Ala Gly Pro  
 170 175 180  
 ggg aga aga tgt ggg agg tgactcccgga gcaggcagca gcg 684  
 Gly Arg Arg Cys Gly Arg  
 185

&lt;210&gt; 400

&lt;211&gt; 187

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 400

Val Thr Lys Lys Ile Leu Ile Leu Gly Ser Thr Gly Ser Ile Gly Thr  
 1 5 10 15  
 Gln Ala Leu Asp Val Ile Ala Asp Asn Ser Asp Lys Phe Glu Val Val  
 20 25 30  
 Gly Ile Ala Ala Gly Gly Ser Gln Pro Asp Leu Val Ile Ser Gln Ala  
 35 40 45  
 Gln Gln Leu Gly Leu Ala Ala Asp Lys Val Ala Val Ala Asp Ala Gln  
 50 55 60  
 Ala Ala Ala Val Ile Ser Lys Ala Leu Gly Gly Glu Ile Ile Ser Gly  
 65 70 75 80  
 Thr Asp Ala Ala Lys Ile Leu Val Glu Thr Thr Lys Ala Asp Thr Val  
 85 90 95  
 Leu Asn Ala Leu Val Gly Ser Leu Gly Leu Ala Ala Thr Leu Ala Thr  
 100 105 110  
 Leu Glu Ser Gly Ala His Leu Ala Leu Ala Asn Lys Glu Ser Leu Val  
 115 120 125  
 Ala Gly Gly Glu Phe Val Thr Ser Lys Ala Lys Leu Gly Gln Ile Ile  
 130 135 140  
 Pro Val Asp Ser Glu His Ser Ala Met Ala Gln Cys Leu Arg Ser Gly  
 145 150 155 160

<400> 401																
ctgccatggc	gcagtgtttg	cgttcgggta	ctcgtgatga	ggttgcgcg	attgtgctga											60
cagcttcggg	cggacctttc	agggctggac	cagggagaag	atg	tgg	gag	gtg	act								115
				Met	Trp	Glu	Val	Thr								
				1				5								
ccc	gag	cag	gca	gca	gcg	cac	cca	acg	tgg	gcg	atg	ggg	cag	atg	aac	163
Pro	Glu	Gln	Ala	Ala	Ala	His	Pro	Thr	Trp	Ala	Met	Gly	Gln	Met	Asn	
				10					15					20		
acg	ttg	aac	tcc	gcc	acc	ctt	att	aat	aaa	ggc	ctc	gaa	ctc	atc	gag	211
Thr	Leu	Asn	Ser	Ala	Thr	Leu	Ile	Asn	Lys	Gly	Leu	Glu	Leu	Ile	Glu	
			25					30					35			
gcg	acc	ctg	ctg	ttt	gaa	acg	gat	gcg	gat	ctc	att	gat	gtg	acg	gtg	259
Ala	Thr	Leu	Leu	Phe	Glu	Thr	Asp	Ala	Asp	Leu	Ile	Asp	Val	Thr	Val	
		40					45					50				
cat	ccg	cag	tcg	atc	atc	cac	tcc	atg	atc	acg	ttt	acg	gat	ggc	gcg	307
His	Pro	Gln	Ser	Ile	Ile	His	Ser	Met	Ile	Thr	Phe	Thr	Asp	Gly	Ala	
	55					60					65					
acc	atc	gcg	cag	gcg	tcg	cca	cca	tcg	atg	aaa	ctg	ccg	atc	gcg	ttg	355
Thr	Ile	Ala	Gln	Ala	Ser	Pro	Pro	Ser	Met	Lys	Leu	Pro	Ile	Ala	Leu	
70					75					80					85	
gcg	ctt	gat	tgg	cca	cat	cgg	gtg	ccg	aag	gct	cag	ccg	gcg	ctg	gat	403
Ala	Leu	Asp	Trp	Pro	His	Arg	Val	Pro	Lys	Ala	Gln	Pro	Ala	Leu	Asp	
				90					95					100		
ttc	acc	gct	gct	cat	acc	tgg	gct	ttt	gag	ccg	gtg	gat	gat	gcc	gca	451
Phe	Thr	Ala	Ala	His	Thr	Trp	Ala	Phe	Glu	Pro	Val	Asp	Asp	Ala	Ala	
			105					110					115			
ttc	cct	gcg	gtg	cag	ctg	gct	agg	cac	gtc	gca	aag	caa	aaa	ggc	acg	499
Phe	Pro	Ala	Val	Gln	Leu	Ala	Arg	His	Val	Ala	Lys	Gln	Lys	Gly	Thr	
		120					125					130				
tac	ccc	gcg	gtg	tat	aac	gcc	gcc	aac	gag	gag	gcg	gct	gag	gcg	ttt	547
Tyr	Pro	Ala	Val	Tyr	Asn	Ala	Ala	Asn	Glu	Glu	Ala	Ala	Glu	Ala	Phe	
	135					140					145					

ttg cgc ggg cga atc aag ttt ccg cag atc gtg gac gtg gtg gac gag 595  
 Leu Arg Gly Arg Ile Lys Phe Pro Gln Ile Val Asp Val Val Asp Glu  
 150 155 160 165  
  
 gtc ctc caa gga gct tct cag ttt gct ggt gta gca tca cac gtc gat 643  
 Val Leu Gln Gly Ala Ser Gln Phe Ala Gly Val Ala Ser His Val Asp  
 170 175 180  
  
 gat att ttg gca acc gaa tct gag gca cgc gcg cgt gcg aat gct ttg 691  
 Asp Ile Leu Ala Thr Glu Ser Glu Ala Arg Ala Arg Ala Asn Ala Leu  
 185 190 195  
  
 atc aac cgg ttg gca acc aac ttg taagctaagg agcttccgcc tcg 738  
 Ile Asn Arg Leu Ala Thr Asn Leu  
 200 205

&lt;210&gt; 402

&lt;211&gt; 205

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 402

Met Trp Glu Val Thr Pro Glu Gln Ala Ala Ala His Pro Thr Trp Ala  
 1 5 10 15  
  
 Met Gly Gln Met Asn Thr Leu Asn Ser Ala Thr Leu Ile Asn Lys Gly  
 20 25 30  
  
 Leu Glu Leu Ile Glu Ala Thr Leu Leu Phe Glu Thr Asp Ala Asp Leu  
 35 40 45  
  
 Ile Asp Val Thr Val His Pro Gln Ser Ile Ile His Ser Met Ile Thr  
 50 55 60  
  
 Phe Thr Asp Gly Ala Thr Ile Ala Gln Ala Ser Pro Pro Ser Met Lys  
 65 70 75 80  
  
 Leu Pro Ile Ala Leu Ala Leu Asp Trp Pro His Arg Val Pro Lys Ala  
 85 90 95  
  
 Gln Pro Ala Leu Asp Phe Thr Ala Ala His Thr Trp Ala Phe Glu Pro  
 100 105 110  
  
 Val Asp Asp Ala Ala Phe Pro Ala Val Gln Leu Ala Arg His Val Ala  
 115 120 125  
  
 Lys Gln Lys Gly Thr Tyr Pro Ala Val Tyr Asn Ala Ala Asn Glu Glu  
 130 135 140  
  
 Ala Ala Glu Ala Phe Leu Arg Gly Arg Ile Lys Phe Pro Gln Ile Val  
 145 150 155 160  
  
 Asp Val Val Asp Glu Val Leu Gln Gly Ala Ser Gln Phe Ala Gly Val  
 165 170 175  
  
 Ala Ser His Val Asp Asp Ile Leu Ala Thr Glu Ser Glu Ala Arg Ala  
 180 185 190  
  
 Arg Ala Asn Ala Leu Ile Asn Arg Leu Ala Thr Asn Leu  
 195 200 205





170										175										180									
cca	acc	att	ggc	gga	ttt	gcg	gaa	aac	ctt	gcg	ggc	ctt	cgc	atg	cag					691									
Pro	Thr	Ile	Gly	Gly	Phe	Ala	Glu	Asn	Leu	Ala	Gly	Leu	Arg	Met	Gln														
			185					190					195																
cct	ttc	tat	gat	cgc	ttc	atg	gaa	aag	ggc	aag	acg	tcc	ctg	aaa	tcc					739									
Pro	Phe	Tyr	Asp	Arg	Phe	Met	Glu	Lys	Gly	Lys	Thr	Ser	Leu	Lys	Ser														
		200					205					210																	
atg	ggg	tgg	gta	ggg	gag	cgt	act	ttt	gaa	gcg	ctc	cat	gca	ttt	aaa					787									
Met	Gly	Trp	Val	Gly	Glu	Arg	Thr	Phe	Glu	Ala	Leu	His	Ala	Phe	Lys														
	215					220					225																		
gaa	ggg	gtg	aag	agc	acc	gtc	att	ccc	acc	gaa	atg	ttc	cct	gaa	ctg					835									
Glu	Gly	Val	Lys	Ser	Thr	Val	Ile	Pro	Thr	Glu	Met	Phe	Pro	Glu	Leu														
	230				235					240					245														
ggc	atg	aaa	tac	gtg	ggg	ccg	gtt	gat	gga	cat	aac	caa	aaa	gct	gtc					883									
Gly	Met	Lys	Tyr	Val	Gly	Pro	Val	Asp	Gly	His	Asn	Gln	Lys	Ala	Val														
			250					255					260																
gac	aat	gcg	ctg	aaa	tac	gct	cat	gat	tat	gat	ggc	ccc	atc	atc	gtg					931									
Asp	Asn	Ala	Leu	Lys	Tyr	Ala	His	Asp	Tyr	Asp	Gly	Pro	Ile	Ile	Val														
		265					270					275																	
cac	atg	gtc	acc	gaa	aag	ggg	cgt	ggg	tac	gcg	cct	gct	gag	cag	gat					979									
His	Met	Val	Thr	Glu	Lys	Gly	Arg	Gly	Tyr	Ala	Pro	Ala	Glu	Gln	Asp														
		280					285				290																		
ttg	gac	gaa	ttg	atg	cac	tcc	acg	ggc	gtc	atc	gat	ccg	ctc	aca	gga					1027									
Leu	Asp	Glu	Leu	Met	His	Ser	Thr	Gly	Val	Ile	Asp	Pro	Leu	Thr	Gly														
	295					300					305																		
gct	cct	aaa	tct	gca	tca	aag	ccc	ggg	tgg	acc	tct	gtg	ttc	agc	gat					1075									
Ala	Pro	Lys	Ser	Ala	Ser	Lys	Pro	Gly	Trp	Thr	Ser	Val	Phe	Ser	Asp														
	310				315				320					325															
gag	ctg	gtc	aag	att	ggg	gcg	cag	aat	gaa	aac	gtt	gtt	gcc	atc	acc					1123									
Glu	Leu	Val	Lys	Ile	Gly	Ala	Gln	Asn	Glu	Asn	Val	Val	Ala	Ile	Thr														
			330					335					340																
gcc	gcg	atg	gca	ggg	cct	acc	ggg	ctg	tcc	aag	ttc	gaa	gcc	aat	ttc					1171									
Ala	Ala	Met	Ala	Gly	Pro	Thr	Gly	Leu	Ser	Lys	Phe	Glu	Ala	Asn	Phe														
		345					350					355																	
ccc	aac	cga	ttc	ttt	gat	gtc	ggc	att	gct	gag	cag	cac	gcg	gta	act					1219									
Pro	Asn	Arg	Phe	Phe	Asp	Val	Gly	Ile	Ala	Glu	Gln	His	Ala	Val	Thr														
		360				365					370																		
tct	gcc	gca	ggc	ctc	gca	ttg	ggg	gga	aaa	cac	cct	gtg	gtg	gct	att					1267									
Ser	Ala	Ala	Gly	Leu	Ala	Leu	Gly	Gly	Lys	His	Pro	Val	Val	Ala	Ile														
	375					380					385																		
tac	tcc	acg	ttc	ttg	aac	cgc	gct	ttt	gat	cag	ctg	ctc	atg	gat	gtg					1315									
Tyr	Ser	Thr	Phe	Leu	Asn	Arg	Ala	Phe	Asp	Gln	Leu	Leu	Met	Asp	Val														
	390				395				400				405																
ggc	atg	ctc	aac	cag	cct	gtt	act	ttg	gtg	ctt	gat	cgc	tca	ggg	gtc					1363									
Gly	Met	Leu	Asn	Gln	Pro	Val	Thr	Leu	Val	Leu	Asp	Arg	Ser	Gly	Val														
			410					415					420																

acg ggt tcg gat gga gcg agc cac aat ggc gtc tgg gat atg gcg ctg 1411  
 Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp Met Ala Leu  
 425 430 435

acc tcg atc gtt cca ggc gtg cag gtg gcg gca cca cgt gat gag gat 1459  
 Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg Asp Glu Asp  
 440 445 450

tcc ttg cgt gag ctg ctc aat gag gct att tcc atc gat gat ggc ccc 1507  
 Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp Asp Gly Pro  
 455 460 465

aca gtt gtg cgt ttc ccc aag ggc gac ttg cca act cca att gtt gct 1555  
 Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro Ile Val Ala  
 470 475 480 485

atc gac acc ttg gaa gac ggc gtg gat gtc ctc gca tat gaa gac gcc 1603  
 Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr Glu Asp Ala  
 490 495 500

act gac gtt gaa tca acc gac gat gcg cca tca gtt ctc atc att gcg 1651  
 Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu Ile Ile Ala  
 505 510 515

gta ggc gag cgc gca act gtt gca ctt gac gtt gct tcc agg att aaa 1699  
 Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser Arg Ile Lys  
 520 525 530

cag cac ggc gtg aac gtc acg gtt gtt gac ccc cgc tgg att gtc ccc 1747  
 Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp Ile Val Pro  
 535 540 545

atc ccg cag tcc ttg gtc gcg ctg tct gat gat cat gac ctc gtg atc 1795  
 Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp Leu Val Ile  
 550 555 560 565

acc atc gaa gac ggc gtc atc cac ggc ggc gtg gga tcc ttg ctc tct 1843  
 Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser Leu Leu Ser  
 570 575 580

gat gcg ctt aac gcc tct gag gtg gat acc cct cgc cga caa atc gcc 1891  
 Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg Gln Ile Ala  
 585 590 595

gtg ccc cag aag tac ctg gat cac gcg tcc cgc aat gaa gtg ctc gcc 1939  
 Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu Val Leu Ala  
 600 605 610

gat tat ggc ctc gac gcc gac ggc att gaa acc act gtt gtt gga tgg 1987  
 Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val Val Gly Trp  
 615 620 625

ctg gat tcc ctg ttc ggg gaa taaaaccctg cttatcgacg ccg 2031  
 Leu Asp Ser Leu Phe Gly Glu  
 630 635

&lt;210&gt; 404

&lt;211&gt; 636

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 404

```

Met Gly Ile Leu Asn Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu
 1           5           10           15

Asn Asp Glu Asp Leu Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu
      20           25           30

Val Asp Lys Val Ala Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly
      35           40           45

Val Val Glu Leu Thr Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln
      50           55           60

Asp Pro Ile Ile Phe Asp Thr Ser His Gln Ser Tyr Val His Lys Ile
      65           70           75           80

Leu Thr Gly Arg Ala Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly
      85           90           95

Leu Ser Gly Tyr Thr Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu
      100          105          110

Ser Ser His Ala Ser Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys
      115          120          125

Ala Lys Gln Leu Asp Gly Asp Thr Thr His Ser Val Val Ala Val Val
      130          135          140

Gly Asp Gly Ala Leu Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn
      145          150          155          160

Ile Ala Ala Gly Lys Asp Arg Lys Val Val Val Val Asn Asp Asn
      165          170          175

Gly Arg Ser Tyr Ser Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala
      180          185          190

Gly Leu Arg Met Gln Pro Phe Tyr Asp Arg Phe Met Glu Lys Gly Lys
      195          200          205

Thr Ser Leu Lys Ser Met Gly Trp Val Gly Glu Arg Thr Phe Glu Ala
      210          215          220

Leu His Ala Phe Lys Glu Gly Val Lys Ser Thr Val Ile Pro Thr Glu
      225          230          235          240

Met Phe Pro Glu Leu Gly Met Lys Tyr Val Gly Pro Val Asp Gly His
      245          250          255

Asn Gln Lys Ala Val Asp Asn Ala Leu Lys Tyr Ala His Asp Tyr Asp
      260          265          270

Gly Pro Ile Ile Val His Met Val Thr Glu Lys Gly Arg Gly Tyr Ala
      275          280          285

Pro Ala Glu Gln Asp Leu Asp Glu Leu Met His Ser Thr Gly Val Ile
      290          295          300

Asp Pro Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr

```

305		310		315		320
Ser Val Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn						
		325		330		335
Val Val Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys						
		340		345		350
Phe Glu Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu						
		355		360		365
Gln His Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His						
		370		375		380
Pro Val Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln						
		385		390		395
Leu Leu Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu						
		405		410		415
Asp Arg Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val						
		420		425		430
Trp Asp Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala						
		435		440		445
Pro Arg Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser						
		450		455		460
Ile Asp Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro						
		465		470		475
Thr Pro Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu						
		485		490		495
Ala Tyr Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser						
		500		505		510
Val Leu Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val						
		515		520		525
Ala Ser Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro						
		530		535		540
Arg Trp Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp						
		545		550		555
His Asp Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val						
		565		570		575
Gly Ser Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro						
		580		585		590
Arg Arg Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg						
		595		600		605
Asn Glu Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr						
		610		615		620
Thr Val Val Gly Trp Leu Asp Ser Leu Phe Gly Glu						
		625		630		635

<210> 405  
 <211> 1061  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1038)  
 <223> FRXA01562

<400> 405  
 gag cag gat ttg gac gaa ttg atg cac tcc acg ggc gtc atc gat ccg 48  
 Glu Gln Asp Leu Asp Glu Leu Met His Ser Thr Gly Val Ile Asp Pro  
 1 5 10 15  
 ctc aca gga gct cct aaa tct gca tca aag ccc ggt tgg acc tct gtg 96  
 Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr Ser Val  
 20 25 30  
 ttc agc gat gag ctg gtc aag att ggt gcg cag aat gaa aac gtt gtt 144  
 Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val  
 35 40 45  
 gcc atc acc gcc gcg atg gca ggt cct acc ggt ctg tcc aag ttc gaa 192  
 Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu  
 50 55 60  
 gcc aat ttc ccc aac cga ttc ttt gat gtc ggc att gct gag cag cac 240  
 Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His  
 65 70 75 80  
 gcg gta act tct gcc gca ggc ctc gca ttg ggt gga aaa cac cct gtg 288  
 Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val  
 85 90 95  
 gtg gct att tac tcc acg ttc ttg aac cgc gct ttt gat cag ctg ctc 336  
 Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu  
 100 105 110  
 atg gat gtg ggc atg ctc aac cag cct gtt act ttg gtg ctt gat cgc 384  
 Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg  
 115 120 125  
 tca ggt gtc acg ggt tcg gat gga gcg agc cac aat ggc gtc tgg gat 432  
 Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp  
 130 135 140  
 atg gcg ctg acc tcg atc gtt cca ggc gtg cag gtg gcg gca cca cgt 480  
 Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg  
 145 150 155 160  
 gat gag gat tcc ttg cgt gag ctg ctc aat gag gct att tcc atc gat 528  
 Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp  
 165 170 175  
 gat ggc ccc aca gtt gtg cgt ttc ccc aag ggc gac ttg cca act cca 576  
 Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro  
 180 185 190

```

att gtt gct atc gac acc ttg gaa gac ggc gtg gat gtc ctc gca tat 624
Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr
    195                200                205

gaa gac gcc act gac gtt gaa tca acc gac gat gcg cca tca gtt ctc 672
Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu
    210                215                220

atc att gcg gta ggc gag cgc gca act gtt gca ctt gac gtt gct tcc 720
Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser
    225                230                235                240

agg att aaa cag cac ggc gtg aac gtc acg gtt gtt gac ccc cgc tgg 768
Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp
    245                250                255

att gtc ccc atc ccg cag tcc ttg gtc gcg ctg tct gat gat cat gac 816
Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp
    260                265                270

ctc gtg atc acc atc gaa gac ggc gtc atc cac ggc ggc gtg gga tcc 864
Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser
    275                280                285

ttg ctc tct gat gcg ctt aac gcc tct gag gtg gat acc cct cgc cga 912
Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg
    290                295                300

caa atc gcc gtg ccc cag aag tac ctg gat cac gcg tcc cgc aat gaa 960
Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu
    305                310                315                320

gtg ctc gcc gat tat ggc ctc gac gcc gac ggc att gaa acc act gtt 1008
Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val
    325                330                335

gtt gga tgg ctg gat tcc ctg ttc ggg gaa taaaaccctg cttatcgacg 1058
Val Gly Trp Leu Asp Ser Leu Phe Gly Glu
    340                345

ccg 1061

```

&lt;210&gt; 406

&lt;211&gt; 346

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 406

```

Glu Gln Asp Leu Asp Glu Leu Met His Ser Thr Gly Val Ile Asp Pro
 1                5                10                15

```

```

Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr Ser Val
    20                25                30

```

```

Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val
    35                40                45

```

```

Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu
    50                55                60

```

Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His  
 65 70 75 80  
 Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val  
 85 90 95  
 Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu  
 100 105 110  
 Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg  
 115 120 125  
 Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp  
 130 135 140  
 Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg  
 145 150 155 160  
 Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp  
 165 170 175  
 Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro  
 180 185 190  
 Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr  
 195 200 205  
 Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu  
 210 215 220  
 Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser  
 225 230 235 240  
 Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp  
 245 250 255  
 Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp  
 260 265 270  
 Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser  
 275 280 285  
 Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg  
 290 295 300  
 Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu  
 305 310 315 320  
 Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val  
 325 330 335  
 Val Gly Trp Leu Asp Ser Leu Phe Gly Glu  
 340 345

&lt;210&gt; 407

&lt;211&gt; 703

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(703)

&lt;223&gt; FRXA01705

&lt;400&gt; 407

gcaggtgcac atttgttttg tcacctgcac aaaagtgtcg ccagcccgat acttgtacaa 60

ccgtccgcat ccgagaagca aaggtgtctg actcgcgcca atg gga att ctg aac 115  
 Met Gly Ile Leu Asn  
 1 5

agt att tca aca cct gct gac tta aag gcc ctt aat gat gag gat ttg 163  
 Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu Asn Asp Glu Asp Leu  
 10 15 20

gac gct ctt gcc aaa gaa atc cga act ttc ctg gtc gat aaa gtc gca 211  
 Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu Val Asp Lys Val Ala  
 25 30 35

gca act ggt ggc cac tta ggt cca aat ttg ggc gta gtg gaa tta acc 259  
 Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly Val Val Glu Leu Thr  
 40 45 50

atc ggt ctt cat cga gtt ttc gat tcg cct caa gac ccg atc atc ttt 307  
 Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln Asp Pro Ile Ile Phe  
 55 60 65

gat act tct cac cag tcc tat gtg cat aag atc ctg acg ggt cgc gct 355  
 Asp Thr Ser His Gln Ser Tyr Val His Lys Ile Leu Thr Gly Arg Ala  
 70 75 80 85

aaa gat ttt gat tct ttg cgt caa aaa gat ggc ctt tct ggt tac acc 403  
 Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly Leu Ser Gly Tyr Thr  
 90 95 100

tgc cgt gct gaa agt gag cac gat tgg act gag tct tcg cat gct tcg 451  
 Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu Ser Ser His Ala Ser  
 105 110 115

gcg gcc ttg tct tat gcg gat ggt ttg tct aaa gcc aag cag ttg gat 499  
 Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys Ala Lys Gln Leu Asp  
 120 125 130

ggc gat acc acg cat agt gtg gtt gct gtc gtt ggt gat ggc gct cta 547  
 Gly Asp Thr Thr His Ser Val Val Ala Val Val Gly Asp Gly Ala Leu  
 135 140 145

act ggc ggc atg tgt tgg gaa gca ctg aac aat att gct gct ggt aaa 595  
 Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn Ile Ala Ala Gly Lys  
 150 155 160 165

gac cgc aaa gtt gtt gtc gta gtc aat gac aat ggc cgg agt tat tct 643  
 Asp Arg Lys Val Val Val Val Val Asn Asp Asn Gly Arg Ser Tyr Ser  
 170 175 180

cca acc att ggc gga ttt gcg gaa aac ctt gcg ggc ctt cgc atg cag 691  
 Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala Gly Leu Arg Met Gln  
 185 190 195

cct ttc tat gat 703  
 Pro Phe Tyr Asp



200

&lt;210&gt; 408

&lt;211&gt; 201

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 408

Met Gly Ile Leu Asn Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu  
 1 5 10 15

Asn Asp Glu Asp Leu Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu  
 20 25 30

Val Asp Lys Val Ala Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly  
 35 40 45

Val Val Glu Leu Thr Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln  
 50 55 60

Asp Pro Ile Ile Phe Asp Thr Ser His Gln Ser Tyr Val His Lys Ile  
 65 70 75 80

Leu Thr Gly Arg Ala Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly  
 85 90 95

Leu Ser Gly Tyr Thr Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu  
 100 105 110

Ser Ser His Ala Ser Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys  
 115 120 125

Ala Lys Gln Leu Asp Gly Asp Thr Thr His Ser Val Val Ala Val Val  
 130 135 140

Gly Asp Gly Ala Leu Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn  
 145 150 155 160

Ile Ala Ala Gly Lys Asp Arg Lys Val Val Val Val Val Asn Asp Asn  
 165 170 175

Gly Arg Ser Tyr Ser Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala  
 180 185 190

Gly Leu Arg Met Gln Pro Phe Tyr Asp  
 195 200

&lt;210&gt; 409

&lt;211&gt; 2241

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2218)

&lt;223&gt; RXN00879

&lt;400&gt; 409

caccccaaag cccaatccaa aagatgtatt ttctaacaaa cttaccctca cgctacaaat 60

```

atgctgtgcc cacacgctat tagtggcata atgttggtgtt gtg act gct cgc aga 115
                               Val Thr Ala Arg Arg
                               1           5

ttt ttg aat gaa ctc gcc gat ctc tac ggc gta gca act tcc tac act 163
Phe Leu Asn Glu Leu Ala Asp Leu Tyr Gly Val Ala Thr Ser Tyr Thr
                10                15                20

gat tac aaa ggt gcc cat att gag gtc agc gat gac aca tta gtg aaa 211
Asp Tyr Lys Gly Ala His Ile Glu Val Ser Asp Asp Thr Leu Val Lys
                25                30                35

atc ctg cgt gct ctg ggt gtg aat tta gat aca agc aac ctc ccc aac 259
Ile Leu Arg Ala Leu Gly Val Asn Leu Asp Thr Ser Asn Leu Pro Asn
                40                45                50

gat gac gct atc caa cgc caa att gcc ctc ttc cat gat cga gag ttc 307
Asp Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe His Asp Arg Glu Phe
                55                60                65

act cgc cca ctg cct cca tcg gtg gtt gca gtt gaa ggt gat gaa cta 355
Thr Arg Pro Leu Pro Pro Ser Val Val Ala Val Glu Gly Asp Glu Leu
                70                75                80                85

gtt ttc ccg gtg cat gtg cac gac ggt tcc cct gca gat gtc cac atc 403
Val Phe Pro Val His Val His Asp Gly Ser Pro Ala Asp Val His Ile
                90                95                100

gaa ttg gaa gac ggc acg cag cgg gat gtt tct cag gtg gaa aac tgg 451
Glu Leu Glu Asp Gly Thr Gln Arg Asp Val Ser Gln Val Glu Asn Trp
                105                110                115

aca gcg cca cgg gaa att gat ggg att agg tgg ggc gag gca tcg ttt 499
Thr Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp Gly Glu Ala Ser Phe
                120                125                130

aag att cct ggt gat ctc ccc ttg ggt tgg cac aag ctt cac ctt aaa 547
Lys Ile Pro Gly Asp Leu Pro Leu Gly Trp His Lys Leu His Leu Lys
                135                140                145

tcc aat gaa cgc tca gct gag tgc ggt ttg atc atc acc ccg gct cgt 595
Ser Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile Ile Thr Pro Ala Arg
                150                155                160                165

ctg tct act gct gat aag tat ctt gat tcc cct cgc agt ggt gtc atg 643
Leu Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro Arg Ser Gly Val Met
                170                175                180

gcg cag atc tac tct gtg cgt tcc acg ttg tcg tgg ggc atg ggt gat 691
Ala Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser Trp Gly Met Gly Asp
                185                190                195

ttc aat gat tta gga aac ttg gca agt gtg gtt gcc cag gat gga gca 739
Phe Asn Asp Leu Gly Asn Leu Ala Ser Val Val Ala Gln Asp Gly Ala
                200                205                210

gac ttc ctg ctc atc aac ccc atg cac gct gca gag ccg ctg cct cct 787
Asp Phe Leu Leu Ile Asn Pro Met His Ala Ala Glu Pro Leu Pro Pro
                215                220                225

```

act gag gac tct cct tat ctg ccc aca acc agg cgc ttt atc aac ccg	835
Thr Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg Arg Phe Ile Asn Pro	
230 235 240 245	
atc tac att cgg gta gaa gat att ccg gag ttt aat cag ctt gag att	883
Ile Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe Asn Gln Leu Glu Ile	
250 255 260	
gat cta cgc gat gat atc gca gag atg gct gcg gaa ttc cgc gaa cgc	931
Asp Leu Arg Asp Asp Ile Ala Glu Met Ala Ala Glu Phe Arg Glu Arg	
265 270 275	
aat ctg acc tca gac atc att gag cgc aat gac gtc tac gct gca aag	979
Asn Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp Val Tyr Ala Ala Lys	
280 285 290	
ctt caa gtg ctg cgc gcc att ttt gaa atg cct cgt tcc agc gaa cgt	1027
Leu Gln Val Leu Arg Ala Ile Phe Glu Met Pro Arg Ser Ser Glu Arg	
295 300 305	
gaa gcc aac ttt gtc tcc ttc gtg caa cgg gaa ggc caa ggt ctt att	1075
Glu Ala Asn Phe Val Ser Phe Val Gln Arg Glu Gly Gln Gly Leu Ile	
310 315 320 325	
gat ttc gcc acc tgg tgc gcg gac cgc gaa act gca cag tct gaa tct	1123
Asp Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser	
330 335 340	
gtc cac gga act gag cca gac cgc gat gag ctg acc atg ttc tac atg	1171
Val His Gly Thr Glu Pro Asp Arg Asp Glu Leu Thr Met Phe Tyr Met	
345 350 355	
tgg ttg cag tgg cta tgt gat gag cag ctg gcg gca gct caa aag cgc	1219
Trp Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala Ala Gln Lys Arg	
360 365 370	
gct gtc gat gcc gga atg tcg atc ggc atc atg gca gac ctg gca gtt	1267
Ala Val Asp Ala Gly Met Ser Ile Gly Ile Met Ala Asp Leu Ala Val	
375 380 385	
ggg gtg cat cca ggt ggt gct gat gcc cag aac ctc agc cac gta ctt	1315
Gly Val His Pro Gly Gly Ala Asp Ala Gln Asn Leu Ser His Val Leu	
390 395 400 405	
gct ccg gat gcg tca gtg ggc gcc cca cca gat gga tac aac cag cag	1363
Ala Pro Asp Ala Ser Val Gly Ala Pro Pro Asp Gly Tyr Asn Gln Gln	
410 415 420	
ggc caa gac tgg tcc cag cca cca tgg cat cca gtg cgt ctt gca gag	1411
Gly Gln Asp Trp Ser Gln Pro Pro Trp His Pro Val Arg Leu Ala Glu	
425 430 435	
gaa ggc tac att ccg tgg cgt aat ctg ctg cgc act gtg ctg cgt cac	1459
Glu Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg Thr Val Leu Arg His	
440 445 450	
tcc ggc gga atc cgc gtg gac cac gtt ctt ggt ttg ttc agg ctc ttt	1507
Ser Gly Gly Ile Arg Val Asp His Val Leu Gly Leu Phe Arg Leu Phe	
455 460 465	
gtc atg cca cgc atg caa tcc cct gct acg ggc acc tat atc cgc ttc	1555

Val	Met	Pro	Arg	Met	Gln	Ser	Pro	Ala	Thr	Gly	Thr	Tyr	Ile	Arg	Phe	
470					475					480					485	
gac	cat	aat	gcg	ttg	gta	ggc	att	cta	gcc	cta	gaa	gca	gaa	ctc	gca	1603
Asp	His	Asn	Ala	Leu	Val	Gly	Ile	Leu	Ala	Leu	Glu	Ala	Glu	Leu	Ala	
				490					495					500		
ggc	gcc	gtt	gtc	att	ggg	gaa	gat	ctg	gga	acg	ttt	gag	cct	tgg	gta	1651
Gly	Ala	Val	Val	Ile	Gly	Glu	Asp	Leu	Gly	Thr	Phe	Glu	Pro	Trp	Val	
			505					510					515			
caa	gat	gca	ttg	gct	cag	cgt	ggc	atc	atg	ggc	acc	tcg	atc	cta	tgg	1699
Gln	Asp	Ala	Leu	Ala	Gln	Arg	Gly	Ile	Met	Gly	Thr	Ser	Ile	Leu	Trp	
		520					525					530				
ttc	gag	cat	tcc	cca	agc	cag	ccg	ggg	cct	cgc	cgc	cag	gaa	gag	tat	1747
Phe	Glu	His	Ser	Pro	Ser	Gln	Pro	Gly	Pro	Arg	Arg	Gln	Glu	Glu	Tyr	
	535					540					545					
cgt	ccg	ctg	gcc	ttg	acc	act	gtg	acc	act	cat	gat	ctc	cct	ccg	act	1795
Arg	Pro	Leu	Ala	Leu	Thr	Thr	Val	Thr	Thr	His	Asp	Leu	Pro	Pro	Thr	
550					555					560					565	
gct	ggg	tat	ttg	gag	ggc	gag	cac	att	gct	ctt	cgt	gag	cga	ttg	ggg	1843
Ala	Gly	Tyr	Leu	Glu	Gly	Glu	His	Ile	Ala	Leu	Arg	Glu	Arg	Leu	Gly	
				570					575					580		
gtg	ctc	aac	act	gat	cct	gct	gca	gaa	ctc	gct	gag	gat	ctg	cag	tgg	1891
Val	Leu	Asn	Thr	Asp	Pro	Ala	Ala	Glu	Leu	Ala	Glu	Asp	Leu	Gln	Trp	
			585					590					595			
caa	gcg	gag	atc	ctt	gat	gtc	gca	gca	tct	gcc	aac	gca	ttg	cca	gcc	1939
Gln	Ala	Glu	Ile	Leu	Asp	Val	Ala	Ala	Ser	Ala	Asn	Ala	Leu	Pro	Ala	
		600					605					610				
cgg	gaa	tac	gtg	gga	ctc	gaa	cgc	gat	cag	cgc	ggg	gag	ttg	gct	gag	1987
Arg	Glu	Tyr	Val	Gly	Leu	Glu	Arg	Asp	Gln	Arg	Gly	Glu	Leu	Ala	Glu	
	615					620					625					
ctg	ttg	gaa	ggc	ctg	cac	act	ttc	gtt	gcg	aaa	acc	cct	tca	gca	ctg	2035
Leu	Leu	Glu	Gly	Leu	His	Thr	Phe	Val	Ala	Lys	Thr	Pro	Ser	Ala	Leu	
630					635					640					645	
acc	tgt	gtc	tgc	ttg	gta	gac	atg	gtc	ggg	gaa	aag	cgg	gca	cag	aat	2083
Thr	Cys	Val	Cys	Leu	Val	Asp	Met	Val	Gly	Glu	Lys	Arg	Ala	Gln	Asn	
				650					655					660		
cag	ccg	ggc	aca	acg	agg	gat	atg	tat	ccc	aac	tgg	tgt	atc	cca	ctg	2131
Gln	Pro	Gly	Thr	Thr	Arg	Asp	Met	Tyr	Pro	Asn	Trp	Cys	Ile	Pro	Leu	
			665					670					675			
tgt	gac	agc	gaa	ggc	aac	tcc	gtg	ctc	att	gaa	tcg	ctg	cgt	gaa	aat	2179
Cys	Asp	Ser	Glu	Gly	Asn	Ser	Val	Leu	Ile	Glu	Ser	Leu	Arg	Glu	Asn	
		680					685					690				
gag	ctg	tat	cac	cgt	gtg	gca	aag	gca	agc	aag	cga	gat	taggtccgct			2228
Glu	Leu	Tyr	His	Arg	Val	Ala	Lys	Ala	Ser	Lys	Arg	Asp				
	695					700					705					
tcagttgtgg	tggtg															2241

&lt;210&gt; 410

&lt;211&gt; 706

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 410

Val Thr Ala Arg Arg Phe Leu Asn Glu Leu Ala Asp Leu Tyr Gly Val  
 1 5 10 15  
 Ala Thr Ser Tyr Thr Asp Tyr Lys Gly Ala His Ile Glu Val Ser Asp  
 20 25 30  
 Asp Thr Leu Val Lys Ile Leu Arg Ala Leu Gly Val Asn Leu Asp Thr  
 35 40 45  
 Ser Asn Leu Pro Asn Asp Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe  
 50 55 60  
 His Asp Arg Glu Phe Thr Arg Pro Leu Pro Pro Ser Val Val Ala Val  
 65 70 75 80  
 Glu Gly Asp Glu Leu Val Phe Pro Val His Val His Asp Gly Ser Pro  
 85 90 95  
 Ala Asp Val His Ile Glu Leu Glu Asp Gly Thr Gln Arg Asp Val Ser  
 100 105 110  
 Gln Val Glu Asn Trp Thr Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp  
 115 120 125  
 Gly Glu Ala Ser Phe Lys Ile Pro Gly Asp Leu Pro Leu Gly Trp His  
 130 135 140  
 Lys Leu His Leu Lys Ser Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile  
 145 150 155 160  
 Ile Thr Pro Ala Arg Leu Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro  
 165 170 175  
 Arg Ser Gly Val Met Ala Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser  
 180 185 190  
 Trp Gly Met Gly Asp Phe Asn Asp Leu Gly Asn Leu Ala Ser Val Val  
 195 200 205  
 Ala Gln Asp Gly Ala Asp Phe Leu Leu Ile Asn Pro Met His Ala Ala  
 210 215 220  
 Glu Pro Leu Pro Pro Thr Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg  
 225 230 235 240  
 Arg Phe Ile Asn Pro Ile Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe  
 245 250 255  
 Asn Gln Leu Glu Ile Asp Leu Arg Asp Asp Ile Ala Glu Met Ala Ala  
 260 265 270  
 Glu Phe Arg Glu Arg Asn Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp  
 275 280 285

Val Tyr Ala Ala Lys Leu Gln Val Leu Arg Ala Ile Phe Glu Met Pro  
 290 295 300  
 Arg Ser Ser Glu Arg Glu Ala Asn Phe Val Ser Phe Val Gln Arg Glu  
 305 310 315 320  
 Gly Gln Gly Leu Ile Asp Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr  
 325 330 335  
 Ala Gln Ser Glu Ser Val His Gly Thr Glu Pro Asp Arg Asp Glu Leu  
 340 345 350  
 Thr Met Phe Tyr Met Trp Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala  
 355 360 365  
 Ala Ala Gln Lys Arg Ala Val Asp Ala Gly Met Ser Ile Gly Ile Met  
 370 375 380  
 Ala Asp Leu Ala Val Gly Val His Pro Gly Gly Ala Asp Ala Gln Asn  
 385 390 395 400  
 Leu Ser His Val Leu Ala Pro Asp Ala Ser Val Gly Ala Pro Pro Asp  
 405 410 415  
 Gly Tyr Asn Gln Gln Gly Gln Asp Trp Ser Gln Pro Pro Trp His Pro  
 420 425 430  
 Val Arg Leu Ala Glu Glu Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg  
 435 440 445  
 Thr Val Leu Arg His Ser Gly Gly Ile Arg Val Asp His Val Leu Gly  
 450 455 460  
 Leu Phe Arg Leu Phe Val Met Pro Arg Met Gln Ser Pro Ala Thr Gly  
 465 470 475 480  
 Thr Tyr Ile Arg Phe Asp His Asn Ala Leu Val Gly Ile Leu Ala Leu  
 485 490 495  
 Glu Ala Glu Leu Ala Gly Ala Val Val Ile Gly Glu Asp Leu Gly Thr  
 500 505 510  
 Phe Glu Pro Trp Val Gln Asp Ala Leu Ala Gln Arg Gly Ile Met Gly  
 515 520 525  
 Thr Ser Ile Leu Trp Phe Glu His Ser Pro Ser Gln Pro Gly Pro Arg  
 530 535 540  
 Arg Gln Glu Glu Tyr Arg Pro Leu Ala Leu Thr Thr Val Thr Thr His  
 545 550 555 560  
 Asp Leu Pro Pro Thr Ala Gly Tyr Leu Glu Gly Glu His Ile Ala Leu  
 565 570 575  
 Arg Glu Arg Leu Gly Val Leu Asn Thr Asp Pro Ala Ala Glu Leu Ala  
 580 585 590  
 Glu Asp Leu Gln Trp Gln Ala Glu Ile Leu Asp Val Ala Ala Ser Ala  
 595 600 605  
 Asn Ala Leu Pro Ala Arg Glu Tyr Val Gly Leu Glu Arg Asp Gln Arg

610                      615                      620

Gly Glu Leu Ala Glu Leu Leu Glu Gly Leu His Thr Phe Val Ala Lys  
625                      630                      635                      640

Thr Pro Ser Ala Leu Thr Cys Val Cys Leu Val Asp Met Val Gly Glu  
645                      650                      655

Lys Arg Ala Gln Asn Gln Pro Gly Thr Thr Arg Asp Met Tyr Pro Asn  
660                      665                      670

Trp Cys Ile Pro Leu Cys Asp Ser Glu Gly Asn Ser Val Leu Ile Glu  
675                      680                      685

Ser Leu Arg Glu Asn Glu Leu Tyr His Arg Val Ala Lys Ala Ser Lys  
690                      695                      700

Arg Asp  
705

<210> 411  
<211> 2223  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(2200)  
<223> FRXA00879

<400> 411  
aaaagatgta ttttctaaca aacttacct cacgtacaa atatgctgtg cccacacgct 60

attagtggca taatgttggtg ttgtgactgc tcgcagattt ttg aat gaa ctc gcc 115  
Leu Asn Glu Leu Ala  
1 5

gat ctc tac ggc gta gca act tcc tac act gat tac aaa ggt gcc cat 163  
Asp Leu Tyr Gly Val Ala Thr Ser Tyr Thr Asp Tyr Lys Gly Ala His  
10 15 20

att gag gtc agc gat gac aca tta gtg aaa atc ctg cgt gct ctg ggt 211  
Ile Glu Val Ser Asp Asp Thr Leu Val Lys Ile Leu Arg Ala Leu Gly  
25 30 35

gtg aat tta gat aca agc aac ctc ccc aac gat gac gct atc caa cgc 259  
Val Asn Leu Asp Thr Ser Asn Leu Pro Asn Asp Asp Ala Ile Gln Arg  
40 45 50

caa att gcc ctc ttc cat gat cga gag ttc act cgc cca ctg cct cca 307  
Gln Ile Ala Leu Phe His Asp Arg Glu Phe Thr Arg Pro Leu Pro Pro  
55 60 65

tcg gtg gtt gca gtt gaa ggt gat gaa cta gtt ttc ccg gtg cat gtg 355  
Ser Val Val Ala Val Glu Gly Asp Glu Leu Val Phe Pro Val His Val  
70 75 80 85

cac gac ggt tcc cct gca gat gtc cac atc gaa ttg gaa gac ggc acg 403  
His Asp Gly Ser Pro Ala Asp Val His Ile Glu Leu Glu Asp Gly Thr  
90 95 100

cag cgg gat gtt tct cag gtg gaa aac tgg aca gcg cca cgg gaa att	451
Gln Arg Asp Val Ser Gln Val Glu Asn Trp Thr Ala Pro Arg Glu Ile	
105 110 115	
gat ggg att agg tgg ggc gag gca tgc ttt aag att cct ggt gat ctc	499
Asp Gly Ile Arg Trp Gly Glu Ala Ser Phe Lys Ile Pro Gly Asp Leu	
120 125 130	
ccc ttg ggt tgg cac aag ctt cac ctt aaa tcc aat gaa cgc tca gct	547
Pro Leu Gly Trp His Lys Leu His Leu Lys Ser Asn Glu Arg Ser Ala	
135 140 145	
gag tgc ggt ttg atc atc acc ccg gct cgt ctg tct act gct gat aag	595
Glu Cys Gly Leu Ile Ile Thr Pro Ala Arg Leu Ser Thr Ala Asp Lys	
150 155 160 165	
tat ctt gat tcc cct cgc agt ggt gtc atg gcg cag atc tac tct gtg	643
Tyr Leu Asp Ser Pro Arg Ser Gly Val Met Ala Gln Ile Tyr Ser Val	
170 175 180	
cgt tcc acg ttg tgc tgg ggc atg ggt gat ttc aat gat tta gga aac	691
Arg Ser Thr Leu Ser Trp Gly Met Gly Asp Phe Asn Asp Leu Gly Asn	
185 190 195	
ttg gca agt gtg gtt gcc cag gat gga gca gac ttc ctg ctc atc aac	739
Leu Ala Ser Val Val Ala Gln Asp Gly Ala Asp Phe Leu Leu Ile Asn	
200 205 210	
ccc atg cac gct gca gag ccg ctg cct cct act gag gac tct cct tat	787
Pro Met His Ala Ala Glu Pro Leu Pro Pro Thr Glu Asp Ser Pro Tyr	
215 220 225	
ctg ccc aca acc agg cgc ttt atc aac ccg atc tac att cgg gta gaa	835
Leu Pro Thr Thr Arg Phe Ile Asn Pro Ile Tyr Ile Arg Val Glu	
230 235 240 245	
gat att ccg gag ttt aat cag ctt gag att gat cta cgc gat gat atc	883
Asp Ile Pro Glu Phe Asn Gln Leu Glu Ile Asp Leu Arg Asp Asp Ile	
250 255 260	
gca gag atg gct gcg gaa ttc cgc gaa cgc aat ctg acc tca gac atc	931
Ala Glu Met Ala Ala Glu Phe Arg Glu Arg Asn Leu Thr Ser Asp Ile	
265 270 275	
att gag cgc aat gac gtc tac gct gca aag ctt caa gtg ctg cgc gcc	979
Ile Glu Arg Asn Asp Val Tyr Ala Ala Lys Leu Gln Val Leu Arg Ala	
280 285 290	
att ttt gaa atg cct cgt tcc agc gaa cgt gaa gcc aac ttt gtc tcc	1027
Ile Phe Glu Met Pro Arg Ser Ser Glu Arg Glu Ala Asn Phe Val Ser	
295 300 305	
ttc gtg caa cgg gaa ggc caa ggt ctt att gat ttc gcc acc tgg tgc	1075
Phe Val Gln Arg Glu Gly Gln Gly Leu Ile Asp Phe Ala Thr Trp Cys	
310 315 320 325	
gcg gac cgc gaa act gca cag tct gaa tct gtc cac gga act gag cca	1123
Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser Val His Gly Thr Glu Pro	
330 335 340	



gac cgc gat gag ctg acc atg ttc tac atg tgg ttg cag tgg cta tgt	1171
Asp Arg Asp Glu Leu Thr Met Phe Tyr Met Trp Leu Gln Trp Leu Cys	
345 350 355	
gat gag cag ctg gcg gca gct caa aag cgc gct gtc gat gcc gga atg	1219
Asp Glu Gln Leu Ala Ala Ala Gln Lys Arg Ala Val Asp Ala Gly Met	
360 365 370	
tcg atc ggc atc atg gca gac ctg gca gtt ggt gtg cat cca ggt ggt	1267
Ser Ile Gly Ile Met Ala Asp Leu Ala Val Gly Val His Pro Gly Gly	
375 380 385	
gct gat gcc cag aac ctc agc cac gta ctt gct ccg gat gcg tca gtg	1315
Ala Asp Ala Gln Asn Leu Ser His Val Leu Ala Pro Asp Ala Ser Val	
390 395 400 405	
ggc gcc cca cca gat gga tac aac cag cag ggc caa gac tgg tcc cag	1363
Gly Ala Pro Pro Asp Gly Tyr Asn Gln Gln Gly Gln Asp Trp Ser Gln	
410 415 420	
cca cca tgg cat cca gtg cgt ctt gca gag gaa ggc tac att ccg tgg	1411
Pro Pro Trp His Pro Val Arg Leu Ala Glu Glu Gly Tyr Ile Pro Trp	
425 430 435	
cgt aat ctg ctg cgc act gtg ctg cgt cac tcc ggc gga atc cgc gtg	1459
Arg Asn Leu Leu Arg Thr Val Leu Arg His Ser Gly Gly Ile Arg Val	
440 445 450	
gac cac gtt ctt ggt ttg ttc agg ctc ttt gtc atg cca cgc atg caa	1507
Asp His Val Leu Gly Leu Phe Arg Leu Phe Val Met Pro Arg Met Gln	
455 460 465	
tcc cct gct acg ggc acc tat atc cgc ttc gac cat aat gcg ttg gta	1555
Ser Pro Ala Thr Gly Thr Tyr Ile Arg Phe Asp His Asn Ala Leu Val	
470 475 480 485	
ggc att cta gcc cta gaa gca gaa ctc gca ggc gcc gtt gtc att ggt	1603
Gly Ile Leu Ala Leu Glu Ala Glu Leu Ala Gly Ala Val Val Ile Gly	
490 495 500	
gaa gat ctg gga acg ttt gag cct tgg gta caa gat gca ttg gct cag	1651
Glu Asp Leu Gly Thr Phe Glu Pro Trp Val Gln Asp Ala Leu Ala Gln	
505 510 515	
cgt ggc atc atg ggc acc tcg atc cta tgg ttc gag cat tcc cca agc	1699
Arg Gly Ile Met Gly Thr Ser Ile Leu Trp Phe Glu His Ser Pro Ser	
520 525 530	
cag ccg ggt cct cgc cgc cag gaa gag tat cgt ccg ctg gcc ttg acc	1747
Gln Pro Gly Pro Arg Arg Gln Glu Glu Tyr Arg Pro Leu Ala Leu Thr	
535 540 545	
act gtg acc act cat gat ctc cct ccg act gct ggt tat ttg gag ggc	1795
Thr Val Thr Thr His Asp Leu Pro Pro Thr Ala Gly Tyr Leu Glu Gly	
550 555 560 565	
gag cac att gct ctt cgt gag cga ttg ggg gtg ctc aac act gat cct	1843
Glu His Ile Ala Leu Arg Glu Arg Leu Gly Val Leu Asn Thr Asp Pro	
570 575 580	
gct gca gaa ctc gct gag gat ctg cag tgg caa gcg gag atc ctt gat	1891

Ala Ala Glu Leu Ala Glu Asp Leu Gln Trp Gln Ala Glu Ile Leu Asp  
585 590 595

gtc gca gca tct gcc aac gca ttg cca gcc cgg gaa tac gtg gga ctc 1939  
Val Ala Ala Ser Ala Asn Ala Leu Pro Ala Arg Glu Tyr Val Gly Leu  
600 605 610

gaa cgc gat cag cgc ggt gag ttg gct gag ctg ttg gaa ggc ctg cac 1987  
Glu Arg Asp Gln Arg Gly Glu Leu Ala Glu Leu Leu Glu Gly Leu His  
615 620 625

act ttc gtt gcg aaa acc cct tca gca ctg acc tgt gtc tgc ttg gta 2035  
Thr Phe Val Ala Lys Thr Pro Ser Ala Leu Thr Cys Val Cys Leu Val  
630 635 640 645

gac atg gtc ggt gaa aag cgg gca cag aat cag ccg ggc aca acg agg 2083  
Asp Met Val Gly Glu Lys Arg Ala Gln Asn Gln Pro Gly Thr Thr Arg  
650 655 660

gat atg tat ccc aac tgg tgt atc cca ctg tgt gac agc gaa ggc aac 2131  
Asp Met Tyr Pro Asn Trp Cys Ile Pro Leu Cys Asp Ser Glu Gly Asn  
665 670 675

tcc gtg ctc att gaa tcg ctg cgt gaa aat gag ctg tat cac cgt gtg 2179  
Ser Val Leu Ile Glu Ser Leu Arg Glu Asn Glu Leu Tyr His Arg Val  
680 685 690

gca aag gca agc aag cga gat taggtccgct tcagttgtgg tgg 2223  
Ala Lys Ala Ser Lys Arg Asp  
695 700

&lt;210&gt; 412

&lt;211&gt; 700

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 412

Leu Asn Glu Leu Ala Asp Leu Tyr Gly Val Ala Thr Ser Tyr Thr Asp  
1 5 10 15

Tyr Lys Gly Ala His Ile Glu Val Ser Asp Asp Thr Leu Val Lys Ile  
20 25 30

Leu Arg Ala Leu Gly Val Asn Leu Asp Thr Ser Asn Leu Pro Asn Asp  
35 40 45

Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe His Asp Arg Glu Phe Thr  
50 55 60

Arg Pro Leu Pro Pro Ser Val Val Ala Val Glu Gly Asp Glu Leu Val  
65 70 75 80

Phe Pro Val His Val His Asp Gly Ser Pro Ala Asp Val His Ile Glu  
85 90 95

Leu Glu Asp Gly Thr Gln Arg Asp Val Ser Gln Val Glu Asn Trp Thr  
100 105 110

Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp Gly Glu Ala Ser Phe Lys  
115 120 125

Ile Pro Gly Asp Leu Pro Leu Gly Trp His Lys Leu His Leu Lys Ser  
 130 135 140  
 Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile Ile Thr Pro Ala Arg Leu  
 145 150 155 160  
 Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro Arg Ser Gly Val Met Ala  
 165 170 175  
 Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser Trp Gly Met Gly Asp Phe  
 180 185 190  
 Asn Asp Leu Gly Asn Leu Ala Ser Val Val Ala Gln Asp Gly Ala Asp  
 195 200 205  
 Phe Leu Leu Ile Asn Pro Met His Ala Ala Glu Pro Leu Pro Pro Thr  
 210 215 220  
 Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg Arg Phe Ile Asn Pro Ile  
 225 230 235 240  
 Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe Asn Gln Leu Glu Ile Asp  
 245 250 255  
 Leu Arg Asp Asp Ile Ala Glu Met Ala Ala Glu Phe Arg Glu Arg Asn  
 260 265 270  
 Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp Val Tyr Ala Ala Lys Leu  
 275 280 285  
 Gln Val Leu Arg Ala Ile Phe Glu Met Pro Arg Ser Ser Glu Arg Glu  
 290 295 300  
 Ala Asn Phe Val Ser Phe Val Gln Arg Glu Gly Gln Gly Leu Ile Asp  
 305 310 315 320  
 Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser Val  
 325 330 335  
 His Gly Thr Glu Pro Asp Arg Asp Glu Leu Thr Met Phe Tyr Met Trp  
 340 345 350  
 Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala Ala Ala Gln Lys Arg Ala  
 355 360 365  
 Val Asp Ala Gly Met Ser Ile Gly Ile Met Ala Asp Leu Ala Val Gly  
 370 375 380  
 Val His Pro Gly Gly Ala Asp Ala Gln Asn Leu Ser His Val Leu Ala  
 385 390 395 400  
 Pro Asp Ala Ser Val Gly Ala Pro Pro Asp Gly Tyr Asn Gln Gln Gly  
 405 410 415  
 Gln Asp Trp Ser Gln Pro Pro Trp His Pro Val Arg Leu Ala Glu Glu  
 420 425 430  
 Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg Thr Val Leu Arg His Ser  
 435 440 445

Gly Gly Ile Arg Val Asp His Val Leu Gly Leu Phe Arg Leu Phe Val  
 450 455 460  
 Met Pro Arg Met Gln Ser Pro Ala Thr Gly Thr Tyr Ile Arg Phe Asp  
 465 470 475 480  
 His Asn Ala Leu Val Gly Ile Leu Ala Leu Glu Ala Glu Leu Ala Gly  
 485 490 495  
 Ala Val Val Ile Gly Glu Asp Leu Gly Thr Phe Glu Pro Trp Val Gln  
 500 505 510  
 Asp Ala Leu Ala Gln Arg Gly Ile Met Gly Thr Ser Ile Leu Trp Phe  
 515 520 525  
 Glu His Ser Pro Ser Gln Pro Gly Pro Arg Arg Gln Glu Glu Tyr Arg  
 530 535 540  
 Pro Leu Ala Leu Thr Thr Val Thr Thr His Asp Leu Pro Pro Thr Ala  
 545 550 555 560  
 Gly Tyr Leu Glu Gly Glu His Ile Ala Leu Arg Glu Arg Leu Gly Val  
 565 570 575  
 Leu Asn Thr Asp Pro Ala Ala Glu Leu Ala Glu Asp Leu Gln Trp Gln  
 580 585 590  
 Ala Glu Ile Leu Asp Val Ala Ala Ser Ala Asn Ala Leu Pro Ala Arg  
 595 600 605  
 Glu Tyr Val Gly Leu Glu Arg Asp Gln Arg Gly Glu Leu Ala Glu Leu  
 610 615 620  
 Leu Glu Gly Leu His Thr Phe Val Ala Lys Thr Pro Ser Ala Leu Thr  
 625 630 635 640  
 Cys Val Cys Leu Val Asp Met Val Gly Glu Lys Arg Ala Gln Asn Gln  
 645 650 655  
 Pro Gly Thr Thr Arg Asp Met Tyr Pro Asn Trp Cys Ile Pro Leu Cys  
 660 665 670  
 Asp Ser Glu Gly Asn Ser Val Leu Ile Glu Ser Leu Arg Glu Asn Glu  
 675 680 685  
 Leu Tyr His Arg Val Ala Lys Ala Ser Lys Arg Asp  
 690 695 700

&lt;210&gt; 413

&lt;211&gt; 1287

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1264)

&lt;223&gt; RXN00043

&lt;400&gt; 413

aacagcaggc ctcaagtccg aagataatta acctaaatcc gtagacataa gacatcatac 60

gtcctatgct tgctggaagg aagcaaataa cctcagaaag atg gca gaa gtg gtg	115
Met Ala Glu Val Val	
1 5	
cat tat caa gaa aat gca ggt caa gca gtt aaa aaa att gaa gga aga	163
His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys Lys Ile Glu Gly Arg	
10 15 20	
att gtt acc ccc cac ggg gtg att gat ggc ttt ctc caa ctc gaa aac	211
Ile Val Thr Pro His Gly Val Ile Asp Gly Phe Leu Gln Leu Glu Asn	
25 30 35	
ggc atc atc acg gaa ctc tct gga gaa cca gca cct aaa aac gca gga	259
Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala Pro Lys Asn Ala Gly	
40 45 50	
ttc cac ccc gaa ctc ccc acg att gtt ccc agt ttt att gat ctt cat	307
Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser Phe Ile Asp Leu His	
55 60 65	
aat cac ggt gga aac ggt ggc gcg ttt cct acg gga acg cag gac cag	355
Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr Gly Thr Gln Asp Gln	
70 75 80 85	
gcg agg aat gcc gcg cag tat cac cgc gaa cat ggc acg acc gtg atg	403
Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His Gly Thr Thr Val Met	
90 95 100	
ttg gca agc atg gtt tcg gcg ccg gct gac gca ctg gca gcg cag gtg	451
Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala Leu Ala Ala Gln Val	
105 110 115	
gaa aac ctt att ccc ttg tgt gaa gag ggc ctg ctg tgc ggc att cac	499
Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu Leu Cys Gly Ile His	
120 125 130	
ctc gag ggt cct ttc atc aac gca tgc cgt tgt ggt gct caa aac ccg	547
Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys Gly Ala Gln Asn Pro	
135 140 145	
gat ttt att ttt ccc ggc aac cca aca gat ctt gcc cag gtg atc cat	595
Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu Ala Gln Val Ile His	
150 155 160 165	
gcg gga aaa ggt tgg atc aaa tcg atc aca gta gcg ccg gaa act gac	643
Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val Ala Pro Glu Thr Asp	
170 175 180	
aat ctt act gag ctt ctc gat ctc tgc gca gcg cac cac atc att gct	691
Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala His His Ile Ile Ala	
185 190 195	
tcc ttc ggg cac act gat gca gat ttt gat acc act acc agc gca att	739
Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr Thr Thr Ser Ala Ile	
200 205 210	
gcc ttg gct aaa gag aaa aat gtg acg gtc acg gct acg cat ttg ttc	787
Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr Ala Thr His Leu Phe	
215 220 225	

aat gcg atg cct ccg ctg cat cat agg gat ccc ggc agc gtg ggc gct 835  
 Asn Ala Met Pro Pro Leu His His Arg Asp Pro Gly Ser Val Gly Ala  
 230 235 240 245  
  
 ttg ctt gct gcg gca cgt gcc ggg gac gca tat gtt gag ttg atc gcc 883  
 Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr Val Glu Leu Ile Ala  
 250 255 260  
  
 gac ggc gtg cat ttg gcc gat gga acg gtc gat cta gct cgt tcc aac 931  
 Asp Gly Val His Leu Ala Asp Gly Thr Val Asp Leu Ala Arg Ser Asn  
 265 270 275  
  
 aac gcc ttt ttc atc acg gac gcc atg gaa gcc gcc gga atg cca gac 979  
 Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala Ala Gly Met Pro Asp  
 280 285 290  
  
 ggt gag tac att ttg ggc gtt ttg aac gtc acc gtc acc gat ggc gtc 1027  
 Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr Val Thr Asp Gly Val  
 295 300 305  
  
 gcc cgt ctg cgc gat ggc gcc gcc atc gcc ggg ggt acc agc aca cta 1075  
 Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly Gly Thr Ser Thr Leu  
 310 315 320 325  
  
 gcg agt cag ttc gtg cac cac gtg cgc agg ggt atg acg ctt atc gac 1123  
 Ala Ser Gln Phe Val His His Val Arg Arg Gly Met Thr Leu Ile Asp  
 330 335 340  
  
 gcg acc ctc cac acc tca acc gtc gcc gcc aaa att ctc gga ctt agc 1171  
 Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys Ile Leu Gly Leu Ser  
 345 350 355  
  
 gat cac gaa atc gtt aaa tcc aac cct gta aat ttt gtg gtc ttt gac 1219  
 Asp His Glu Ile Val Lys Ser Asn Pro Val Asn Phe Val Val Phe Asp  
 360 365 370  
  
 tca aac ggc cag tta caa cag gtc cat tta gac cat caa gta att 1264  
 Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp His Gln Val Ile  
 375 380 385  
  
 taaatacgag caaaactttc ctg 1287

&lt;210&gt; 414

&lt;211&gt; 388

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 414

Met Ala Glu Val Val His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys  
 1 5 10 15  
  
 Lys Ile Glu Gly Arg Ile Val Thr Pro His Gly Val Ile Asp Gly Phe  
 20 25 30  
  
 Leu Gln Leu Glu Asn Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala  
 35 40 45  
  
 Pro Lys Asn Ala Gly Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser  
 50 55 60

Phe Ile Asp Leu His Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr  
 65 70 75 80  
 Gly Thr Gln Asp Gln Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His  
 85 90 95  
 Gly Thr Thr Val Met Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala  
 100 105 110  
 Leu Ala Ala Gln Val Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu  
 115 120 125  
 Leu Cys Gly Ile His Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys  
 130 135 140  
 Gly Ala Gln Asn Pro Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu  
 145 150 155 160  
 Ala Gln Val Ile His Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val  
 165 170 175  
 Ala Pro Glu Thr Asp Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala  
 180 185 190  
 His His Ile Ile Ala Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr  
 195 200 205  
 Thr Thr Ser Ala Ile Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr  
 210 215 220  
 Ala Thr His Leu Phe Asn Ala Met Pro Pro Leu His His Arg Asp Pro  
 225 230 235 240  
 Gly Ser Val Gly Ala Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr  
 245 250 255  
 Val Glu Leu Ile Ala Asp Gly Val His Leu Ala Asp Gly Thr Val Asp  
 260 265 270  
 Leu Ala Arg Ser Asn Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala  
 275 280 285  
 Ala Gly Met Pro Asp Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr  
 290 295 300  
 Val Thr Asp Gly Val Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly  
 305 310 315 320  
 Gly Thr Ser Thr Leu Ala Ser Gln Phe Val His His Val Arg Arg Gly  
 325 330 335  
 Met Thr Leu Ile Asp Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys  
 340 345 350  
 Ile Leu Gly Leu Ser Asp His Glu Ile Val Lys Ser Asn Pro Val Asn  
 355 360 365  
 Phe Val Val Phe Asp Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp  
 370 375 380  
 His Gln Val Ile





Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val Ala Pro Glu Thr Asp  
170 175 180

aat ctt act gag ctt ctc gat ctc tgc gca gcg cac cac atc att gct 691  
Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala His His Ile Ile Ala  
185 190 195

tcc ttc ggg cac act gat gca gat ttt gat acc act acc agc gca att 739  
Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr Thr Thr Ser Ala Ile  
200 205 210

gcc ttg gct aaa gag aaa aat gtg acg gtc acg gct acg cat ttg ttc 787  
Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr Ala Thr His Leu Phe  
215 220 225

aat gcg atg cct ccg ctg cat cat agg gat ccc ggc agc gtg ggc gct 835  
Asn Ala Met Pro Pro Leu His His Arg Asp Pro Gly Ser Val Gly Ala  
230 235 240 245

ttg ctt gct gcg gca cgt gcc ggg gac gca tat gtt gag ttg atc gcc 883  
Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr Val Glu Leu Ile Ala  
250 255 260

gac ggc gtg cat ttg gcc gat gga acg gtc gat cta gct cgt tcc aac 931  
Asp Gly Val His Leu Ala Asp Gly Thr Val Asp Leu Ala Arg Ser Asn  
265 270 275

aac gcc ttt ttc atc acg gac gcc atg gaa gcc gcc gga atg cca gac 979  
Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala Ala Gly Met Pro Asp  
280 285 290

ggt gag tac att ttg ggc gtt ttg aac gtc acc gtc acc gat ggc gtc 1027  
Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr Val Thr Asp Gly Val  
295 300 305

gcc cgt ctg cgc gat ggc ggc gcc atc gcc ggg ggt acc agc aca cta 1075  
Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly Gly Thr Ser Thr Leu  
310 315 320 325

gcg agt cag ttc gtg cac cac gtg cgc agg ggt atg acg ctt atc gac 1123  
Ala Ser Gln Phe Val His His Val Arg Arg Gly Met Thr Leu Ile Asp  
330 335 340

gcg acc ctc cac acc tca acc gtc gcc gcc aaa att ctc gga ctt agc 1171  
Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys Ile Leu Gly Leu Ser  
345 350 355

gat cac gaa atc gtt aaa tcc aac cct gta aat ttt gtg gtc ttt gac 1219  
Asp His Glu Ile Val Lys Ser Asn Pro Val Asn Phe Val Val Phe Asp  
360 365 370

tca aac ggc cag tta caa cag gtc cat tta gac cat caa gta att 1264  
Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp His Gln Val Ile  
375 380 385

taaatacgag caaaactttc ctg 1287

&lt;210&gt; 416

&lt;211&gt; 388

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 416

```

Met Ala Glu Val Val His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys
 1             5             10             15

Lys Ile Glu Gly Arg Ile Val Thr Pro His Gly Val Ile Asp Gly Phe
          20          25          30

Leu Gln Leu Glu Asn Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala
 35          40          45

Pro Lys Asn Ala Gly Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser
 50          55          60

Phe Ile Asp Leu His Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr
 65          70          75          80

Gly Thr Gln Asp Gln Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His
          85          90          95

Gly Thr Thr Val Met Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala
 100         105         110

Leu Ala Ala Gln Val Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu
 115         120         125

Leu Cys Gly Ile His Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys
 130         135         140

Gly Ala Gln Asn Pro Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu
 145         150         155         160

Ala Gln Val Ile His Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val
          165         170         175

Ala Pro Glu Thr Asp Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala
 180         185         190

His His Ile Ile Ala Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr
 195         200         205

Thr Thr Ser Ala Ile Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr
 210         215         220

Ala Thr His Leu Phe Asn Ala Met Pro Pro Leu His His Arg Asp Pro
 225         230         235         240

Gly Ser Val Gly Ala Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr
          245         250         255

Val Glu Leu Ile Ala Asp Gly Val His Leu Ala Asp Gly Thr Val Asp
 260         265         270

Leu Ala Arg Ser Asn Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala
 275         280         285

Ala Gly Met Pro Asp Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr
 290         295         300

Val Thr Asp Gly Val Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly

```

305	310	315	320
Gly Thr Ser Thr Leu Ala Ser Gln Phe Val His His Val Arg Arg Gly			
	325	330	335
Met Thr Leu Ile Asp Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys			
	340	345	350
Ile Leu Gly Leu Ser Asp His Glu Ile Val Lys Ser Asn Pro Val Asn			
	355	360	365
Phe Val Val Phe Asp Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp			
	370	375	380
His Gln Val Ile			
385			
<210> 417			
<211> 1584			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(1561)			
<223> RXN01752			
<400> 417			
gaaatgacgt gaccatcgat accaatacccc aattgaaaga tcttgacctg gtcagccaag 60			
ttggccgtca gatcggtggca gaacaacagg tggggagggtc atg atg gaa caa gat			115
		Met Met Glu Gln Asp	
		1 5	
ctc agc tac cgt gaa att ctt ccc ctc aac gcg agt gag gag aag aaa			163
Leu Ser Tyr Arg Glu Ile Leu Pro Leu Asn Ala Ser Glu Glu Lys Lys			
	10	15	20
aag gct gca ctg att gat gcc att gaa ggg tta agg gtg cgc gat ccg			211
Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu Arg Val Arg Asp Pro			
	25	30	35
cta ctc tct gcc tcg att gca ttt act aga ggg cag aaa gtc gcc ttc			259
Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly Gln Lys Val Ala Phe			
	40	45	50
att gct gtg gtg gtg ggc ttt atc ttg atg ctc att ttt gct cgg caa			307
Ile Ala Val Val Val Gly Phe Ile Leu Met Leu Ile Phe Ala Arg Gln			
	55	60	65
gca gca ctt att gga ctg tca gca acg tgt acg ttc atg tac ctc att			355
Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr Phe Met Tyr Leu Ile			
	70	75	80
aca ttg ttg gac aga ttt atc atg ttt tcc aga ggt atc cgc gcg gaa			403
Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg Gly Ile Arg Ala Glu			
	90	95	100
tcc atc atc cag gta tcg gat gaa gat gcg ctg gct ttc cct gag gac			451
Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu Ala Phe Pro Glu Asp			

105										110					115					
aag	ctg	aaa	acc	tac	acg	gtg	ttg	gtg	ccc	gcc	tat	ggc	gaa	cct	gag	499				
Lys	Leu	Lys	Thr	Tyr	Thr	Val	Leu	Val	Pro	Ala	Tyr	Gly	Glu	Pro	Glu					
		120						125					130							
gtg	att	gcg	cag	ctg	ctg	gca	tcc	atg	cac	gct	ttt	gat	tac	ccc	aag	547				
Val	Ile	Ala	Gln	Leu	Leu	Ala	Ser	Met	His	Ala	Phe	Asp	Tyr	Pro	Lys					
	135					140					145									
cat	ctt	ctg	cag	gta	ttg	ctc	atg	ttg	gag	gaa	gat	gat	ctg	ccc	acg	595				
His	Leu	Leu	Gln	Val	Leu	Leu	Met	Leu	Glu	Glu	Asp	Asp	Leu	Pro	Thr					
150					155					160				165						
atc	gcc	gcg	gca	gag	gca	gcg	gga	gtg	gat	cag	gtg	gca	acg	atc	att	643				
Ile	Ala	Ala	Ala	Glu	Ala	Ala	Gly	Val	Asp	Gln	Val	Ala	Thr	Ile	Ile					
				170					175					180						
aag	gtg	ccg	cca	gcg	cag	ccc	cgc	acc	aag	ccg	aag	gcc	tgt	aac	tat	691				
Lys	Val	Pro	Pro	Ala	Gln	Pro	Arg	Thr	Lys	Pro	Lys	Ala	Cys	Asn	Tyr					
			185					190					195							
gga	ttg	cac	ttt	gcc	acg	ggg	gaa	att	gtc	acg	atc	ttt	gac	gcg	gaa	739				
Gly	Leu	His	Phe	Ala	Thr	Gly	Glu	Ile	Val	Thr	Ile	Phe	Asp	Ala	Glu					
	200						205					210								
gac	atg	cca	gat	ccc	ctc	caa	ctg	cgt	cgc	gtg	gtg	gtg	gca	ttt	gaa	787				
Asp	Met	Pro	Asp	Pro	Leu	Gln	Leu	Arg	Arg	Val	Val	Val	Ala	Phe	Glu					
	215					220					225									
cgc	tcg	gct	tcc	aat	acg	gtg	tgc	gtc	cag	tca	agg	ttg	tcg	tat	cga	835				
Arg	Ser	Ala	Ser	Asn	Thr	Val	Cys	Val	Gln	Ser	Arg	Leu	Ser	Tyr	Arg					
230					235					240					245					
aac	gcc	agg	cag	aat	ctg	cta	act	gcg	tgg	ttc	acc	att	gaa	tat	gac	883				
Asn	Ala	Arg	Gln	Asn	Leu	Leu	Thr	Ala	Trp	Phe	Thr	Ile	Glu	Tyr	Asp					
				250					255					260						
gtg	tgg	ttt	aac	ttc	ctg	ctg	cca	ggc	gtc	atg	cgc	atg	aac	gca	cct	931				
Val	Trp	Phe	Asn	Phe	Leu	Leu	Pro	Gly	Val	Met	Arg	Met	Asn	Ala	Pro					
			265					270					275							
gtc	cca	ttg	ggc	ggt	acc	tcc	aac	cat	ctg	ctc	acg	ggt	gtc	ctg	aaa	979				
Val	Pro	Leu	Gly	Gly	Thr	Ser	Asn	His	Leu	Leu	Thr	Gly	Val	Leu	Lys					
		280					285					290								
gat	ctc	ggc	gcg	tgg	gat	cct	ttc	aat	gtc	aca	gaa	aat	gcc	gac	ctc	1027				
Asp	Leu	Gly	Ala	Trp	Asp	Pro	Phe	Asn	Val	Thr	Glu	Asn	Ala	Asp	Leu					
	295					300					305									
ggc	gta	ccc	atc	gcg	gca	aaa	gga	tat	tcc	acc	gcg	gtg	ttg	gat	tcg	1075				
Gly	Val	Pro	Ile	Ala	Ala	Lys	Gly	Tyr	Ser	Thr	Ala	Val	Leu	Asp	Ser					
310					315					320				325						
gtg	acg	tgg	gag	gaa	gca	aac	tcc	gac	acc	atc	aac	tgg	ttg	cgc	cag	1123				
Val	Thr	Trp	Glu	Glu	Ala	Asn	Ser	Asp	Thr	Ile	Asn	Trp	Leu	Arg	Gln					
				330					335					340						
cgt	tct	cgc	tgg	tac	aag	ggc	tat	ctg	caa	aca	tgg	ctt	gtg	tat	atg	1171				
Arg	Ser	Arg	Trp	Tyr	Lys	Gly	Tyr	Leu	Gln	Thr	Trp	Leu	Val	Tyr	Met					
			345					350					355							

cgc agg cca aag tgg tta gtc caa gag ctt ggc atc att cct gct gtg 1219  
 Arg Arg Pro Lys Trp Leu Val Gln Glu Leu Gly Ile Ile Pro Ala Val  
 360 365 370  
 cgt ttt acc ttc ctc atg gca ggc acc ccg atc att gcg gtg ctc aat 1267  
 Arg Phe Thr Phe Leu Met Ala Gly Thr Pro Ile Ile Ala Val Leu Asn  
 375 380 385  
 ctg ctc ttt tgg tac ttg tgc ctc acg tgg att ctg ggc cag ccc ggc 1315  
 Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp Ile Leu Gly Gln Pro Gly  
 390 395 400 405  
 acc att gag cag atg ttc cca cct gcg gtg tac tac cca gcg ttg gtg 1363  
 Thr Ile Glu Gln Met Phe Pro Pro Ala Val Tyr Tyr Pro Ala Leu Val  
 410 415 420  
 tgt ttg gtg gtg gcc aat gct gcg acc atc ttt atg aat ctc att ggc 1411  
 Cys Leu Val Val Ala Asn Ala Ala Thr Ile Phe Met Asn Leu Ile Gly  
 425 430 435  
 tgc cgg gaa ggc cgc gac ccc ttg ctg ctc atc gcg gtt ctc acg ttc 1459  
 Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu Ile Ala Val Leu Thr Phe  
 440 445 450  
 ccg ctg tat tgg ctg ctc atg agc att gca gcg ttg aaa ggc acg tgg 1507  
 Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala Ala Leu Lys Gly Thr Trp  
 455 460 465  
 caa ttg atc acg cga cca tcc tat tgg gag aaa act gcc cac gga ttg 1555  
 Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu Lys Thr Ala His Gly Leu  
 470 475 480 485  
 gag gcg taagcgggtgc ccacgtcaa acc 1584  
 Glu Ala

&lt;210&gt; 418

&lt;211&gt; 487

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 418

Met Met Glu Gln Asp Leu Ser Tyr Arg Glu Ile Leu Pro Leu Asn Ala  
 1 5 10 15  
 Ser Glu Glu Lys Lys Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu  
 20 25 30  
 Arg Val Arg Asp Pro Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly  
 35 40 45  
 Gln Lys Val Ala Phe Ile Ala Val Val Val Gly Phe Ile Leu Met Leu  
 50 55 60  
 Ile Phe Ala Arg Gln Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr  
 65 70 75 80  
 Phe Met Tyr Leu Ile Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg  
 85 90 95

Gly Ile Arg Ala Glu Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu  
 100 105 110  
 Ala Phe Pro Glu Asp Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala  
 115 120 125  
 Tyr Gly Glu Pro Glu Val Ile Ala Gln Leu Leu Ala Ser Met His Ala  
 130 135 140  
 Phe Asp Tyr Pro Lys His Leu Leu Gln Val Leu Leu Met Leu Glu Glu  
 145 150 155 160  
 Asp Asp Leu Pro Thr Ile Ala Ala Ala Glu Ala Ala Gly Val Asp Gln  
 165 170 175  
 Val Ala Thr Ile Ile Lys Val Pro Pro Ala Gln Pro Arg Thr Lys Pro  
 180 185 190  
 Lys Ala Cys Asn Tyr Gly Leu His Phe Ala Thr Gly Glu Ile Val Thr  
 195 200 205  
 Ile Phe Asp Ala Glu Asp Met Pro Asp Pro Leu Gln Leu Arg Arg Val  
 210 215 220  
 Val Val Ala Phe Glu Arg Ser Ala Ser Asn Thr Val Cys Val Gln Ser  
 225 230 235 240  
 Arg Leu Ser Tyr Arg Asn Ala Arg Gln Asn Leu Leu Thr Ala Trp Phe  
 245 250 255  
 Thr Ile Glu Tyr Asp Val Trp Phe Asn Phe Leu Leu Pro Gly Val Met  
 260 265 270  
 Arg Met Asn Ala Pro Val Pro Leu Gly Gly Thr Ser Asn His Leu Leu  
 275 280 285  
 Thr Gly Val Leu Lys Asp Leu Gly Ala Trp Asp Pro Phe Asn Val Thr  
 290 295 300  
 Glu Asn Ala Asp Leu Gly Val Pro Ile Ala Ala Lys Gly Tyr Ser Thr  
 305 310 315 320  
 Ala Val Leu Asp Ser Val Thr Trp Glu Glu Ala Asn Ser Asp Thr Ile  
 325 330 335  
 Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln Thr  
 340 345 350  
 Trp Leu Val Tyr Met Arg Arg Pro Lys Trp Leu Val Gln Glu Leu Gly  
 355 360 365  
 Ile Ile Pro Ala Val Arg Phe Thr Phe Leu Met Ala Gly Thr Pro Ile  
 370 375 380  
 Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp Ile  
 385 390 395 400  
 Leu Gly Gln Pro Gly Thr Ile Glu Gln Met Phe Pro Pro Ala Val Tyr  
 405 410 415

Tyr Pro Ala Leu Val Cys Leu Val Val Ala Asn Ala Ala Thr Ile Phe  
 420 425 430

Met Asn Leu Ile Gly Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu Ile  
 435 440 445

Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala Ala  
 450 455 460

Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu Lys  
 465 470 475 480

Thr Ala His Gly Leu Glu Ala  
 485

<210> 419  
 <211> 689  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (19)..(666)  
 <223> FRXA01839

<400> 419  
 ttccctgctgc caggtgtcatg cgc atg aac gca cct gtc cca ttg ggc ggt 51  
 Met Arg Met Asn Ala Pro Val Pro Leu Gly Gly  
 1 5 10

acc tcc aac cat ctg ctc acg ggt gtc ctg aaa gat ctc ggc gcg tgg 99  
 Thr Ser Asn His Leu Leu Thr Gly Val Leu Lys Asp Leu Gly Ala Trp  
 15 20 25

gat cct ttc aat gtc aca gaa gat gcg gac ctc ggc gta cgc atc gcg 147  
 Asp Pro Phe Asn Val Thr Glu Asp Ala Asp Leu Gly Val Arg Ile Ala  
 30 35 40

gca aag gga tat tcc acc gcg gtg ttg gat tcg gtg acg tgg gag gaa 195  
 Ala Lys Gly Tyr Ser Thr Ala Val Leu Asp Ser Val Thr Trp Glu Glu  
 45 50 55

gca aac tcc gac acc atc aac tgg ttg cgc cag cgt tct cgc tgg tac 243  
 Ala Asn Ser Asp Thr Ile Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr  
 60 65 70 75

aag ggc tat ctg caa aca tgg ctt gtg tat atg cgc agg cca aag tgg 291  
 Lys Gly Tyr Leu Gln Thr Trp Leu Val Tyr Met Arg Arg Pro Lys Trp  
 80 85 90

tta gtc caa gag ctt ggc atc att cct gct gtg cgt ttt acc ttc ctc 339  
 Leu Val Gln Glu Leu Gly Ile Ile Pro Ala Val Arg Phe Thr Phe Leu  
 95 100 105

atg gca ggc acc ccg atc att gcg gtg ctc aat ctg ctc ttt tgg tac 387  
 Met Ala Gly Thr Pro Ile Ile Ala Val Leu Asn Leu Phe Trp Tyr  
 110 115 120

ttg tcg ctc acg tgg att ctg ggc cag ccc ggc acc att gag cag atg 435  
 Leu Ser Leu Thr Trp Ile Leu Gly Gln Pro Gly Thr Ile Glu Gln Met

125	130	135	
ttc cca cct gcg gtg tac tac cca gcg ttg gtg tgt ttg gtg gtg gcc			483
Phe Pro Pro Ala Val Tyr Tyr Pro Ala Leu Val Cys Leu Val Val Ala			
140	145	150	155
aat gct gcg acc atc ttt atg aat ctc att ggc tgc cgg gaa ggc cgc			531
Asn Ala Ala Thr Ile Phe Met Asn Leu Ile Gly Cys Arg Glu Gly Arg			
	160	165	170
gac ccc ttg ctg ctc atc gcg gtt ctc acg ttc ccg ctg tat tgg ctg			579
Asp Pro Leu Leu Leu Ile Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu			
	175	180	185
ctc atg agc att gca gcg ttg aaa ggc acg tgg caa ttg atc acg cga			627
Leu Met Ser Ile Ala Ala Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg			
	190	195	200
cca tcc tat tgg gag aaa act gcc cac gga ttg gag gcg taagcgggtgc			676
Pro Ser Tyr Trp Glu Lys Thr Ala His Gly Leu Glu Ala			
205	210	215	
ccatcgtcaa acc			689
<210> 420			
<211> 216			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 420			
Met Arg Met Asn Ala Pro Val Pro Leu Gly Gly Thr Ser Asn His Leu			
1	5	10	15
Leu Thr Gly Val Leu Lys Asp Leu Gly Ala Trp Asp Pro Phe Asn Val			
	20	25	30
Thr Glu Asp Ala Asp Leu Gly Val Arg Ile Ala Ala Lys Gly Tyr Ser			
	35	40	45
Thr Ala Val Leu Asp Ser Val Thr Trp Glu Glu Ala Asn Ser Asp Thr			
	50	55	60
Ile Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln			
	65	70	75
Thr Trp Leu Val Tyr Met Arg Arg Pro Lys Trp Leu Val Gln Glu Leu			
	85	90	95
Gly Ile Ile Pro Ala Val Arg Phe Thr Phe Leu Met Ala Gly Thr Pro			
	100	105	110
Ile Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp			
	115	120	125
Ile Leu Gly Gln Pro Gly Thr Ile Glu Gln Met Phe Pro Pro Ala Val			
	130	135	140
Tyr Tyr Pro Ala Leu Val Cys Leu Val Val Ala Asn Ala Ala Thr Ile			
145	150	155	160



Phe Met Asn Leu Ile Gly Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu  
                           165                          170                          175

Ile Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala  
                           180                          185                          190

Ala Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu  
                           195                          200                          205

Lys Thr Ala His Gly Leu Glu Ala  
           210                          215

<210> 421  
 <211> 1050  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1027)  
 <223> RXA01859

<400> 421  
 tacgccccagg gtttccatat tggtaaactct aagccgattg atgaatttat agctacttat 60

ctcgagacga accaaaccgc tacctggggg taggaagaat atg aaa aag aag agc 115  
   Met Lys Lys Lys Ser  
   1                          5

ttt cca atc gca aga gtc atc ggt atc ggc gtc ctt ggc atc gcc ggg 163  
 Phe Pro Ile Ala Arg Val Ile Gly Ile Gly Val Leu Gly Ile Ala Gly  
                           10                          15                          20

atg gga ata ttg ttg cta tgg ctt gca gtt acc ctg tct gat cca gca 211  
 Met Gly Ile Leu Leu Leu Trp Leu Ala Val Thr Leu Ser Asp Pro Ala  
                           25                          30                          35

tca ccg ggt gcc aaa gaa acc gaa gtc ttt gat agg tgg aaa gtg ctc 259  
 Ser Pro Gly Ala Lys Glu Thr Glu Val Phe Asp Arg Trp Lys Val Leu  
                           40                          45                          50

ttt gat gac tat att cca cca gtc agg gta ttg gtt gct gcg att atc 307  
 Phe Asp Asp Tyr Ile Pro Pro Val Arg Val Leu Val Ala Ala Ile Ile  
                           55                          60                          65

gtt gca tta att ttc gtc ttt atc gct gcc aca gtg gaa cga acc gta 355  
 Val Ala Leu Ile Phe Val Phe Ile Ala Ala Thr Val Glu Arg Thr Val  
                           70                          75                          80                          85

acc aac cgc tac cga agc tcc gta gac ggc gaa aga gtg cca tta gcg 403  
 Thr Asn Arg Tyr Arg Ser Ser Val Asp Gly Glu Arg Val Pro Leu Ala  
                           90                          95                          100

ccg aag att gtg atg gca gaa acc cga ggg gta ttt cat gga ccg att 451  
 Pro Lys Ile Val Met Ala Glu Thr Arg Gly Val Phe His Gly Pro Ile  
                           105                          110                          115

acc att aac gtg ctc gtg cca gca cac aat gag gcg gaa aga att act 499  
 Thr Ile Asn Val Leu Val Pro Ala His Asn Glu Ala Glu Arg Ile Thr  
                           120                          125                          130

gga aca att cag gca ttg aaa tca caa cat gag cct cca gaa cgc atc 547  
 Gly Thr Ile Gln Ala Leu Lys Ser Gln His Glu Pro Pro Glu Arg Ile  
 135 140 145  
 gtt gta gtt gcc gat aat tgc act gat gaa act acg gaa tta gcc cgt 595  
 Val Val Val Ala Asp Asn Cys Thr Asp Glu Thr Thr Glu Leu Ala Arg  
 150 155 160 165  
 gct gag gga gtg gag gtc ttg gaa aca gtc aat aat aag ttt aag aag 643  
 Ala Glu Gly Val Glu Val Leu Glu Thr Val Asn Asn Lys Phe Lys Lys  
 170 175 180  
 gcc gga gga ctc aat cag gct ttg agc cgg atg ctt ccc aca ttg ggg 691  
 Ala Gly Gly Leu Asn Gln Ala Leu Ser Arg Met Leu Pro Thr Leu Gly  
 185 190 195  
 gag aat gac att gtg atg atc gtt gac gct gat aca gca ctt gat caa 739  
 Glu Asn Asp Ile Val Met Ile Val Asp Ala Asp Thr Ala Leu Asp Gln  
 200 205 210  
 ggt ttc ctc aag gaa gca cgg cgc cgc ttt gag tct gat cgc gct cta 787  
 Gly Phe Leu Lys Glu Ala Arg Arg Arg Phe Glu Ser Asp Arg Ala Leu  
 215 220 225  
 atg gcc gtg ggc gga ttg ttc tac ggt gag tca ggc tcc gga tgg ctt 835  
 Met Ala Val Gly Gly Leu Phe Tyr Gly Glu Ser Gly Ser Gly Trp Leu  
 230 235 240 245  
 ggc caa tat cag cgc aac gaa tac acc cgt tat agc cgt gac atc tat 883  
 Gly Gln Tyr Gln Arg Asn Glu Tyr Thr Arg Tyr Ser Arg Asp Ile Tyr  
 250 255 260  
 cga cgc cgc gga cgt gtg ttt gtt ttg act gga aca gcg tcg gct ttt 931  
 Arg Arg Arg Gly Arg Val Phe Val Leu Thr Gly Thr Ala Ser Ala Phe  
 265 270 275  
 cgg cca cgc ggc ctg cgg aca gta gcg gaa tca cgc ggg aca ttg atc 979  
 Arg Pro Arg Gly Leu Arg Thr Val Ala Glu Ser Arg Gly Thr Leu Ile  
 280 285 290  
 ccc gga cgt aaa gcc gat gtt tat gac acc gcg ggc gtt gac cga aga 1027  
 Pro Gly Arg Lys Ala Asp Val Tyr Asp Thr Ala Gly Val Asp Arg Arg  
 295 300 305  
 taatgagttg accctggcctt tga 1050

&lt;210&gt; 422

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 422

Met Lys Lys Lys Ser Phe Pro Ile Ala Arg Val Ile Gly Ile Gly Val  
 1 5 10 15

Leu Gly Ile Ala Gly Met Gly Ile Leu Leu Leu Trp Leu Ala Val Thr  
 20 25 30

Leu Ser Asp Pro Ala Ser Pro Gly Ala Lys Glu Thr Glu Val Phe Asp

35	40	45
Arg Trp Lys Val Leu Phe Asp	Asp Tyr Ile Pro	Pro Val Arg Val Leu
50	55	60
Val Ala Ala Ile Ile Val Ala Leu Ile Phe Val Phe Ile Ala Ala Thr		
65	70	75 80
Val Glu Arg Thr Val Thr Asn Arg Tyr Arg Ser Ser Val Asp Gly Glu		
	85	90 95
Arg Val Pro Leu Ala Pro Lys Ile Val Met Ala Glu Thr Arg Gly Val		
	100	105 110
Phe His Gly Pro Ile Thr Ile Asn Val Leu Val Pro Ala His Asn Glu		
	115	120 125
Ala Glu Arg Ile Thr Gly Thr Ile Gln Ala Leu Lys Ser Gln His Glu		
	130	135 140
Pro Pro Glu Arg Ile Val Val Val Ala Asp Asn Cys Thr Asp Glu Thr		
	145	150 155 160
Thr Glu Leu Ala Arg Ala Glu Gly Val Glu Val Leu Glu Thr Val Asn		
	165	170 175
Asn Lys Phe Lys Lys Ala Gly Gly Leu Asn Gln Ala Leu Ser Arg Met		
	180	185 190
Leu Pro Thr Leu Gly Glu Asn Asp Ile Val Met Ile Val Asp Ala Asp		
	195	200 205
Thr Ala Leu Asp Gln Gly Phe Leu Lys Glu Ala Arg Arg Arg Phe Glu		
	210	215 220
Ser Asp Arg Ala Leu Met Ala Val Gly Gly Leu Phe Tyr Gly Glu Ser		
	225	230 235 240
Gly Ser Gly Trp Leu Gly Gln Tyr Gln Arg Asn Glu Tyr Thr Arg Tyr		
	245	250 255
Ser Arg Asp Ile Tyr Arg Arg Arg Gly Arg Val Phe Val Leu Thr Gly		
	260	265 270
Thr Ala Ser Ala Phe Arg Pro Arg Gly Leu Arg Thr Val Ala Glu Ser		
	275	280 285
Arg Gly Thr Leu Ile Pro Gly Arg Lys Ala Asp Val Tyr Asp Thr Ala		
	290	295 300
Gly Val Asp Arg Arg		
305		

&lt;210&gt; 423

&lt;211&gt; 882

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(859)

&lt;223&gt; RXA00042

&lt;400&gt; 423

```

gtggtctttg actcaaacgg ccagttacaa caggtccatt tagaccatca agtaatttaa 60
atacgagcaa aacttttctg ataataaaag gagtccgacc atg gac atc atc atc 115
                                         Met Asp Ile Ile Ile
                                         1           5

tgc aaa gac gag caa gaa gtc ggc aaa gca gcg gca gcc ctg atc gca 163
Cys Lys Asp Glu Gln Glu Val Gly Lys Ala Ala Ala Ala Leu Ile Ala
              10              15              20

ccc ttc gca act aag ggc gga acc ttg ggg ctt gca act gga tgc tca 211
Pro Phe Ala Thr Lys Gly Gly Thr Leu Gly Leu Ala Thr Gly Ser Ser
              25              30              35

cct ttg agc acc tac caa gag ctc att cgc atg tat gaa gct ggg gaa 259
Pro Leu Ser Thr Tyr Gln Glu Leu Ile Arg Met Tyr Glu Ala Gly Glu
              40              45              50

gtg tca ttc aag aac tgc aag gca ttc ttg ttg gat gaa tac gtg gga 307
Val Ser Phe Lys Asn Cys Lys Ala Phe Leu Leu Asp Glu Tyr Val Gly
              55              60              65

tta acg cgc gac gat gaa aac agc tac ttc aaa acc att cgt aaa gag 355
Leu Thr Arg Asp Asp Glu Asn Ser Tyr Phe Lys Thr Ile Arg Lys Glu
              70              75              80              85

ttc act gac cac atc gac atc gtt gat gaa gag gtc tac agc cca gat 403
Phe Thr Asp His Ile Asp Ile Val Asp Glu Glu Val Tyr Ser Pro Asp
              90              95              100

ggg gca aac cct gat cca tac gaa gca gct gca gag tat gag gca aag 451
Gly Ala Asn Pro Asp Pro Tyr Glu Ala Ala Ala Glu Tyr Glu Ala Lys
              105              110              115

atc gct gca gaa tcc gtt gat gtt caa atc ctt ggc atc ggc gga aac 499
Ile Ala Ala Glu Ser Val Asp Val Gln Ile Leu Gly Ile Gly Gly Asn
              120              125              130

ggc cac atc gct ttc aat gag cca tca tct tct ctg tca gga ctg aca 547
Gly His Ile Ala Phe Asn Glu Pro Ser Ser Ser Leu Ser Gly Leu Thr
              135              140              145

aag gtc cag gcg ctg cac cct aaa act gtg gag gac aac gct cga ttc 595
Lys Val Gln Ala Leu His Pro Lys Thr Val Glu Asp Asn Ala Arg Phe
              150              155              160              165

ttc aac acc atc gaa gag gtc cca acc cac gcc ctc acc cag ggt ttg 643
Phe Asn Thr Ile Glu Glu Val Pro Thr His Ala Leu Thr Gln Gly Leu
              170              175              180

ggc act ttg tcc cgc gcg caa aac atc gtg ttg gtg gca act ggt gaa 691
Gly Thr Leu Ser Arg Ala Gln Asn Ile Val Leu Val Ala Thr Gly Glu
              185              190              195

gga aaa gcc gac gcc atc cgc gga act gtg gaa gcc cca ctg acc gcc 739
Gly Lys Ala Asp Ala Ile Arg Gly Thr Val Glu Gly Pro Leu Thr Ala
              200              205              210

```

atg tgc cca ggt tcc atc ctg cag atg cac aac aat gcc acc atc atc 787  
 Met Cys Pro Gly Ser Ile Leu Gln Met His Asn Asn Ala Thr Ile Ile  
 215 220 225

gtt gat gaa gca gca gca tcc aag ctg gaa aac gct gat cac tac cgt 835  
 Val Asp Glu Ala Ala Ala Ser Lys Leu Glu Asn Ala Asp His Tyr Arg  
 230 235 240 245

ctc atg gag caa tta aag ctg cgc tagaaacaaa aaggaaagta gtg 882  
 Leu Met Glu Gln Leu Lys Leu Arg  
 250

<210> 424

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 424

Met Asp Ile Ile Ile Cys Lys Asp Glu Gln Glu Val Gly Lys Ala Ala  
 1 5 10 15

Ala Ala Leu Ile Ala Pro Phe Ala Thr Lys Gly Gly Thr Leu Gly Leu  
 20 25 30

Ala Thr Gly Ser Ser Pro Leu Ser Thr Tyr Gln Glu Leu Ile Arg Met  
 35 40 45

Tyr Glu Ala Gly Glu Val Ser Phe Lys Asn Cys Lys Ala Phe Leu Leu  
 50 55 60

Asp Glu Tyr Val Gly Leu Thr Arg Asp Asp Glu Asn Ser Tyr Phe Lys  
 65 70 75 80

Thr Ile Arg Lys Glu Phe Thr Asp His Ile Asp Ile Val Asp Glu Glu  
 85 90 95

Val Tyr Ser Pro Asp Gly Ala Asn Pro Asp Pro Tyr Glu Ala Ala Ala  
 100 105 110

Glu Tyr Glu Ala Lys Ile Ala Ala Glu Ser Val Asp Val Gln Ile Leu  
 115 120 125

Gly Ile Gly Gly Asn Gly His Ile Ala Phe Asn Glu Pro Ser Ser Ser  
 130 135 140

Leu Ser Gly Leu Thr Lys Val Gln Ala Leu His Pro Lys Thr Val Glu  
 145 150 155 160

Asp Asn Ala Arg Phe Phe Asn Thr Ile Glu Glu Val Pro Thr His Ala  
 165 170 175

Leu Thr Gln Gly Leu Gly Thr Leu Ser Arg Ala Gln Asn Ile Val Leu  
 180 185 190

Val Ala Thr Gly Glu Gly Lys Ala Asp Ala Ile Arg Gly Thr Val Glu  
 195 200 205

Gly Pro Leu Thr Ala Met Cys Pro Gly Ser Ile Leu Gln Met His Asn  
 210 215 220

Asn Ala Thr Ile Ile Val Asp Glu Ala Ala Ala Ser Lys Leu Glu Asn  
 225 230 235 240

Ala Asp His Tyr Arg Leu Met Glu Gln Leu Lys Leu Arg  
 245 250

<210> 425

<211> 1998

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1975)

<223> RXA01482

<400> 425

```

ttgcgtgctg caacttaatt atggtcctcc cagctcagtg tgctgtgtgg attgtttatt 60

ctcgtccatt aagtgatcga. gaaaaagttg ttgtaaagtc atg cgc atg tgt gga 115
                                         Met Arg Met Cys Gly
                                         1 5

att gtt gga tat att ggc caa gcg ggc gac tcc cgt gat tac ttt gct 163
Ile Val Gly Tyr Ile Gly Gln Ala Gly Asp Ser Arg Asp Tyr Phe Ala
                        10 15 20

cta gat gta gtt gtt gaa gga cta cgt cgc ctg gaa tac cgc gga tat 211
Leu Asp Val Val Val Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr
                        25 30 35

gac tcc gca ggt att gct att cac gcc aat ggt gag att agc tac cga 259
Asp Ser Ala Gly Ile Ala Ile His Ala Asn Gly Glu Ile Ser Tyr Arg
                        40 45 50

aag aag gcc gga aag gtt gct gca cta gat gca gaa atc gct aaa gca 307
Lys Lys Ala Gly Lys Val Ala Ala Leu Asp Ala Glu Ile Ala Lys Ala
                        55 60 65

cct ctt cca gat tct att ttg gga att gga cac acc cgt tgg gca act 355
Pro Leu Pro Asp Ser Ile Leu Gly Ile Gly His Thr Arg Trp Ala Thr
                        70 75 80 85

cat ggt ggc cca acc gat gtc aac gct cac ccc cac gtt gtt tcc aat 403
His Gly Gly Pro Thr Asp Val Asn Ala His Pro His Val Val Ser Asn
                        90 95 100

ggc aag ctt gcc gta gta cac aac ggc atc atc gaa aac ttt gcg gaa 451
Gly Lys Leu Ala Val Val His Asn Gly Ile Ile Glu Asn Phe Ala Glu
                        105 110 115

ctg cgc tct gag ctt tcc gct aag ggc tac aac ttt gta tcc gat acc 499
Leu Arg Ser Glu Leu Ser Ala Lys Gly Tyr Asn Phe Val Ser Asp Thr
                        120 125 130

gat acc gaa gtt gct gct tct ttg ctt gct gaa att tac aat act cag 547
Asp Thr Glu Val Ala Ala Ser Leu Leu Ala Glu Ile Tyr Asn Thr Gln
                        135 140 145

```

gca aac ggt gac ctc acc ctt gct atg cag ctg acc ggt cag cgc ctt	595
Ala Asn Gly Asp Leu Thr Leu Ala Met Gln Leu Thr Gly Gln Arg Leu	
150 155 160 165	
gag ggt gct ttc acc ctg cta gct att cat gct gat cac gat gac cgc	643
Glu Gly Ala Phe Thr Leu Leu Ala Ile His Ala Asp His Asp Asp Arg	
170 175 180	
atc gtt gca gct cgt cgt aac tct cct ttg gtt atc ggc gtc ggc gag	691
Ile Val Ala Ala Arg Arg Asn Ser Pro Leu Val Ile Gly Val Gly Glu	
185 190 195	
ggc gag aac ttc ctc gga tct gac gtt tct ggc ttt att gat tac acc	739
Gly Glu Asn Phe Leu Gly Ser Asp Val Ser Gly Phe Ile Asp Tyr Thr	
200 205 210	
cgc aag gct gta gag ctg gct aat gac cag gtt gtt acc atc acc gct	787
Arg Lys Ala Val Glu Leu Ala Asn Asp Gln Val Val Thr Ile Thr Ala	
215 220 225	
gat gat tac gcc atc acc aac ttt gat gga tca gaa gca gtt ggc aag	835
Asp Asp Tyr Ala Ile Thr Asn Phe Asp Gly Ser Glu Ala Val Gly Lys	
230 235 240 245	
cct ttc gac gtg gag tgg gac gct gca gct gct gaa aag ggt ggc ttc	883
Pro Phe Asp Val Glu Trp Asp Ala Ala Ala Glu Lys Gly Gly Phe	
250 255 260	
ggt tcc ttc atg gag aag gaa atc cac gat cag cca gca gct gtt cgc	931
Gly Ser Phe Met Glu Lys Glu Ile His Asp Gln Pro Ala Ala Val Arg	
265 270 275	
gat acc ctg atg ggc cgt ctt gat gaa gat ggc aag ctc gtt ctt gat	979
Asp Thr Leu Met Gly Arg Leu Asp Glu Asp Gly Lys Leu Val Leu Asp	
280 285 290	
gag ctg cgc atc gat gaa gct att ctg cgt agt gtc gac aag atc gtc	1027
Glu Leu Arg Ile Asp Glu Ala Ile Leu Arg Ser Val Asp Lys Ile Val	
295 300 305	
att gtt gct tgt ggt act gca gct tat gca ggc cag gtt gct cgt tac	1075
Ile Val Ala Cys Gly Thr Ala Ala Tyr Ala Gly Gln Val Ala Arg Tyr	
310 315 320 325	
gcc att gag cac tgg tgc cgc atc cca acc gag gtg gag ctg gct cac	1123
Ala Ile Glu His Trp Cys Arg Ile Pro Thr Glu Val Glu Leu Ala His	
330 335 340	
gag ttc cgt tac cgc gac cca atc ctc aac gag aag acc ctt gtt gtg	1171
Glu Phe Arg Tyr Arg Asp Pro Ile Leu Asn Glu Lys Thr Leu Val Val	
345 350 355	
gca ttg tcc cag tcc ggc gag acc atg gat acc ctc atg gct gtt cgc	1219
Ala Leu Ser Gln Ser Gly Glu Thr Met Asp Thr Leu Met Ala Val Arg	
360 365 370	
cac gca cgt gag cag ggt gcc aag gtt gtt gct att tgt aac act gtt	1267
His Ala Arg Glu Gln Gly Ala Lys Val Val Ala Ile Cys Asn Thr Val	
375 380 385	
gga tcc act ctt cca cgt gaa gca gat gcg tcc ctg tac acc tac gct	1315

Gly 390	Ser	Thr	Leu	Pro	Arg 395	Glu	Ala	Asp	Ala	Ser 400	Leu	Tyr	Thr	Tyr	Ala 405	
ggc cct gag atc gct gtg gcg tcc acc aag gcg ttc ttg gct cag atc																1363
Gly Pro Glu Ile				Ala Val	Ala Ser	Thr	Lys	Ala	Phe	Leu	Ala	Gln	Ile			
				410			415					420				
act gct tct tac ttg ctt ggc ctg tac ttg gct cag ctg cgc ggc aac																1411
Thr Ala Ser Tyr				Leu Leu	Gly Leu	Tyr	Leu	Ala	Gln	Leu	Arg	Gly	Asn			
				425			430				435					
aag ttc gct gat gag gtt tct tcc att ctg gac agc ctg cgt gag atg																1459
Lys Phe				Ala Asp	Glu Val	Ser	Ile	Leu	Asp	Ser	Leu	Arg	Glu	Met		
				440			445				450					
cct gag aag att cag cag gtc atc gat gca gaa gag cag atc aag aag																1507
Pro Glu Lys Ile				Gln Gln	Val Ile	Asp	Ala	Glu	Glu	Gln	Ile	Lys	Lys			
				455			460				465					
ctt ggc caa gat atg gca gat gct aag tct gtg ctg ttc ctg ggc cgc																1555
Leu Gly Gln Asp				Met Ala	Asp Ala	Lys	Ser	Val	Leu	Phe	Leu	Gly	Arg			
				470			475				480		485			
cac gtt ggt ttc cca gtt gcg ctt gag ggt gcg ttg aag ctc aag gag																1603
His Val Gly Phe				Pro Val	Ala Leu	Glu	Gly	Ala	Leu	Lys	Leu	Lys	Glu			
				490			495					500				
atc gca tac ctg cac gct gaa ggt ttc gct gca ggc gag ctc aag cac																1651
Ile Ala Tyr				Leu His	Ala Glu	Gly	Phe	Ala	Ala	Gly	Glu	Leu	Lys	His		
				505			510					515				
ggc cca att gct ttg gtt gag gaa ggc cag ccg atc ttc gtt atc gtg																1699
Gly Pro Ile Ala				Leu Val	Glu Glu	Gly	Gln	Pro	Ile	Phe	Val	Ile	Val			
				520			525				530					
cct tca cct cgt ggt cgc gat tcc ctg cac tcc aag gtt gtc tcc aac																1747
Pro Ser Pro Arg				Gly Arg	Asp Ser	Leu	His	Ser	Lys	Val	Val	Ser	Asn			
				535			540				545					
att cag gag atc cgt gca cgt ggc gct gtc acc atc gtg att gca gag																1795
Ile Gln Glu Ile				Arg Ala	Arg Gly	Ala	Val	Thr	Ile	Val	Ile	Ala	Glu			
				550			555				560		565			
gaa ggc gat gag gct gtc aac gat tac gcc aac ttc atc atc cgc att																1843
Glu Gly Asp Glu				Ala Val	Asn Asp	Tyr	Ala	Asn	Phe	Ile	Ile	Arg	Ile			
				570			575					580				
cct cag gcc cca acc ctg atg cag cct ctg ctg tcc acc gtg cct ctg																1891
Pro Gln Ala Pro				Thr Leu	Met Gln	Pro	Leu	Leu	Ser	Thr	Val	Pro	Leu			
				585			590					595				
cag atc ttt gcg tgc gct gtg gca acc gca aag ggc tac aac gtg gat																1939
Gln Ile Phe Ala				Cys Ala	Val Ala	Thr	Ala	Lys	Gly	Tyr	Asn	Val	Asp			
				600			605				610					
cag cct cgt aac ctg gca aag tct gtc acc gtc gaa taaaaagatt																1985
Gln Pro Arg Asn				Leu Ala	Lys Ser	Val	Thr	Val	Glu							
				615			620		625							
tcgcttctcg acg																1998



&lt;210&gt; 426

&lt;211&gt; 625

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 426

Met Arg Met Cys Gly Ile Val Gly Tyr Ile Gly Gln Ala Gly Asp Ser  
 1 5 10 15

Arg Asp Tyr Phe Ala Leu Asp Val Val Val Glu Gly Leu Arg Arg Leu  
 20 25 30

Glu Tyr Arg Gly Tyr Asp Ser Ala Gly Ile Ala Ile His Ala Asn Gly  
 35 40 45

Glu Ile Ser Tyr Arg Lys Lys Ala Gly Lys Val Ala Ala Leu Asp Ala  
 50 55 60

Glu Ile Ala Lys Ala Pro Leu Pro Asp Ser Ile Leu Gly Ile Gly His  
 65 70 75 80

Thr Arg Trp Ala Thr His Gly Gly Pro Thr Asp Val Asn Ala His Pro  
 85 90 95

His Val Val Ser Asn Gly Lys Leu Ala Val Val His Asn Gly Ile Ile  
 100 105 110

Glu Asn Phe Ala Glu Leu Arg Ser Glu Leu Ser Ala Lys Gly Tyr Asn  
 115 120 125

Phe Val Ser Asp Thr Asp Thr Glu Val Ala Ala Ser Leu Leu Ala Glu  
 130 135 140

Ile Tyr Asn Thr Gln Ala Asn Gly Asp Leu Thr Leu Ala Met Gln Leu  
 145 150 155 160

Thr Gly Gln Arg Leu Glu Gly Ala Phe Thr Leu Leu Ala Ile His Ala  
 165 170 175

Asp His Asp Asp Arg Ile Val Ala Ala Arg Arg Asn Ser Pro Leu Val  
 180 185 190

Ile Gly Val Gly Glu Gly Glu Asn Phe Leu Gly Ser Asp Val Ser Gly  
 195 200 205

Phe Ile Asp Tyr Thr Arg Lys Ala Val Glu Leu Ala Asn Asp Gln Val  
 210 215 220

Val Thr Ile Thr Ala Asp Asp Tyr Ala Ile Thr Asn Phe Asp Gly Ser  
 225 230 235 240

Glu Ala Val Gly Lys Pro Phe Asp Val Glu Trp Asp Ala Ala Ala Ala  
 245 250 255

Glu Lys Gly Gly Phe Gly Ser Phe Met Glu Lys Glu Ile His Asp Gln  
 260 265 270

Pro Ala Ala Val Arg Asp Thr Leu Met Gly Arg Leu Asp Glu Asp Gly  
 275 280 285

Lys Leu Val Leu Asp Glu Leu Arg Ile Asp Glu Ala Ile Leu Arg Ser  
 290 295 300  
 Val Asp Lys Ile Val Ile Val Ala Cys Gly Thr Ala Ala Tyr Ala Gly  
 305 310 315 320  
 Gln Val Ala Arg Tyr Ala Ile Glu His Trp Cys Arg Ile Pro Thr Glu  
 325 330 335  
 Val Glu Leu Ala His Glu Phe Arg Tyr Arg Asp Pro Ile Leu Asn Glu  
 340 345 350  
 Lys Thr Leu Val Val Ala Leu Ser Gln Ser Gly Glu Thr Met Asp Thr  
 355 360 365  
 Leu Met Ala Val Arg His Ala Arg Glu Gln Gly Ala Lys Val Val Ala  
 370 375 380  
 Ile Cys Asn Thr Val Gly Ser Thr Leu Pro Arg Glu Ala Asp Ala Ser  
 385 390 395 400  
 Leu Tyr Thr Tyr Ala Gly Pro Glu Ile Ala Val Ala Ser Thr Lys Ala  
 405 410 415  
 Phe Leu Ala Gln Ile Thr Ala Ser Tyr Leu Leu Gly Leu Tyr Leu Ala  
 420 425 430  
 Gln Leu Arg Gly Asn Lys Phe Ala Asp Glu Val Ser Ser Ile Leu Asp  
 435 440 445  
 Ser Leu Arg Glu Met Pro Glu Lys Ile Gln Gln Val Ile Asp Ala Glu  
 450 455 460  
 Glu Gln Ile Lys Lys Leu Gly Gln Asp Met Ala Asp Ala Lys Ser Val  
 465 470 475 480  
 Leu Phe Leu Gly Arg His Val Gly Phe Pro Val Ala Leu Glu Gly Ala  
 485 490 495  
 Leu Lys Leu Lys Glu Ile Ala Tyr Leu His Ala Glu Gly Phe Ala Ala  
 500 505 510  
 Gly Glu Leu Lys His Gly Pro Ile Ala Leu Val Glu Glu Gly Gln Pro  
 515 520 525  
 Ile Phe Val Ile Val Pro Ser Pro Arg Gly Arg Asp Ser Leu His Ser  
 530 535 540  
 Lys Val Val Ser Asn Ile Gln Glu Ile Arg Ala Arg Gly Ala Val Thr  
 545 550 555 560  
 Ile Val Ile Ala Glu Glu Gly Asp Glu Ala Val Asn Asp Tyr Ala Asn  
 565 570 575  
 Phe Ile Ile Arg Ile Pro Gln Ala Pro Thr Leu Met Gln Pro Leu Leu  
 580 585 590  
 Ser Thr Val Pro Leu Gln Ile Phe Ala Cys Ala Val Ala Thr Ala Lys  
 595 600 605  
 Gly Tyr Asn Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val

610 615 620

Glu  
625

<210> 427  
<211> 666  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (1)..(666)  
<223> RXN03179

<400> 427

gct cgt gag gca tgg cgc att ttc atg tcc cac tgg gat ctc tac gca	48
Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala	
1 5 10 15	
gga acc gca act ggc tac tgg gtg gag cag gaa ttt gag cac gtt ttc	96
Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe	
20 25 30	
ggc atc aac gcg gag cgc ctg aat gtt ggc acc cca gaa cat gct gac	144
Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp	
35 40 45	
gcc atc ttt gat gag ctg acc gat att ctt gcc aag cca gat ttc cga	192
Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg	
50 55 60	
cca cgc gca ctg gct gag cag ttc aac ttg gaa gtt cta gcc acc acc	240
Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr	
65 70 75 80	
gac gat ccg ctc gat gac ctg gca gat cac aag gca ctg gca gat gat	288
Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp	
85 90 95	
cca acc ttc tcc cct cgt gtg ctc cct acc ttc cgc cca gac gca tac	336
Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr	
100 105 110	
acc aag atg tac aac gct ggt tgg gca gaa aaa acc acc aag ctt atc	384
Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile	
115 120 125	
gat acc gca ggt gac ggc aag gca ggc tgg gag ggt tac ctt cag gca	432
Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala	
130 135 140	
atg cgc aac cgc cgc cag tac ttc atc aat cac ggt gca acc tcc gcg	480
Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala	
145 150 155 160	
gac cac ggt ctc cac gac acc gac acc acc cca ctg agc cac aaa gat	528
Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp	
165 170 175	

gcc cag aag atc ttg gac aag ggt ctc gct ggc aca gca acc ttg gct 576  
 Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala  
           180                          185                          190

gaa atg cat gcc ttc gaa gcc aac acc acc tac cgt tcg cgg aaa tgt 624  
 Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Ser Arg Lys Cys  
           195                          200                          205

cca aga aga cgg ctg gtc atg acc atc cac cag gtg tgt acc 666  
 Pro Arg Arg Arg Leu Val Met Thr Ile His Gln Val Cys Thr  
           210                          215                          220

<210> 428

<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 428

Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala  
       1                          5                          10                          15

Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe  
           20                          25                          30

Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp  
           35                          40                          45

Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg  
       50                          55                          60

Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr  
       65                          70                          75                          80

Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp  
           85                          90                          95

Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr  
           100                          105                          110

Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile  
           115                          120                          125

Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala  
       130                          135                          140

Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala  
       145                          150                          155                          160

Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp  
           165                          170                          175

Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala  
           180                          185                          190

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Ser Arg Lys Cys  
           195                          200                          205

Pro Arg Arg Arg Leu Val Met Thr Ile His Gln Val Cys Thr  
       210                          215                          220

<210> 429  
 <211> 672  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(672)  
 <223> FRXA02872

<400> 429  
 gct cgt gag gca tgg cgc att ttc atg tcc cac tgg gat ctc tac gca 48  
 Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala  
 1 5 10 15  
 gga acc gca act ggc tac tgg gtg gag cag gaa ttt gag cac gtt ttc 96  
 Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe  
 20 25 30  
 ggc atc aac gcg gag cgc ctg aat gtt ggc acc cca gaa cat gct gac 144  
 Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp  
 35 40 45  
 gcc atc ttt gat gag ctg acc gat att ctt gcc aag cca gat ttc cga 192  
 Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg  
 50 55 60  
 cca cgc gca ctg gct gag cag ttc aac ttg gaa gtt cta gcc acc acc 240  
 Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr  
 65 70 75 80  
 gac gat ccg ctc gat gac ctg gca gat cac aag gca ctg gca gat gat 288  
 Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp  
 85 90 95  
 cca acc ttc tcc cct cgt gtg ctc cct acc ttc cgc cca gac gca tac 336  
 Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr  
 100 105 110  
 acc aag atg tac aac gct ggt tgg gca gaa aaa acc acc aag ctt atc 384  
 Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile  
 115 120 125  
 gat acc gca ggt gac ggc aag gca ggc tgg gag ggt tac ctt cag gca 432  
 Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala  
 130 135 140  
 atg cgc aac cgc cgc cag tac ttc atc aat cac ggt gca acc tcc gcg 480  
 Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala  
 145 150 155 160  
 gac cac ggt ctc cac gac acc gac acc acc cca ctg agc cac aaa gat 528  
 Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp  
 165 170 175  
 gcc cag aag atc ttg gac aag ggt ctc gct ggc aca gca acc ttg gct 576  
 Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala  
 180 185 190  
 gaa atg cat gcc ttc gaa gcc aac acc acc tac cgt ttc gcg gaa atg 624

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Phe Ala Glu Met  
 195 200 205

tcc caa gaa gac ggc ctg gtc atg acc atc cac cca ggt gtg tac cgc 672  
 Ser Gln Glu Asp Gly Leu Val Met Thr Ile His Pro Gly Val Tyr Arg  
 210 215 220

<210> 430

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 430

Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala  
 1 5 10 15

Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe  
 20 25 30

Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp  
 35 40 45

Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg  
 50 55 60

Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr  
 65 70 75 80

Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp  
 85 90 95

Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr  
 100 105 110

Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile  
 115 120 125

Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala  
 130 135 140

Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala  
 145 150 155 160

Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp  
 165 170 175

Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala  
 180 185 190

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Phe Ala Glu Met  
 195 200 205

Ser Gln Glu Asp Gly Leu Val Met Thr Ile His Pro Gly Val Tyr Arg  
 210 215 220

<210> 431

<211> 533  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(510)  
 <223> RXN03180

<400> 431  
 ttc ggt gag aac aaa gat ctc atc tct gac agc agt ttc aac cgc tgg 48  
 Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp  
 1 5 10 15  
 ctg cgt acg gtt tcc ctc gga tcg acc cag gat gcc gat atg gct gca 96  
 Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala  
 20 25 30  
 gct tcc aac ttg gca gcc aat tct aaa atg gcc cgc cag aac acc cgc 144  
 Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg  
 35 40 45  
 gat atc ctc gac gca gtc tct gat ggt ggc gtc atg ctc ggc cga aac 192  
 Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn  
 50 55 60  
 ggt gcc cta gtg ttg gga cct gtg gtt gga act ctc cac att aaa ttc 240  
 Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe  
 65 70 75 80  
 att gcg cct ttg aac aag cgt gtg gaa aga gtc atg tac aaa act gga 288  
 Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly  
 85 90 95  
 ctc tca gaa gct gct gca gct gag caa tgt gct ttg gag gat cgt ctc 336  
 Leu Ser Glu Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu  
 100 105 110  
 cgc gaa gag atg gcc cac gct ttg tat caa tgg aat ccg gga cgc gat 384  
 Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp  
 115 120 125  
 gaa aac tat gac ctc gtg atc aac acc ggt tcg atg aca tac gaa caa 432  
 Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln  
 130 135 140  
 atc gtt gat cta gtt gtg gaa act tac gcc agg aag tat ccg ctc cac 480  
 Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His  
 145 150 155 160  
 gtg aga atc att ccg aac gga aaa gac caa taaacataca gtccccgtga 530  
 Val Arg Ile Ile Pro Asn Gly Lys Asp Gln  
 165 170  
 tgt 533

<210> 432  
 <211> 170  
 <212> PRT  
 <213> Corynebacterium glutamicum

&lt;400&gt; 432

Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp  
 1 5 10 15

Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala  
 20 25 30

Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg  
 35 40 45

Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn  
 50 55 60

Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe  
 65 70 75 80

Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly  
 85 90 95

Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu  
 100 105 110

Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp  
 115 120 125

Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln  
 130 135 140

Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His  
 145 150 155 160

Val Arg Ile Ile Pro Asn Gly Lys Asp Gln  
 165 170

&lt;210&gt; 433

&lt;211&gt; 533

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(510)

&lt;223&gt; FRXA02873

&lt;400&gt; 433

ttc ggt gag aac aaa gat ctc atc tct gac agc agt ttc aac cgc tgg 48  
 Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp  
 1 5 10 15

ctg cgt acg gtt tcc ctc gga tcg acc cag gat gcc gat atg gct gca 96  
 Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala  
 20 25 30

gct tcc aac ttg gca gcc aat tct aaa atg gcc cgc cag aac acc cgc 144  
 Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg  
 35 40 45

gat atc ctc gac gca gtc tct gat ggt ggc gtc atg ctc ggc cga aac 192  
 Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn



50	55	60	
ggt gcc cta gtg ttg gga cct gtg gtt gga act ctc cac att aaa ttc			240
Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe			
65	70	75	80
att gcg cct ttg aac aag cgt gtg gaa aga gtc atg tac aaa act gga			288
Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly			
	85	90	95
ctc tca gaa gct gct gca gct gag caa tgt gct ttg gag gat cgt ctc			336
Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu			
	100	105	110
cgc gaa gag atg gcc cac gct ttg tat caa tgg aat ccg gga cgc gat			384
Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp			
	115	120	125
gaa aac tat gac ctc gtg atc aac acc ggt tcg atg aca tac gaa caa			432
Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln			
	130	135	140
atc gtt gat cta gtt gtg gaa act tac gcc agg aag tat ccg ctc cac			480
Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His			
	145	150	155
gtg aga atc att ccg aac gga aaa gac caa taaacataca gtccccgtga			530
Val Arg Ile Ile Pro Asn Gly Lys Asp Gln			
	165	170	
tgt			533

&lt;210&gt; 434

&lt;211&gt; 170

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 434

Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp			
1	5	10	15
Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala			
	20	25	30
Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg			
	35	40	45
Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn			
	50	55	60
Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe			
	65	70	75
Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly			
	85	90	95
Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu			
	100	105	110
Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp			

```

115          120          125
Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln
130          135          140

Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His
145          150          155          160

Val Arg Ile Ile Pro Asn Gly Lys Asp Gln
165          170

<210> 435
<211> 798
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(775)
<223> RXA02292

<400> 435
tgcaccacgc cagctgcaac cctgcgcggt ggtctgggaa gttggtggag gggatcgtcg 60

aaaagcgtag gcactaaagt tctcctgcac aatggaggat atg gac aat gac ttt 115
Met Asp Asn Asp Phe
1 5

gaa tct atc gag aaa atg agc agc ggc gat tgg tac gtg gct acc ggc 163
Glu Ser Ile Glu Lys Met Ser Ser Gly Asp Trp Tyr Val Ala Thr Gly
10 15 20

gcg gaa cgt gaa gaa gtg gca caa aaa aca gcg tta ctt ttc cac gaa 211
Ala Glu Arg Glu Glu Val Ala Gln Lys Thr Ala Leu Leu Phe His Glu
25 30 35

tac aac caa att gga cct aca gac ccc gca cga act gcc gaa ata cta 259
Tyr Asn Gln Ile Gly Pro Thr Asp Pro Ala Arg Thr Ala Glu Ile Leu
40 45 50

aga act gta cta aat cct gcc agc gga acc tgc acg atc aaa gcg cca 307
Arg Thr Val Leu Asn Pro Ala Ser Gly Thr Cys Thr Ile Lys Ala Pro
55 60 65

gcc atc att gaa tac ggc ttc aac acc acg atc ggc gag cat gtg ttc 355
Ala Ile Ile Glu Tyr Gly Phe Asn Thr Thr Ile Gly Glu His Val Phe
70 75 80 85

atc aac ttt ggc ctc acc att tta gat atc gca ccg gtt cgc atc ggg 403
Ile Asn Phe Gly Leu Thr Ile Leu Asp Ile Ala Pro Val Arg Ile Gly
90 95 100

gca cgc agc atg ctc ggg cca aac tgt cag ctc ttc acc gca ggt cac 451
Ala Arg Ser Met Leu Gly Pro Asn Cys Gln Leu Phe Thr Ala Gly His
105 110 115

ccg gtc gat gac tgg gaa atg cgc tcc ggt ggg tgg gaa aat ggc gca 499
Pro Val Asp Asp Trp Glu Met Arg Ser Gly Gly Trp Glu Asn Gly Ala
120 125 130

```

ccc att tcc att ggc gag gat acg tgg ctg ggt gga aat gtc acc gtc 547  
 Pro Ile Ser Ile Gly Glu Asp Thr Trp Leu Gly Gly Asn Val Thr Val  
 135 140 145

gtt ggt ggc gtg agc att ggc gat agg tgt gtg att ggc gcg ggg ccc 595  
 Val Gly Gly Val Ser Ile Gly Asp Arg Cys Val Ile Gly Ala Gly Pro  
 150 155 160 165

gtg gtg acc aag gat att ccg gat gat tct att gct gtg ggc aac cct 643  
 Val Val Thr Lys Asp Ile Pro Asp Asp Ser Ile Ala Val Gly Asn Pro  
 170 175 180

gcg cga gta gtg cgg aaa cgt gat gat agc cgg ctc gaa cgt tcg cag 691  
 Ala Arg Val Val Arg Lys Arg Asp Asp Ser Arg Leu Glu Arg Ser Gln  
 185 190 195

ctg cca gaa ggt gct tcc gtg gat gcg ttg ggg att ctt cct aca aaa 739  
 Leu Pro Glu Gly Ala Ser Val Asp Ala Leu Gly Ile Leu Pro Thr Lys  
 200 205 210

tca cct agg ctg tca gaa aat att gcc gaa aaa tat taaatacgca 785  
 Ser Pro Arg Leu Ser Glu Asn Ile Ala Glu Lys Tyr  
 215 220 225

ggcactaaga aga 798

<210> 436  
 <211> 225  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 436  
 Met Asp Asn Asp Phe Glu Ser Ile Glu Lys Met Ser Ser Gly Asp Trp  
 1 5 10 15

Tyr Val Ala Thr Gly Ala Glu Arg Glu Glu Val Ala Gln Lys Thr Ala  
 20 25 30

Leu Leu Phe His Glu Tyr Asn Gln Ile Gly Pro Thr Asp Pro Ala Arg  
 35 40 45

Thr Ala Glu Ile Leu Arg Thr Val Leu Asn Pro Ala Ser Gly Thr Cys  
 50 55 60

Thr Ile Lys Ala Pro Ala Ile Ile Glu Tyr Gly Phe Asn Thr Thr Ile  
 65 70 75 80

Gly Glu His Val Phe Ile Asn Phe Gly Leu Thr Ile Leu Asp Ile Ala  
 85 90 95

Pro Val Arg Ile Gly Ala Arg Ser Met Leu Gly Pro Asn Cys Gln Leu  
 100 105 110

Phe Thr Ala Gly His Pro Val Asp Asp Trp Glu Met Arg Ser Gly Gly  
 115 120 125

Trp Glu Asn Gly Ala Pro Ile Ser Ile Gly Glu Asp Thr Trp Leu Gly  
 130 135 140

Gly Asn Val Thr Val Val Gly Gly Val Ser Ile Gly Asp Arg Cys Val

145									150									155									160
Ile	Gly	Ala	Gly	Pro	Val	Val	Thr	Lys	Asp	Ile	Pro	Asp	Asp	Ser	Ile												
				165					170					175													
Ala	Val	Gly	Asn	Pro	Ala	Arg	Val	Val	Arg	Lys	Arg	Asp	Asp	Ser	Arg												
				180					185					190													
Leu	Glu	Arg	Ser	Gln	Leu	Pro	Glu	Gly	Ala	Ser	Val	Asp	Ala	Leu	Gly												
				195					200					205													
Ile	Leu	Pro	Thr	Lys	Ser	Pro	Arg	Leu	Ser	Glu	Asn	Ile	Ala	Glu	Lys												
				210					215					220													

Tyr  
225

```
<210> 437
<211> 891
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(868)  
<223> RXA02666
```

<400> 437																
gctcggcgac	gaggaagaga	agaaggacgc	attcgacgac	ttcgacgatt	ccgacgtgga	60										
tcttgacgat	ctgagcttcg	acgacgaaga	ttagacgccc	atg	tcg	tct	aca	cga	115							
				Met	Ser	Ser	Thr	Arg								
				1				5								
atc	ccc	gtc	atc	gca	ctc	ctc	gcg	gcg	gcg	ggg	cgc	gga	acc	cgc	ctc	163
Ile	Pro	Val	Ile	Ala	Leu	Leu	Ala	Ala	Ala	Gly	Arg	Gly	Thr	Arg	Leu	
				10				15						20		
ggc	gga	ccc	atc	ccc	aaa	gca	ttc	gtc	acg	ttg	cgt	gaa	cgc	aca	ctt	211
Gly	Gly	Pro	Ile	Pro	Lys	Ala	Phe	Val	Thr	Leu	Arg	Glu	Arg	Thr	Leu	
			25					30					35			
tta	gag	cgc	tcg	ctc	caa	gcc	atg	ctc	acc	tcc	gaa	agc	gtc	gac	gaa	259
Leu	Glu	Arg	Ser	Leu	Gln	Ala	Met	Leu	Thr	Ser	Glu	Ser	Val	Asp	Glu	
		40					45					50				
atc	atc	atc	ctc	gtc	agc	ccc	gac	atg	gaa	acc	tac	gcc	cgc	gat	ttg	307
Ile	Ile	Ile	Leu	Val	Ser	Pro	Asp	Met	Glu	Thr	Tyr	Ala	Arg	Asp	Leu	
		55				60					65					
ctg	cgc	aaa	cgc	ggc	ctt	ttg	aac	gac	ccc	gaa	ggg	gta	cgc	gta	cgg	355
Leu	Arg	Lys	Arg	Gly	Leu	Leu	Asn	Asp	Pro	Glu	Gly	Val	Arg	Val	Arg	
	70				75					80					85	
ctc	gtg	cac	ggc	ggc	ggg	gag	cgc	gcg	gac	tcg	gtc	tgg	gca	ggc	ctt	403
Leu	Val	His	Gly	Gly	Gly	Glu	Arg	Ala	Asp	Ser	Val	Trp	Ala	Gly	Leu	
			90						95					100		
cag	gca	att	tcg	ctt	gac	gac	gcc	acc	ccc	gat	gca	att	gtc	tta	atc	451
Gln	Ala	Ile	Ser	Leu	Asp	Asp	Ala	Thr	Pro	Asp	Ala	Ile	Val	Leu	Ile	

105	110	115	
cac gac agc gcc cga gcg ctc aca cca ccc ggc atg att gcg cgc gtg His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly Met Ile Ala Arg Val 120 125 130			499
gtg cgc aaa gtc cac gaa ggc gcc acc gca gtc atc cca gta ctg cca Val Arg Lys Val His Glu Gly Ala Thr Ala Val Ile Pro Val Leu Pro 135 140 145			547
gta tcg gac acc atc aaa cga gtg tcc cct gat ggc gga gta gtt gtc Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp Gly Gly Val Val Val 150 155 160 165			595
gac aca ccc aac cgt gca gaa ctt cgc gcc gtc caa acc cca caa ggc Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val Gln Thr Pro Gln Gly 170 175 180			643
ttc ctg ctg tcc gaa ctt gtt gca gcg aat gag aaa ttc ttc gcc gac Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu Lys Phe Phe Ala Asp 185 190 195			691
ccc aac cca ggc ttc atc cca acc gat gac gcc agc ttg atg gaa tgg Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala Ser Leu Met Glu Trp 200 205 210			739
tac ggc gca gat gta gtc tgc gta caa ggc gac cca atg gcg ttt aaa Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp Pro Met Ala Phe Lys 215 220 225			787
gta aca acc ccc att gat atg atg ctg gca caa cgc atc acc gac gaa Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln Arg Ile Thr Asp Glu 230 235 240 245			835
gcc gaa ccc aca ata ttt gag gta cca ggt gac taacccaatc atccccgcg Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp 250 255			888

tag 891

<210> 438

<211> 256

<212> PRT

<213> Corynebacterium glutamicum

<400> 438

Met Ser Ser Thr Arg Ile Pro Val Ile Ala Leu Leu Ala Ala Ala Gly 1 5 10 15
Arg Gly Thr Arg Leu Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu 20 25 30
Arg Glu Arg Thr Leu Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser 35 40 45
Glu Ser Val Asp Glu Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr 50 55 60
Tyr Ala Arg Asp Leu Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu 65 70 75 80

Gly	Val	Arg	Val	Arg	Leu	Val	His	Gly	Gly	Gly	Glu	Arg	Ala	Asp	Ser		
				85					90					95			
Val	Trp	Ala	Gly	Leu	Gln	Ala	Ile	Ser	Leu	Asp	Asp	Ala	Thr	Pro	Asp		
				100					105					110			
Ala	Ile	Val	Leu	Ile	His	Asp	Ser	Ala	Arg	Ala	Leu	Thr	Pro	Pro	Gly		
				115					120					125			
Met	Ile	Ala	Arg	Val	Val	Arg	Lys	Val	His	Glu	Gly	Ala	Thr	Ala	Val		
				130					135					140			
Ile	Pro	Val	Leu	Pro	Val	Ser	Asp	Thr	Ile	Lys	Arg	Val	Ser	Pro	Asp		
145					150					155					160		
Gly	Gly	Val	Val	Val	Asp	Thr	Pro	Asn	Arg	Ala	Glu	Leu	Arg	Ala	Val		
				165					170					175			
Gln	Thr	Pro	Gln	Gly	Phe	Leu	Leu	Ser	Glu	Leu	Val	Ala	Ala	Asn	Glu		
				180					185					190			
Lys	Phe	Phe	Ala	Asp	Pro	Asn	Pro	Gly	Phe	Ile	Pro	Thr	Asp	Asp	Ala		
				195					200					205			
Ser	Leu	Met	Glu	Trp	Tyr	Gly	Ala	Asp	Val	Val	Cys	Val	Gln	Gly	Asp		
				210					215					220			
Pro	Met	Ala	Phe	Lys	Val	Thr	Thr	Pro	Ile	Asp	Met	Met	Leu	Ala	Gln		
225					230					235					240		
Arg	Ile	Thr	Asp	Glu	Ala	Glu	Pro	Thr	Ile	Phe	Glu	Val	Pro	Gly	Asp		
				245					250					255			

```
<210> 439
<211> 1065
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1042)  
<223> RXA00202
```

```

<400> 439
ctggcagcag attgtcatcg gttgtgtcat cgcgcttgcg gtgggcttcg atgtcatccg 60

aaacaaaacc tctaagtaat tcctgaaagg aaattttcac atg tac gct cgt aaa 115
                                         Met Tyr Ala Arg Lys
                                         1                               5

ctt att gct ctg tcc gct tct gtc gtt ttg gct ttc agc ttg tct gct 163
Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala Phe Ser Leu Ser Ala
                        10                               15                               20

tgc aac cgt gaa tct tct ggc acc agc gca gac ggc ggt tct gcg gat 211
Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp Gly Gly Ser Ala Asp

```

	25	30	35	
ggg tcg atc acc ttg gct ctg tct acc cag acc aac ccg ttc ttt gtg				259
Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr Asn Pro Phe Phe Val				
	40	45	50	
cag ctt cgt gat ggt gcc cag gaa aag gct gat gaa ttg ggc gtg acc				307
Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp Glu Leu Gly Val Thr				
	55	60	65	
ctc aat gtt cag gat gct tcc gat gac gct gca acg cag gcc aac cag				355
Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala Thr Gln Ala Asn Gln				
	70	75	80	85
ctc aac aac gct gtc acc acc ggt gct ggc gtg gtg att gtc aac cca				403
Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val Val Ile Val Asn Pro				
	90	95	100	
act gat tct gat gct gtg gtg ccg tcg gtg gaa gct ctc aac cag gct				451
Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu Ala Leu Asn Gln Ala				
	105	110	115	
gac att cct gtt gtg gct gtc gac cgt tcc tcc aat ggt ggc gag gtg				499
Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser Asn Gly Gly Glu Val				
	120	125	130	
gcg tcc ttc gtg gca tct gac aac gtt gct ggc ggc gcg cag gct gct				547
Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly Gly Ala Gln Ala Ala				
	135	140	145	
gca gcc ctg gca gag gcg atc ggt ggc gaa ggt gaa atc ctc atg ctg				595
Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly Glu Ile Leu Met Leu				
	150	155	160	165
caa ggc att gcg gga tcc tct gca tca cgt gat cgt gga cag gga ttt				643
Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp Arg Gly Gln Gly Phe				
	170	175	180	
gaa gag gag atc gct aag cat gag ggc att tcc att gtg gct aag cag				691
Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser Ile Val Ala Lys Gln				
	185	190	195	
acc gcc aac ttt gac cgc ggt gag ggc ctg gac gtg gca act aac ctg				739
Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp Val Ala Thr Asn Leu				
	200	205	210	
ctg cag gca cac ccc aat gtg aag gcg atc ttc gcg gaa aac gat gag				787
Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe Ala Glu Asn Asp Glu				
	215	220	225	
atg gcg ttg ggc gca atc gaa gcc ctg ggt gct cgt gct ggt gaa gat				835
Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala Arg Ala Gly Glu Asp				
	230	235	240	245
gtc atc gtt gtc ggt ttc gat ggc acc aat gat ggt ctg gca gcg gtt				883
Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp Gly Leu Ala Ala Val				
	250	255	260	
gaa gat gga cgc atg ttg gcc acc gtt gct cag cag cca gaa gag ctg				931
Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln Gln Pro Glu Glu Leu				
	265	270	275	

gga gca aag gct gtg gaa gaa gca gct aag ctc ctg cgc ggt gag gac 979  
 Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu Leu Arg Gly Glu Asp  
           280                                  285                                  290

gct gaa aca gag gta cca gtt gag gtt gtc act gtg aag ctc gac aac 1027  
 Ala Glu Thr Glu Val Pro Val Glu Val Val Thr Val Lys Leu Asp Asn  
           295                                  300                                  305

gtc gcg gac ttc aag tagtcggcga tgaaaaagtc cgt 1065  
 Val Ala Asp Phe Lys  
 310

&lt;210&gt; 440

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 440

Met Tyr Ala Arg Lys Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala  
   1                                  5                                  10                                  15

Phe Ser Leu Ser Ala Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp  
           20                                  25                                  30

Gly Gly Ser Ala Asp Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr  
           35                                  40                                  45

Asn Pro Phe Phe Val Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp  
   50                                  55                                  60

Glu Leu Gly Val Thr Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala  
   65                                  70                                  75                                  80

Thr Gln Ala Asn Gln Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val  
           85                                  90                                  95

Val Ile Val Asn Pro Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu  
           100                                  105                                  110

Ala Leu Asn Gln Ala Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser  
           115                                  120                                  125

Asn Gly Gly Glu Val Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly  
           130                                  135                                  140

Gly Ala Gln Ala Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly  
   145                                  150                                  155                                  160

Glu Ile Leu Met Leu Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp  
           165                                  170                                  175

Arg Gly Gln Gly Phe Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser  
           180                                  185                                  190

Ile Val Ala Lys Gln Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp  
           195                                  200                                  205

Val Ala Thr Asn Leu Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe  
           210                                  215                                  220



Ala Glu Asn Asp Glu Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala  
 225 230 235 240

Arg Ala Gly Glu Asp Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp  
 245 250 255

Gly Leu Ala Ala Val Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln  
 260 265 270

Gln Pro Glu Glu Leu Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu  
 275 280 285

Leu Arg Gly Glu Asp Ala Glu Thr Glu Val Pro Val Glu Val Val Thr  
 290 295 300

Val Lys Leu Asp Asn Val Ala Asp Phe Lys  
 305 310

<210> 441  
 <211> 963  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(940)  
 <223> RXA02440

<400> 441  
 gctgttaatc acgggttggt cagctaccgg gggagcacca cgggcaacag atggggcatc 60

aggcggagga accgtcgata cgcctcggtt ggttgtcgcg atg gtg agc cac ggc 115  
 Met Val Ser His Gly  
 1 5

gcg ccg ggc gat act ttt tgg gat ttg gtc cga aaa ggt gct gaa gac 163  
 Ala Pro Gly Asp Thr Phe Trp Asp Leu Val Arg Lys Gly Ala Glu Asp  
 10 15 20

gcc gcc caa aaa gac aac gtt gaa ctc cgc tat tcc tct aat ccg gaa 211  
 Ala Ala Gln Lys Asp Asn Val Glu Leu Arg Tyr Ser Ser Asn Pro Glu  
 25 30 35

atc cct gaa caa tcc aac ctc gtg caa aat gcc atc gat tca cgc gtc 259  
 Ile Pro Glu Gln Ser Asn Leu Val Gln Asn Ala Ile Asp Ser Arg Val  
 40 45 50

gac ggc atc gcc atg acc atg cct aat gct caa tca cta gga ccg gtc 307  
 Asp Gly Ile Ala Met Thr Met Pro Asn Ala Gln Ser Leu Gly Pro Val  
 55 60 65

gct caa aag gcc gtg gat gcg ggc att cct gtg gtt ggt ctc aac gct 355  
 Ala Gln Lys Ala Val Asp Ala Gly Ile Pro Val Val Gly Leu Asn Ala  
 70 75 80 85

gga atg aac gaa tac caa gat tat gga atg aca gga ttc ttt ggt caa 403  
 Gly Met Asn Glu Tyr Gln Asp Tyr Gly Met Thr Gly Phe Phe Gly Gln  
 90 95 100

gat gaa tcc gtc gca gga gca tcc gca gga gcg cgc ctt gcc gag gaa 451  
Asp Glu Ser Val Ala Gly Ala Ser Ala Gly Ala Arg Leu Ala Glu Glu  
105 110 115

aac gca caa aaa gtt ttg tgt gtg atc cat gaa cag ggc aac tcc tcc 499  
Asn Ala Gln Lys Val Leu Cys Val Ile His Glu Gln Gly Asn Ser Ser  
120 125 130

cag gaa gct cgc tgt ggt ggc gtg tct gaa ggt ttg ggc aaa caa gta 547  
Gln Glu Ala Arg Cys Gly Gly Val Ser Glu Gly Leu Gly Lys Gln Val  
135 140 145

gaa acc ctg tat gtc aac ggc atg gat ctc acc tca gtg aac tcc acc 595  
Glu Thr Leu Tyr Val Asn Gly Met Asp Leu Thr Ser Val Asn Ser Thr  
150 155 160 165

ctg cag gca aaa ctt gct caa gac cgc agc att gat tgg gtt gtg gga 643  
Leu Gln Ala Lys Leu Ala Gln Asp Arg Ser Ile Asp Trp Val Val Gly  
170 175 180

ctc cag gct ggt gta tca atg gct att tct gat gcg gca gac gct gcg 691  
Leu Gln Ala Gly Val Ser Met Ala Ile Ser Asp Ala Ala Asp Ala Ala  
185 190 195

aac tca gaa gta aag atc gcc acc ttt gat aca aac gca cag ctc atg 739  
Asn Ser Glu Val Lys Ile Ala Thr Phe Asp Thr Asn Ala Gln Leu Met  
200 205 210

acc gct att cgt gat ggc aag atc caa ttc gcc att gat cag caa cca 787  
Thr Ala Ile Arg Asp Gly Lys Ile Gln Phe Ala Ile Asp Gln Gln Pro  
215 220 225

tat ctg cag ggc tac atg gcc gtg gat tcg ctg tgg ttg gcg cac cga 835  
Tyr Leu Gln Gly Tyr Met Ala Val Asp Ser Leu Trp Leu Ala His Arg  
230 235 240 245

aac ggc acc act gtt ggt ggc gga cga ccc gtg tac aca gga cca gcc 883  
Asn Gly Thr Thr Val Gly Gly Gly Arg Pro Val Tyr Thr Gly Pro Ala  
250 255 260

att gtg gat gcc acc aac gtt gat gtc att gct gaa gcc gtt ggg gag 931  
Ile Val Asp Ala Thr Asn Val Asp Val Ile Ala Glu Ala Val Gly Glu  
265 270 275

ggt ctg cga tgacaaaaat caagagtggg gag 963  
Gly Leu Arg  
280

&lt;210&gt; 442

&lt;211&gt; 280

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 442

Met Val Ser His Gly Ala Pro Gly Asp Thr Phe Trp Asp Leu Val Arg  
1 5 10 15

Lys Gly Ala Glu Asp Ala Ala Gln Lys Asp Asn Val Glu Leu Arg Tyr  
20 25 30

<400> 443  
aaggcctaga gcagaccatc gatttgtacc gcgaaaacga ggcctggtgg cgccctgcc 60

agaacaacgt cgaagctacc tacgctaagc agggacaata atg gaa tac ggt aaa	115
Met Glu Tyr Gly Lys	
1 5	
caa ctc acc tcc cac acc acc gac atc gaa ggc cta ctg gtt ttc gat	163
Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly Leu Leu Val Phe Asp	
10 15 20	
ttc ccc gtc cac ggc gac aac cgc ggc tgg ttc aag gaa aat tgg cag	211
Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe Lys Glu Asn Trp Gln	
25 30 35	
cgc acc aag atg acc aac ctg ggg ctg ccc gat ttt ggc ccc gtc caa	259
Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp Phe Gly Pro Val Gln	
40 45 50	
aac aac atg agt ttc aac gcc acc gcc ggc acg act cgc ggc atg cac	307
Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr Thr Arg Gly Met His	
55 60 65	
gct gag ccg tgg gat aaa ttt gtg tcc gtc gcg gtg ggt tcc gtt ttc	355
Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala Val Gly Ser Val Phe	
70 75 80 85	
gga gct tgg gtg gat ctg cgc gcg ggc tcg agc acg tac ggt aac gtc	403
Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser Thr Tyr Gly Asn Val	
90 95 100	
gta acg caa aaa att acc cct gac gtg gga gtt tac gtc ccg cgt ggt	451
Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val Tyr Val Pro Arg Gly	
105 110 115	
gtg gca aac ggc ttc cag gcg ctc gag gac ggc acg ctg tac acc tac	499
Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly Thr Leu Tyr Thr Tyr	
120 125 130	
ctc gtc aac gat cat tgg tcc ccc gac gcg cat tac gcc aac gtc aac	547
Leu Val Asn Asp His Trp Ser Pro Asp Ala His Tyr Ala Asn Val Asn	
135 140 145	
ctc aac atg atc gac tgg ccg ctg ccc atc acc gag atc tcc gaa aaa	595
Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr Glu Ile Ser Glu Lys	
150 155 160 165	
gat aaa aaa cat cca gcg ctt atc gac gcc acc ccc ctg ccc gcc cgc	643
Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr Pro Leu Pro Ala Arg	
170 175 180	
aag gtt ctc gtg gtc ggc gcc ggc gga caa ctg gga acc gcg cta cgc	691
Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu Gly Thr Ala Leu Arg	
185 190 195	
gcg cag ttc cca gac gcg gaa ttt gtc acg cgc caa gaa ctc gat atc	739
Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg Gln Glu Leu Asp Ile	
200 205 210	
acc tca gat ctc acc gag gct cgc gcg tgg aaa caa tac tcc acc atc	787
Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys Gln Tyr Ser Thr Ile	
215 220 225	

ata aac gcc gcc gcc tac act gcc gtt gac cag gca gaa cac gac cgc 835  
 Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln Ala Glu His Asp Arg  
 230 235 240 245  
 gca gca gcg tgg gac atc aac gca gcg gca gtg gct aac ctc gcg acc 883  
 Ala Ala Ala Trp Asp Ile Asn Ala Ala Val Ala Asn Leu Ala Thr  
 250 255 260  
 atc gcg cgc gac aac aac ctc acc ctc gtg cac gtg tcc tca gat tat 931  
 Ile Ala Arg Asp Asn Asn Leu Thr Leu Val His Val Ser Ser Asp Tyr  
 265 270 275  
 gtc ttc gac ggt gcg gcc gaa tcc tac gat gaa aac gca ccg ttt tcc 979  
 Val Phe Asp Gly Ala Ala Glu Ser Tyr Asp Glu Asn Ala Pro Phe Ser  
 280 285 290  
 cca ctc ggc gtg tac ggc caa tcc aaa gca gcc ggc gac atc gga gac 1027  
 Pro Leu Gly Val Tyr Gly Gln Ser Lys Ala Ala Gly Asp Ile Gly Asp  
 295 300 305  
 acc acc gca ccg cgc cac tac att gtg cgc acc agc tgg gtg att ggc 1075  
 Thr Thr Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly  
 310 315 320 325  
 gat ggc aat aat ttt gtc cgc acc atg aaa tcc ctc gac gaa cgc ggc 1123  
 Asp Gly Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly  
 330 335 340  
 atc gca cca tca gta gtt gat gat caa atc ggc cgc cta tcc ttc acc 1171  
 Ile Ala Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr  
 345 350 355  
 gaa gac atc gca gcc ggc atc gcg cac ctt ttg gaa gtg ggt gca gca 1219  
 Glu Asp Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala  
 360 365 370  
 tat ggc acc tac aac ctc acc aac acc ggc gaa ccc gca agc tgg gcc 1267  
 Tyr Gly Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala  
 375 380 385  
 gat gtt gcc cgc gca gta ttt tcc gac ccc acc aaa gtt acc ggc gtg 1315  
 Asp Val Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val  
 390 395 400 405  
 agc acc gcc gag tac ttc gcc aac aaa gac gca gcg ccc cgc cca ctg 1363  
 Ser Thr Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu  
 410 415 420  
 aac tcc gtt ttg gat ctc ggc aaa atc gaa gcc acc gga ttt agc gca 1411  
 Asn Ser Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala  
 425 430 435  
 ccg acc tgg cag acc cgc ctc aac gac tac ctc aag gaa ctc tca aag 1459  
 Pro Thr Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys  
 440 445 450  
 tgaaaggcat catcctcgca ggt 1482

&lt;210&gt; 444

&lt;211&gt; 453

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 444

```

Met Glu Tyr Gly Lys Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly
 1          5          10          15

Leu Leu Val Phe Asp Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe
          20          25          30

Lys Glu Asn Trp Gln Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp
          35          40          45

Phe Gly Pro Val Gln Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr
          50          55          60

Thr Arg Gly Met His Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala
          65          70          75          80

Val Gly Ser Val Phe Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser
          85          90          95

Thr Tyr Gly Asn Val Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val
          100          105          110

Tyr Val Pro Arg Gly Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly
          115          120          125

Thr Leu Tyr Thr Tyr Leu Val Asn Asp His Trp Ser Pro Asp Ala His
          130          135          140

Tyr Ala Asn Val Asn Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr
          145          150          155          160

Glu Ile Ser Glu Lys Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr
          165          170          175

Pro Leu Pro Ala Arg Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu
          180          185          190

Gly Thr Ala Leu Arg Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg
          195          200          205

Gln Glu Leu Asp Ile Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys
          210          215          220

Gln Tyr Ser Thr Ile Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln
          225          230          235          240

Ala Glu His Asp Arg Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val
          245          250          255

Ala Asn Leu Ala Thr Ile Ala Arg Asp Asn Asn Leu Thr Leu Val His
          260          265          270

Val Ser Ser Asp Tyr Val Phe Asp Gly Ala Ala Glu Ser Tyr Asp Glu
          275          280          285

Asn Ala Pro Phe Ser Pro Leu Gly Val Tyr Gly Gln Ser Lys Ala Ala
          290          295          300

```

Gly Asp Ile Gly Asp Thr Thr Ala Pro Arg His Tyr Ile Val Arg Thr  
 305 310 315 320  
 Ser Trp Val Ile Gly Asp Gly Asn Asn Phe Val Arg Thr Met Lys Ser  
 325 330 335  
 Leu Asp Glu Arg Gly Ile Ala Pro Ser Val Val Asp Asp Gln Ile Gly  
 340 345 350  
 Arg Leu Ser Phe Thr Glu Asp Ile Ala Ala Gly Ile Ala His Leu Leu  
 355 360 365  
 Glu Val Gly Ala Ala Tyr Gly Thr Tyr Asn Leu Thr Asn Thr Gly Glu  
 370 375 380  
 Pro Ala Ser Trp Ala Asp Val Ala Arg Ala Val Phe Ser Asp Pro Thr  
 385 390 395 400  
 Lys Val Thr Gly Val Ser Thr Ala Glu Tyr Phe Ala Asn Lys Asp Ala  
 405 410 415  
 Ala Pro Arg Pro Leu Asn Ser Val Leu Asp Leu Gly Lys Ile Glu Ala  
 420 425 430  
 Thr Gly Phe Ser Ala Pro Thr Trp Gln Thr Arg Leu Asn Asp Tyr Leu  
 435 440 445  
 Lys Glu Leu Ser Lys  
 450

&lt;210&gt; 445

&lt;211&gt; 449

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(426)

&lt;223&gt; FRXA01569

&lt;400&gt; 445

gca ccg cgc cac tac att gtg cgc acc agc tgg gtg att ggc gat ggc 48  
 Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly Asp Gly  
 1 5 10 15  
 aat aat ttt gtc cgc acc atg aaa tcc ctc gac gaa cgc ggc atc gca 96  
 Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly Ile Ala  
 20 25 30  
 cca tca gta gtt gat gat caa atc ggc cgc cta tcc ttc acc gaa gac 144  
 Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr Glu Asp  
 35 40 45  
 atc gca gcc ggc atc gcg cac ctt ttg gaa gtg ggt gca gca tat ggc 192  
 Ile Ala Ala Gly Ile Ala His Leu Glu Val Gly Ala Ala Tyr Gly  
 50 55 60  
 acc tac aac ctc acc aac acc ggc gaa ccc gca agc tgg gcc gat gtt 240  
 Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala Asp Val  
 65 70 75 80

gcc cgc gca gta ttt tcc gac ccc acc aaa gtt acc ggc gtg agc acc 288  
 Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val Ser Thr  
                     85                    90                    95

gcc gag tac ttc gcc aac aaa gac gca gcg ccc cgc cca ctg aac tcc 336  
 Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu Asn Ser  
                     100                    105                    110

gtt ttg gat ctc ggc aaa atc gaa gcc acc gga ttt agc gca ccg acc 384  
 Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala Pro Thr  
                     115                    120                    125

tgg cag acc cgc ctc aac gac tac ctc aag gaa ctc tca aag 426  
 Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys  
                     130                    135                    140

tgaaaggcat catcctcgca ggt 449

<210> 446  
 <211> 142  
 <212> PRT  
 <213> Corynebacterium glutamicum.

<400> 446  
 Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly Asp Gly  
   1                    5                    10                    15

Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly Ile Ala  
                     20                    25                    30

Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr Glu Asp  
                     35                    40                    45

Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala Tyr Gly  
                     50                    55                    60

Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala Asp Val  
   65                    70                    75                    80

Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val Ser Thr  
                     85                    90                    95

Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu Asn Ser  
                     100                    105                    110

Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala Pro Thr  
                     115                    120                    125

Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys  
                     130                    135                    140

<210> 447  
 <211> 1028  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS



&lt;222&gt; (101)..(1021)

&lt;223&gt; FRXA02055

&lt;400&gt; 447

```

aaggcctaga gcagaccatc gattggtacc gcgaaaacga ggcctggtgg cgccctgccca 60

agaacaacgt cgaagctacc tacgctaagc agggacaata atg gaa tac ggt aaa 115
                                         Met Glu Tyr Gly Lys
                                         1 5

caa ctc acc tcc cac acc acc gac atc gaa ggc cta ctg gtt ttc gat 163
Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly Leu Leu Val Phe Asp
                10                15                20

ttc ccc gtc cac ggc gac aac cgc ggc tgg ttc aag gaa aat tgg cag 211
Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe Lys Glu Asn Trp Gln
                25                30                35

cgc acc aag atg acc aac ctg ggg ctg ccc gat ttt ggc ccc gtc caa 259
Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp Phe Gly Pro Val Gln
                40                45                50

aac aac atg agt ttc aac gcc acc gcc ggc acg act cgc ggc atg cac 307
Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr Thr Arg Gly Met His
                55                60                65

gct gag ccg tgg gat aaa ttt gtg tcc gtc gcg gtg ggt tcc gtt ttc 355
Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala Val Gly Ser Val Phe
                70                75                80                85

gga gct tgg gtg gat ctg cgc gcg ggc tcg agc acg tac ggt aac gtc 403
Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser Thr Tyr Gly Asn Val
                90                95                100

gta acg caa aaa att acc cct gac gtg gga gtt tac gtc ccg cgt ggt 451
Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val Tyr Val Pro Arg Gly
                105                110                115

gtg gca aac ggc ttc cag gcg ctc gag gac ggc acg ctg tac acc tac 499
Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly Thr Leu Tyr Thr Tyr
                120                125                130

ctc gtc aac gat cat tgg tcc ccc gac gcg cat tac gcc aac gtc aac 547
Leu Val Asn Asp His Trp Ser Pro Asp Ala His Tyr Ala Asn Val Asn
                135                140                145

ctc aac atg atc gac tgg ccg ctg ccc atc acc gag atc tcc gaa aaa 595
Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr Glu Ile Ser Glu Lys
                150                155                160                165

gat aaa aaa cat cca gcg ctt atc gac gcc acc ccc ctg ccc gcc cgc 643
Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr Pro Leu Pro Ala Arg
                170                175                180

aag gtt ctc gtg gtc ggc gcc ggc gga caa ctg gga acc gcg cta cgc 691
Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu Gly Thr Ala Leu Arg
                185                190                195

gcg cag ttc cca gac gcg gaa ttt gtc acg cgc caa gaa ctc gat atc 739
Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg Gln Glu Leu Asp Ile
                200                205                210

```

acc tca gat ctc acc gag gct cgc gcg tgg aaa caa tac tcc acc atc 787  
 Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys Gln Tyr Ser Thr Ile  
 215 220 225

ata aac gcc gcc gcc tac act gcc gtt gac cag gca gaa cac gac cgc 835  
 Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln Ala Glu His Asp Arg  
 230 235 240 245

gca gca gcg tgg gac att aac gca gcg gca gtg gct acc tcg cga cca 883  
 Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val Ala Thr Ser Arg Pro  
 250 255 260

tcg cgc gcg aca aca acc tca ccc tcg tgc acg tgt cct cag att atg 931  
 Ser Arg Ala Thr Thr Thr Ser Pro Ser Cys Thr Cys Pro Gln Ile Met  
 265 270 275

tct tcg acg gtg cgg gcg aat cct acg atg aaa acg cac cgt ttt ccc 979  
 Ser Ser Thr Val Arg Ala Asn Pro Thr Met Lys Thr His Arg Phe Pro  
 280 285 290

cac tcg gcg tgt acg gcc aat cca aag cag ccg gcg aca tcg 1021  
 His Ser Ala Cys Thr Ala Asn Pro Lys Gln Pro Ala Thr Ser  
 295 300 305

taagcac 1028

&lt;210&gt; 448

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 448

Met Glu Tyr Gly Lys Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly  
 1 5 10 15

Leu Leu Val Phe Asp Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe  
 20 25 30

Lys Glu Asn Trp Gln Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp  
 35 40 45

Phe Gly Pro Val Gln Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr  
 50 55 60

Thr Arg Gly Met His Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala  
 65 70 75 80

Val Gly Ser Val Phe Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser  
 85 90 95

Thr Tyr Gly Asn Val Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val  
 100 105 110

Tyr Val Pro Arg Gly Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly  
 115 120 125

Thr Leu Tyr Thr Tyr Leu Val Asn Asp His Trp Ser Pro Asp Ala His  
 130 135 140

Tyr Ala Asn Val Asn Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr  
 145 150 155 160  
 Glu Ile Ser Glu Lys Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr  
 165 170 175  
 Pro Leu Pro Ala Arg Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu  
 180 185 190  
 Gly Thr Ala Leu Arg Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg  
 195 200 205  
 Gln Glu Leu Asp Ile Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys  
 210 215 220  
 Gln Tyr Ser Thr Ile Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln  
 225 230 235 240  
 Ala Glu His Asp Arg Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val  
 245 250 255  
 Ala Thr Ser Arg Pro Ser Arg Ala Thr Thr Thr Ser Pro Ser Cys Thr  
 260 265 270  
 Cys Pro Gln Ile Met Ser Ser Thr Val Arg Ala Asn Pro Thr Met Lys  
 275 280 285  
 Thr His Arg Phe Pro His Ser Ala Cys Thr Ala Asn Pro Lys Gln Pro  
 290 295 300  
 Ala Thr Ser  
 305

<210> 449  
 <211> 1056  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1033)  
 <223> RXA00825

<400> 449  
 cccgttcattg ctgggctttg gtgcggtgat ggcaactatt tgtctgatca ttgtgagttt 60  
 tagtgcacgc cgattctgag aaacaactaa agtgagccac atg cgc aca gta gtt 115  
 Met Arg Thr Val Val  
 1 5  
 acc ggc ggt gcc ggc ttc atc gga tcc cat ctc gtt gac ctt ttg atc 163  
 Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Asp Leu Leu Ile  
 10 15 20  
 aag gaa ggc cac gag gtc gtt gtg atc gat aac ctc tcc cgc gga cgc 211  
 Lys Glu Gly His Glu Val Val Val Ile Asp Asn Leu Ser Arg Gly Arg  
 25 30 35  
 ctg gag aat ctc tcc gat gcg gaa gcc acc gga aaa ctc acc ttt gtg 259  
 Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly Lys Leu Thr Phe Val

40	45	50	
gaa gcc gat ctt ctc gac gtt gat ttc aac gag ttt cta gga acc cac Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu Phe Leu Gly Thr His 55 60 65			307
aag cct gag gtt att ttc cac ctg gca gcg caa atc gat gtg cgc cac Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln Ile Asp Val Arg His 70 75 80 85			355
tct gtt gta gat cct ctt cac gac gcc gaa acc aac att ttg tcc acc Ser Val Val Asp Pro Leu His Asp Ala Glu Thr Asn Ile Leu Ser Thr 90 95 100			403
atc cgc atc gct gac gct gcc cgc cag cac ggt gtt cgc aag gtt gtc Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly Val Arg Lys Val Val 105 110 115			451
ttt acc tcc tca ggc ggt tcc att tac ggt gag cct tcg gaa ttc cca Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu Pro Ser Glu Phe Pro 120 125 130			499
gtt gat gaa acc gtg cca gtg gat cca cat tcc cct tat gcg gca tcc Val Asp Glu Thr Val Pro Val Asp Pro His Ser Pro Tyr Ala Ala Ser 135 140 145			547
aag gtg tcc ggt gaa att tac ctg aac acc ttc cgc cac ctg tac ggc Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe Arg His Leu Tyr Gly 150 155 160 165			595
tta gac tgt tct cac atc gca ccg gca aat gtt tac ggc cca cgc caa Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val Tyr Gly Pro Arg Gln 170 175 180			643
gat cca cac ggt gaa gca gga gtt gtg gcc att ttc gcg ctg cga ctt Asp Pro His Gly Glu Ala Gly Val Val Ala Ile Phe Ala Leu Arg Leu 185 190 195			691
ctg gga ggc ctg gac acc aag gta ttc ggc gac ggc gga aac acc cgc Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp Gly Gly Asn Thr Arg 200 205 210			739
gac tac gtc tac gtc ggt gac gta gtt cgt gct ttc tac ctg gct tct Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala Phe Tyr Leu Ala Ser 215 220 225			787
ggg gaa atc ggt ggg gga gag cgc ttc aac att ggc acc tct gtg gaa Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile Gly Thr Ser Val Glu 230 235 240 245			835
acc tct gac cgc cag ctg cac acc ctc gtg gcc act gcg gca ggt tcc Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala Thr Ala Ala Gly Ser 250 255 260			883
aaa gat gat cct gaa tat gca cct gca cgt ctc ggc gat gtg cca cgc Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu Gly Asp Val Pro Arg 265 270 275			931
agt gca ctc agc ttc ggc aag gcc aaa gag gtg ctt ggt tgg gag cct Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val Leu Gly Trp Glu Pro 280 285 290			979

gag gtg aac atc gaa caa ggt gtg gcc aag act gtg gag tac ttc cgc 1027  
Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr Val Glu Tyr Phe Arg  
295 300 305

act cac taggggaaaaa tccaccacaa atc 1056  
Thr His  
310

<210> 450

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 450

Met Arg Thr Val Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu  
1 5 10 15

Val Asp Leu Leu Ile Lys Glu Gly His Glu Val Val Val Ile Asp Asn  
20 25 30

Leu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly  
35 40 45

Lys Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu  
50 55 60

Phe Leu Gly Thr His Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln  
65 70 75 80

Ile Asp Val Arg His Ser Val Val Asp Pro Leu His Asp Ala Glu Thr  
85 90 95

Asn Ile Leu Ser Thr Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly  
100 105 110

Val Arg Lys Val Val Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu  
115 120 125

Pro Ser Glu Phe Pro Val Asp Glu Thr Val Pro Val Asp Pro His Ser  
130 135 140

Pro Tyr Ala Ala Ser Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe  
145 150 155 160

Arg His Leu Tyr Gly Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val  
165 170 175

Tyr Gly Pro Arg Gln Asp Pro His Gly Glu Ala Gly Val Val Ala Ile  
180 185 190

Phe Ala Leu Arg Leu Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp  
195 200 205

Gly Gly Asn Thr Arg Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala  
210 215 220

Phe Tyr Leu Ala Ser Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile  
225 230 235 240

<400> 451																	
ccta	aatgaac	agcc	ggagca	ccct	ggtcgt	ttgc	cagaata	ggcg	catcga	caac	agctac	60					
taact	ctgcc	agct	cgcccg	gacga	aactaa	ggtag	acggc	atg	act	tct	ttg	ctt	115				
								Met	Thr	Ser	Leu	Leu					
								1				5					
gtg	acc	gga	ggt	gcc	gga	ttt	atc	ggc	gcc	aac	ttc	gtc	cgc	caa	acc	163	
Val	Thr	Gly	Gly	Ala	Gly	Phe	Ile	Gly	Ala	Asn	Phe	Val	Arg	Gln	Thr		
				10					15					20			
gta	gag	cag	cac	cct	gaa	tac	acc	cac	atc	acg	gtg	ctg	gat	aaa	ctc	211	
Val	Glu	Gln	His	Pro	Glu	Tyr	Thr	His	Ile	Thr	Val	Leu	Asp	Lys	Leu		
			25					30					35				
acc	tac	gca	gga	aac	gcc	gac	aat	ctc	aaa	ggc	ctc	ccc	gac	agc	aaa	259	
Thr	Tyr	Ala	Gly	Asn	Ala	Asp	Asn	Leu	Lys	Gly	Leu	Pro	Asp	Ser	Lys		
		40					45					50					
gta	acc	ctc	atc	gaa	ggc	gat	atc	tgc	gat	gct	gaa	tta	gtc	gac	tcc	307	
Val	Thr	Leu	Ile	Glu	Gly	Asp	Ile	Cys	Asp	Ala	Glu	Leu	Val	Asp	Ser		
	55					60					65						
ctg	gtc	aaa	gac	cac	gac	atc	aca	gtc	cac	ttc	gca	gca	gaa	tcc	cac	355	
Leu	Val	Lys	Asp	His	Asp	Ile	Thr	Val	His	Phe	Ala	Ala	Glu	Ser	His		
70					75					80					85		
aac	gac	aac	tcc	ctc	aac	gac	ccc	tcc	ccg	ttt	gtt	cac	act	aac	ctc	403	
Asn	Asp	Asn	Ser	Leu	Asn	Asp	Pro	Ser	Pro	Phe	Val	His	Thr	Asn	Leu		
				90					95					100			
atc	ggc	acc	ttt	gtc	ctg	cta	gaa	gca	gtc	cgc	aag	cac	aac	aaa	cgc	451	
Ile	Gly	Thr	Phe	Val	Leu	Leu	Glu	Ala	Val	Arg	Lys	His	Asn	Lys	Arg		
			105					110					115				

ttc cac cac atc tcc acc gat gaa gtc ttc ggc gat cta gag ctg gat 499  
 Phe His His Ile Ser Thr Asp Glu Val Phe Gly Asp Leu Glu Leu Asp  
 120 125 130

gat cca aac cgc ttc act gaa acc acc gcc tac aag cca tcg tct cca 547  
 Asp Pro Asn Arg Phe Thr Glu Thr Thr Ala Tyr Lys Pro Ser Ser Pro  
 135 140 145

tat tct gca acc aag gca ggg tct gat cac ttg gta cac gca tgg atc 595  
 Tyr Ser Ala Thr Lys Ala Gly Ser Asp His Leu Val His Ala Trp Ile  
 150 155 160 165

cgc tcc ttc gga atc cag gca acc atg tct aac tgc tcc aac aat tac 643  
 Arg Ser Phe Gly Ile Gln Ala Thr Met Ser Asn Cys Ser Asn Asn Tyr  
 170 175 180

ggt ccc tac cag cac att gaa aag ttc atc ccc cgc cag atc acc aat 691  
 Gly Pro Tyr Gln His Ile Glu Lys Phe Ile Pro Arg Gln Ile Thr Asn  
 185 190 195

att ctg gcc ggc ctg aca cca aaa ctt tat gga acc ggc gag cag gtc 739  
 Ile Leu Ala Gly Leu Thr Pro Lys Leu Tyr Gly Thr Gly Glu Gln Val  
 200 205 210

cgc gac tgg atc cac gtc gat gat cac aat gac gcc gtc cac ctg atc 787  
 Arg Asp Trp Ile His Val Asp Asp His Asn Asp Ala Val His Leu Ile  
 215 220 225

ctg agt aag ggc aag atc ggc gaa acc tac atc atc ggc gcc gac aac 835  
 Leu Ser Lys Gly Lys Ile Gly Glu Thr Tyr Ile Ile Gly Ala Asp Asn  
 230 235 240 245

gat cat gtg aat aac aag cag gtc atc gag ctt att tgt gaa ctc atg 883  
 Asp His Val Asn Asn Lys Gln Val Ile Glu Leu Ile Cys Glu Leu Met  
 250 255 260

ggc ctc gac aaa aac gca tac gag cac gtc gca gac cgc ccc ggc cac 931  
 Gly Leu Asp Lys Asn Ala Tyr Glu His Val Ala Asp Arg Pro Gly His  
 265 270 275

gat atg cgt tac gcc atg gat tcc acc aag ctg cgc acc gag ctc ggc 979  
 Asp Met Arg Tyr Ala Met Asp Ser Thr Lys Leu Arg Thr Glu Leu Gly  
 280 285 290

tgg gca cct aaa tac acc gac gtt gat tcc ggc atg cgc aaa ggc cta 1027  
 Trp Ala Pro Lys Tyr Thr Asp Val Asp Ser Gly Met Arg Lys Gly Leu  
 295 300 305

gag cag acc atc gat tgg tac cgc gaa aac gag gcc tgg tgg cgc cct 1075  
 Glu Gln Thr Ile Asp Trp Tyr Arg Glu Asn Glu Ala Trp Trp Arg Pro  
 310 315 320 325

gcc aag aac aac gtc gaa gct acc tac gct aag cag gga caa 1117  
 Ala Lys Asn Asn Val Glu Ala Thr Tyr Ala Lys Gln Gly Gln  
 330 335

taatggaata cggtaaacaa ctc 1140

&lt;210&gt; 452

&lt;211&gt; 339

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 452

```

Met Thr Ser Leu Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ala Asn
 1           5           10           15

Phe Val Arg Gln Thr Val Glu Gln His Pro Glu Tyr Thr His Ile Thr
          20           25           30

Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Ala Asp Asn Leu Lys Gly
          35           40           45

Leu Pro Asp Ser Lys Val Thr Leu Ile Glu Gly Asp Ile Cys Asp Ala
          50           55           60

Glu Leu Val Asp Ser Leu Val Lys Asp His Asp Ile Thr Val His Phe
65           70           75           80

Ala Ala Glu Ser His Asn Asp Asn Ser Leu Asn Asp Pro Ser Pro Phe
          85           90           95

Val His Thr Asn Leu Ile Gly Thr Phe Val Leu Leu Glu Ala Val Arg
          100          105          110

Lys His Asn Lys Arg Phe His His Ile Ser Thr Asp Glu Val Phe Gly
          115          120          125

Asp Leu Glu Leu Asp Asp Pro Asn Arg Phe Thr Glu Thr Thr Ala Tyr
130          135          140

Lys Pro Ser Ser Pro Tyr Ser Ala Thr Lys Ala Gly Ser Asp His Leu
145          150          155          160

Val His Ala Trp Ile Arg Ser Phe Gly Ile Gln Ala Thr Met Ser Asn
          165          170          175

Cys Ser Asn Asn Tyr Gly Pro Tyr Gln His Ile Glu Lys Phe Ile Pro
          180          185          190

Arg Gln Ile Thr Asn Ile Leu Ala Gly Leu Thr Pro Lys Leu Tyr Gly
          195          200          205

Thr Gly Glu Gln Val Arg Asp Trp Ile His Val Asp Asp His Asn Asp
210          215          220

Ala Val His Leu Ile Leu Ser Lys Gly Lys Ile Gly Glu Thr Tyr Ile
225          230          235          240

Ile Gly Ala Asp Asn Asp His Val Asn Asn Lys Gln Val Ile Glu Leu
          245          250          255

Ile Cys Glu Leu Met Gly Leu Asp Lys Asn Ala Tyr Glu His Val Ala
          260          265          270

Asp Arg Pro Gly His Asp Met Arg Tyr Ala Met Asp Ser Thr Lys Leu
          275          280          285

Arg Thr Glu Leu Gly Trp Ala Pro Lys Tyr Thr Asp Val Asp Ser Gly
          290          295          300

```



Met Arg Lys Gly Leu Glu Gln Thr Ile Asp Trp Tyr Arg Glu Asn Glu  
305 310 315 320

Ala Trp Trp Arg Pro Ala Lys Asn Asn Val Glu Ala Thr Tyr Ala Lys  
325 330 335

Gln Gly Gln

<210> 453

<211> 909

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(886)

<223> RXN00427

<400> 453

gcggtcattg tgaccacaaa tcgtgtggaa ttgctgcggc attccctcga gggtgttgcc 60

aatcaaacct atccggtgaa acacattgtg gtggtggata atg ggg cgg atc cta 115  
Met Gly Arg Ile Leu  
1 5

gta ttc tat agt gtc act tta gag gtg gcg gga gac cgt ccc gtt tac 163  
Val Phe Tyr Ser Val Thr Leu Glu Val Ala Gly Asp Arg Pro Val Tyr  
10 15 20

acg cct tcg cgc acc aat ttg ggc gac ggt ggc ggt ttt gct ttt ggt 211  
Thr Pro Ser Arg Thr Asn Leu Gly Asp Gly Gly Gly Phe Ala Phe Gly  
25 30 35

ttt ttg acg gcg ttg gcg ctg ggg gcg aac gcg gtg tgg tgc aca gac 259  
Phe Leu Thr Ala Leu Ala Leu Gly Ala Asn Ala Val Trp Cys Thr Asp  
40 45 50

gat gac ggc cgg ccg gag ggg cca ggg gtg ttg aag acg ctt atc gac 307  
Asp Asp Gly Arg Pro Glu Gly Pro Gly Val Leu Lys Thr Leu Ile Asp  
55 60 65

gcc gct tct cgg cat aat ctg gag gag gtt tct ccg gtg gta tgc aat 355  
Ala Ala Ser Arg His Asn Leu Glu Glu Val Ser Pro Val Val Cys Asn  
70 75 80 85

gct gat gat ccg gag cgg ttg gca ttt ccg ctg cgt cgg ggc ttg gag 403  
Ala Asp Asp Pro Glu Arg Leu Ala Phe Pro Leu Arg Arg Gly Leu Glu  
90 95 100

tgg cgt cgg atg cgc agt gag ttg att gat cca gcc aac ccg gag gat 451  
Trp Arg Arg Met Arg Ser Glu Leu Ile Asp Pro Ala Asn Pro Glu Asp  
105 110 115

gat ttg ctg ccg ggc atc gcc tcc ttg ttc aat ggt gcc ctg atc agc 499  
Asp Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser  
120 125 130

gct tat gca atg gag cgc att ggc gtg ccg gac tat cga ctg ttt att 547  
Ala Tyr Ala Met Glu Arg Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile

135	140	145	
cgc ggc gat gag gtg gag tat cac cgc cgt ttg gtg cgt tcc ggt ttg			595
Arg Gly Asp Glu Val Glu Tyr His Arg Arg Leu Val Arg Ser Gly Leu			
150	155	160	165
ccg ttt ggt acg tgt ttg acc acg gcg tat ttg cac ccg gat ggt tct			643
Pro Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu His Pro Asp Gly Ser			
	170	175	180
gat gag ttc aag ccg att ctg ggt ggg cgg atg cat acg cag tat ccg			691
Asp Glu Phe Lys Pro Ile Leu Gly Gly Arg Met His Thr Gln Tyr Pro			
	185	190	195
gat aat gat ttc aag agg ttt ttc acc tac cgc aac cgt ggc tac ctg			739
Asp Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu			
	200	205	210
atg agc cag ccg gga atg cgc aag ctt ctc cct cag gaa tat gcg cgc			787
Met Ser Gln Pro Gly Met Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg			
	215	220	225
ttt gcg tgg ttc ttc ctg gtt cag aaa cgg gat gtg aag gga ttc cgg			835
Phe Ala Trp Phe Phe Leu Val Gln Lys Arg Asp Val Lys Gly Phe Arg			
230	235	240	245
gag tgg ctg cgc ctg cac aaa ctg ggc cgc gac gag aaa ttc aat agg			883
Glu Trp Leu Arg Leu His Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg			
	250	255	260
ccc tagatcagtt ttagtagttc ctc			909
Pro			

&lt;210&gt; 454

&lt;211&gt; 262

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 454

Met Gly Arg Ile Leu Val Phe Tyr Ser Val Thr Leu Glu Val Ala Gly
1 5 10 15

Asp Arg Pro Val Tyr Thr Pro Ser Arg Thr Asn Leu Gly Asp Gly Gly
20 25 30

Gly Phe Ala Phe Gly Phe Leu Thr Ala Leu Ala Leu Gly Ala Asn Ala
35 40 45

Val Trp Cys Thr Asp Asp Asp Gly Arg Pro Glu Gly Pro Gly Val Leu
50 55 60

Lys Thr Leu Ile Asp Ala Ala Ser Arg His Asn Leu Glu Glu Val Ser
65 70 75 80

Pro Val Val Cys Asn Ala Asp Asp Pro Glu Arg Leu Ala Phe Pro Leu
85 90 95

Arg Arg Gly Leu Glu Trp Arg Arg Met Arg Ser Glu Leu Ile Asp Pro
100 105 110

Ala Asn Pro Glu Asp Asp Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn  
 115 120 125

Gly Ala Leu Ile Ser Ala Tyr Ala Met Glu Arg Ile Gly Val Pro Asp  
 130 135 140

Tyr Arg Leu Phe Ile Arg Gly Asp Glu Val Glu Tyr His Arg Arg Leu  
 145 150 155 160

Val Arg Ser Gly Leu Pro Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu  
 165 170 175

His Pro Asp Gly Ser Asp Glu Phe Lys Pro Ile Leu Gly Gly Arg Met  
 180 185 190

His Thr Gln Tyr Pro Asp Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg  
 195 200 205

Asn Arg Gly Tyr Leu Met Ser Gln Pro Gly Met Arg Lys Leu Leu Pro  
 210 215 220

Gln Glu Tyr Ala Arg Phe Ala Trp Phe Phe Leu Val Gln Lys Arg Asp  
 225 230 235 240

Val Lys Gly Phe Arg Glu Trp Leu Arg Leu His Lys Leu Gly Arg Asp  
 245 250 255

Glu Lys Phe Asn Arg Pro  
 260

<210> 455  
 <211> 555  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(532)  
 <223> FRXA00427

<400> 455  
 tgctgatgat ccggagcggg ttgcatttcc gctgcgtcgg ggcttgaggt ggcgtcggat 60

gcgcagtgag ttgattgac cagccaaccc ggaggatgat ttg ctg ccg ggc atc 115  
 Leu Leu Pro Gly Ile  
 1 5

gcc tcc ttg ttc aat ggt gcc ctg atc agc gct tat gca atg gag cgc 163  
 Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser Ala Tyr Ala Met Glu Arg  
 10 15 20

att ggc gtg ccg gac tat cga ctg ttt att cgc ggc gat gag gtg gag 211  
 Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile Arg Gly Asp Glu Val Glu  
 25 30 35

tat cac cgc cgt ttg gtg cgt tcc ggt ttg ccg ttt ggt acg tgt ttg 259  
 Tyr His Arg Arg Leu Val Arg Ser Gly Leu Pro Phe Gly Thr Cys Leu  
 40 45 50

acc acg gcg tat ttg cac ccg gat ggt tct gat gag ttc aag ccg att 307  
 Thr Thr Ala Tyr Leu His Pro Asp Gly Ser Asp Glu Phe Lys Pro Ile  
           55                                60                                65

ctg ggt ggg cgg atg cat acg cag tat ccg gat aat gat ttc aag agg 355  
 Leu Gly Gly Arg Met His Thr Gln Tyr Pro Asp Asn Asp Phe Lys Arg  
           70                                75                                80                                85

ttt ttc acc tac cgc aac cgt ggc tac ctg atg agc cag ccg gga atg 403  
 Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu Met Ser Gln Pro Gly Met  
                                 90                                95                                100

cgc aag ctt ctc cct cag gaa tat gcg cgc ttt gcg tgg ttc ttc ctg 451  
 Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg Phe Ala Trp Phe Phe Leu  
                                 105                                110                                115

gtt cag aaa cgg gat gtg aag gga ttc cgg gag tgg ctg cgc ctg cac 499  
 Val Gln Lys Arg Asp Val Lys Gly Phe Arg Glu Trp Leu Arg Leu His  
                                 120                                125                                130

aaa ctg ggc cgc gac gag aaa ttc aat agg ccc tagatcagtt ttagtagttc 552  
 Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg Pro  
           135                                140

ctc 555

&lt;210&gt; 456

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 456

Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser Ala  
   1                                5                                10                                15

Tyr Ala Met Glu Arg Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile Arg  
                                 20                                25                                30

Gly Asp Glu Val Glu Tyr His Arg Arg Leu Val Arg Ser Gly Leu Pro  
                                 35                                40                                45

Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu His Pro Asp Gly Ser Asp  
           50                                55                                60

Glu Phe Lys Pro Ile Leu Gly Gly Arg Met His Thr Gln Tyr Pro Asp  
           65                                70                                75                                80

Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu Met  
                                 85                                90                                95

Ser Gln Pro Gly Met Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg Phe  
                                 100                                105                                110

Ala Trp Phe Phe Leu Val Gln Lys Arg Asp Val Lys Gly Phe Arg Glu  
           115                                120                                125

Trp Leu Arg Leu His Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg Pro  
           130                                135                                140

```
<210> 457
<211> 507
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(484)  
<223> RXA00327
```

<400> 457																			
aacgatttttc gccgtcgcaa ccgtgatcac cggtcgcttt ccggcatcgt gtcgtcgcg																60			
ctaggggggcc aggcgcggga tgattggggtt tgtcacgcgcg																115			
Met Ile Gln Ala Ala																1	5		
ttg tgg atc gtg ctc ttt tta ttc gct gat cgc ctg tcc aat ccg ctg																163			
Leu Trp Ile Val Leu Phe Leu Phe Ala Asp Arg Leu Ser Asn Pro Leu																10	15	20	
gtt ttt gtc agc gcc atc atg ttc gcg att tcc ttt agc tcc ccc gtg																211			
Val Phe Val Ser Ala Ile Met Phe Ala Ile Ser Phe Ser Ser Pro Val																25	30	35	
gcg aac ttc ggt ttc gat acg atc tgc gaa aaa ctc gac cgc cgc gtc																259			
Ala Asn Phe Gly Phe Asp Thr Ile Cys Glu Lys Leu Asp Arg Arg Val																40	45	50	
atg gtc gcc ggc acc ggc atg gcc aac atg agc gcc tac att tgc gcg																307			
Met Val Ala Gly Thr Gly Met Ala Asn Met Ser Ala Tyr Ile Cys Ala																55	60	65	
atg ctg gcc aca caa atc atc gga ttt tta ctc gac tgg aac gcc gac																355			
Met Leu Ala Thr Gln Ile Ile Gly Phe Leu Leu Asp Trp Asn Ala Asp																70	75	80	85
ggc cac gcc tac acc tgg tcg aat ttc cag gtg gcg tgg ctt ggt ctg																403			
Gly His Ala Tyr Thr Trp Ser Asn Phe Gln Val Ala Trp Leu Gly Leu																90	95	100	
ggc gcg gtg tgg ctg gca ggc atg atc ggg ctt gca gtc tgc ctc ctg																451			
Gly Ala Val Trp Leu Ala Gly Met Ile Gly Leu Ala Val Cys Leu Leu																105	110	115	
ctg cag cgt cga aaa aat att gct ttt cga cgc taaaaccgga ccgtaaccgc																504			
Leu Gln Arg Arg Lys Asn Ile Ala Phe Arg Arg																120	125		
taq																507			

```
<210> 458
<211> 128
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 458

Met Ile Gln Ala Ala Leu Trp Ile Val Leu Phe Leu Phe Ala Asp Arg  
 1 5 10 15  
 Leu Ser Asn Pro Leu Val Phe Val Ser Ala Ile Met Phe Ala Ile Ser  
 20 25 30  
 Phe Ser Ser Pro Val Ala Asn Phe Gly Phe Asp Thr Ile Cys Glu Lys  
 35 40 45  
 Leu Asp Arg Arg Val Met Val Ala Gly Thr Gly Met Ala Asn Met Ser  
 50 55 60  
 Ala Tyr Ile Cys Ala Met Leu Ala Thr Gln Ile Ile Gly Phe Leu Leu  
 65 70 75 80  
 Asp Trp Asn Ala Asp Gly His Ala Tyr Thr Trp Ser Asn Phe Gln Val  
 85 90 95  
 Ala Trp Leu Gly Leu Gly Ala Val Trp Leu Ala Gly Met Ile Gly Leu  
 100 105 110  
 Ala Val Cys Leu Leu Leu Gln Arg Arg Lys Asn Ile Ala Phe Arg Arg  
 115 120 125

<210> 459  
 <211> 615  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(592)  
 <223> RXA00328

<400> 459  
 gtcacgggat ttgtttagc ccgactcaag ggtggaccgg gccgcagatt actcgcccag 60  
 attaggtcta ccaaggactt ttaaagatcg ggtaaaacct gtg ggc gtt gaa agg 115  
 Val Gly Val Glu Arg  
 1 5  
 ggc aag gtc tct gcc aag gca cta gtt gtc tgg ttg acg gca atg tgc 163  
 Gly Lys Val Ser Ala Lys Ala Leu Val Val Trp Leu Thr Ala Met Cys  
 10 15 20  
 gtg tac atc gtg gcc att gct ggt cga aca tca ttt ggt gtc gcc gga 211  
 Val Tyr Ile Val Ala Ile Ala Gly Arg Thr Ser Phe Gly Val Ala Gly  
 25 30 35  
 gtg cat gcg atc gat cgc ttt gat atc gac gcc tcc cggttg gcc gtg 259  
 Val His Ala Ile Asp Arg Phe Asp Ile Asp Ala Ser Arg Leu Ala Val  
 40 45 50  
 ttc act tct gtt cag gtt gga gtc tat gtt ctc gcg cag att ccc atg 307  
 Phe Thr Ser Val Gln Val Gly Val Tyr Val Leu Ala Gln Ile Pro Met  
 55 60 65

ggc atg ctg gtg gac agg ttc gac gcc cgg aaa ctc ttg ctg gct ggc 355  
 Gly Met Leu Val Asp Arg Phe Asp Ala Arg Lys Leu Leu Leu Ala Gly  
 70 75 80 85  
  
 gct tta att ttg gca gct ggc cag ctc att ttg ggt ttc act gat tct 403  
 Ala Leu Ile Leu Ala Ala Gly Gln Leu Ile Leu Gly Phe Thr Asp Ser  
 90 95 100  
  
 tat atg atc gcc att ttt gcc cga gtg ctc atc agt gtt ggc gat tct 451  
 Tyr Met Ile Ala Ile Phe Ala Arg Val Leu Ile Ser Val Gly Asp Ser  
 105 110 115  
  
 tct gca ttt ttg tcc gtg atg cga ctg ttg ccc aac tgg ttc ccg atg 499  
 Ser Ala Phe Leu Ser Val Met Arg Leu Leu Pro Asn Trp Phe Pro Met  
 120 125 130  
  
 tct tgg aca cct gtg ttg cag cag ctc acg ggc gct ttt ggc ttt gtg 547  
 Ser Trp Thr Pro Val Leu Gln Gln Leu Thr Gly Ala Phe Gly Phe Val  
 135 140 145  
  
 ggg cag ttt tct ccg cgg tgc cgt ttt tgc aca tac tca aca cct 592  
 Gly Gln Phe Ser Pro Arg Cys Arg Phe Cys Thr Tyr Ser Thr Pro  
 150 155 160  
  
 tagggtggac aattcctttc gca 615

<210> 460  
 <211> 164  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 460  
 Val Gly Val Glu Arg Gly Lys Val Ser Ala Lys Ala Leu Val Val Trp  
 1 5 10 15  
  
 Leu Thr Ala Met Cys Val Tyr Ile Val Ala Ile Ala Gly Arg Thr Ser  
 20 25 30  
  
 Phe Gly Val Ala Gly Val His Ala Ile Asp Arg Phe Asp Ile Asp Ala  
 35 40 45  
  
 Ser Arg Leu Ala Val Phe Thr Ser Val Gln Val Gly Val Tyr Val Leu  
 50 55 60  
  
 Ala Gln Ile Pro Met Gly Met Leu Val Asp Arg Phe Asp Ala Arg Lys  
 65 70 75 80  
  
 Leu Leu Leu Ala Gly Ala Leu Ile Leu Ala Ala Gly Gln Leu Ile Leu  
 85 90 95  
  
 Gly Phe Thr Asp Ser Tyr Met Ile Ala Ile Phe Ala Arg Val Leu Ile  
 100 105 110  
  
 Ser Val Gly Asp Ser Ser Ala Phe Leu Ser Val Met Arg Leu Leu Pro  
 115 120 125  
  
 Asn Trp Phe Pro Met Ser Trp Thr Pro Val Leu Gln Gln Leu Thr Gly  
 130 135 140  
  
 Ala Phe Gly Phe Val Gly Gln Phe Ser Pro Arg Cys Arg Phe Cys Thr

655



150	155	160	165	
ggt cgg gat act cca gat cct cag cca aaa cct gtc gaa tca gct cag	643			
Val Arg Asp Thr Pro Asp Pro Gln Pro Lys Pro Val Glu Ser Ala Gln				
170 175 180				
gaa gca gat aaa cca agc ctg cgc gcg agt ttg aag ttg att gtc cgc	691			
Glu Ala Asp Lys Pro Ser Leu Arg Ala Ser Leu Lys Leu Ile Val Arg				
185 190 195				
aat ccg att acg tgg cag ggt ttc ttc att cac tac gta ttg atg gtg	739			
Asn Pro Ile Thr Trp Gln Gly Phe Phe Ile His Tyr Val Leu Met Val				
200 205 210				
tgg cag acc gtg ttc tcc atg atg tgg ggc gtc ccg ctg atg act ttg	787			
Trp Gln Thr Val Phe Ser Met Met Trp Gly Val Pro Leu Met Thr Leu				
215 220 225				
ggc atg gga ctg tct gca acg acg gct ggt ttg gtg ttg agc atc aac	835			
Gly Met Gly Leu Ser Ala Thr Thr Ala Gly Leu Val Leu Ser Ile Asn				
230 235 240 245				
acg ctg tgc atg gtg gta tcg gcg cca atc atc gga ata att tcc gca	883			
Thr Leu Cys Met Val Val Ser Ala Pro Ile Ile Gly Ile Ile Ser Ala				
250 255 260				
cgc ctt ggg tat cgc cgt gac gtg gtc gcc att gcg ctg tcg ttt gtt	931			
Arg Leu Gly Tyr Arg Arg Asp Val Val Ala Ile Ala Leu Ser Phe Val				
265 270 275				
caa tcc gca gta tgg ctg gtg ttc ttg gcc tcc gat gca cct cgt ggt	979			
Gln Ser Ala Val Trp Leu Val Phe Leu Ala Ser Asp Ala Pro Arg Gly				
280 285 290				
ttg atg gct atc atc ttg gtc aac atc gtc atg ggt ctg act act gcg	1027			
Leu Met Ala Ile Ile Leu Val Asn Ile Val Met Gly Leu Thr Thr Ala				
295 300 305				
gct tct ggt tat ggc ttt gac acc att cgt gag cgc cta gat cgc aag	1075			
Ala Ser Gly Tyr Gly Phe Asp Thr Ile Arg Glu Arg Leu Asp Arg Lys				
310 315 320 325				
att ttg gct gcg ggc acg gga ctg gca aac atg ggt gga ttc ttg tca	1123			
Ile Leu Ala Ala Gly Thr Gly Leu Ala Asn Met Gly Gly Phe Leu Ser				
330 335 340				
tcg atg gtt gca gcg cag gtt atg ggg ttc ctt ctt gat cac agc gcg	1171			
Ser Met Val Ala Ala Gln Val Met Gly Phe Leu Leu Asp His Ser Ala				
345 350 355				
cat ggt agc acc tat act tgg gtg gac ttc cgt ttt ggt ttc ctt gcg	1219			
His Gly Ser Thr Tyr Thr Trp Val Asp Phe Arg Phe Gly Phe Leu Ala				
360 365 370				
att ctt gtc aca tgg gcc gtc gga gtc acg gga ttt gtt gta gcc cga	1267			
Ile Leu Val Thr Trp Ala Val Gly Val Thr Gly Phe Val Val Ala Arg				
375 380 385				
ctc aag ggt gga ccg ggc cgc aga tta ctc gcc cag att agg tct acc	1315			
Leu Lys Gly Gly Pro Gly Arg Arg Leu Leu Ala Gln Ile Arg Ser Thr				
390 395 400 405				

aag gac ttt taaagatcgg gtaaaacctg tgg  
Lys Asp Phe

1347

&lt;210&gt; 462

&lt;211&gt; 408

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 462

Met Ala Ala Ile Thr Ser Arg Thr Ser Phe Gly Val Ala Gly Val Glu  
1 5 10 15

Ala Ile Asp Arg Phe Gln Val Asp Ala Thr Arg Ile Ala Val Phe Thr  
20 25 30

Ser Val Gln Val Gly Val Tyr Ala Phe Ala Gln Ile Pro Met Gly Ile  
35 40 45

Leu Ile Asp Lys Phe Gly Pro Arg Lys Leu Leu Ala Ile Gly Ala Leu  
50 55 60

Val Met Gly Ile Gly Gln Leu Ile Leu Gly Phe Thr Asp Ser Tyr Ser  
65 70 75 80

Ile Ala Ile Ile Ala Arg Val Phe Ile Gly Ala Gly Asp Ala Ser Ile  
85 90 95

Phe Leu Ser Val Met Arg Ile Leu Pro Phe Trp Phe Pro Leu Lys His  
100 105 110

Thr Pro Ile Phe Thr Gln Leu Thr Thr Cys Leu Gly Gln Leu Gly Gln  
115 120 125

Phe Phe Ser Ala Val Pro Phe Met Ala Leu Leu Gly Ala Gln Gly Trp  
130 135 140

Pro Val Ala Phe Val Ser Leu Gly Ser Val Val Ala Leu Ile Ala Ile  
145 150 155 160

Ala Ala Leu Val Ala Val Arg Asp Thr Pro Asp Pro Gln Pro Lys Pro  
165 170 175

Val Glu Ser Ala Gln Glu Ala Asp Lys Pro Ser Leu Arg Ala Ser Leu  
180 185 190

Lys Leu Ile Val Arg Asn Pro Ile Thr Trp Gln Gly Phe Phe Ile His  
195 200 205

Tyr Val Leu Met Val Trp Gln Thr Val Phe Ser Met Met Trp Gly Val  
210 215 220

Pro Leu Met Thr Leu Gly Met Gly Leu Ser Ala Thr Thr Ala Gly Leu  
225 230 235 240

Val Leu Ser Ile Asn Thr Leu Cys Met Val Val Ser Ala Pro Ile Ile  
245 250 255

Gly Ile Ile Ser Ala Arg Leu Gly Tyr Arg Arg Asp Val Val Ala Ile

260	265	270
Ala Leu Ser Phe Val Gln Ser	Ala Val Trp Leu Val	Phe Leu Ala Ser
275	280	285
Asp Ala Pro Arg Gly Leu Met	Ala Ile Ile Leu Val	Asn Ile Val Met
290	295	300
Gly Leu Thr Thr Ala Ala Ser	Gly Tyr Gly Phe Asp Thr	Ile Arg Glu
305	310	315
Arg Leu Asp Arg Lys Ile Leu	Ala Ala Gly Thr Gly Leu	Ala Asn Met
325	330	335
Gly Gly Phe Leu Ser Ser Met	Val Ala Ala Gln Val Met	Gly Phe Leu
340	345	350
Leu Asp His Ser Ala His Gly	Ser Thr Tyr Thr Trp Val	Asp Phe Arg
355	360	365
Phe Gly Phe Leu Ala Ile Leu	Val Thr Trp Ala Val Gly	Val Thr Gly
370	375	380
Phe Val Val Ala Arg Leu Lys	Gly Gly Pro Gly Arg Arg	Leu Leu Ala
385	390	395
Gln Ile Arg Ser Thr Lys Asp	Phe	
405		

<210> 463  
 <211> 2265  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2242)  
 <223> RXN01554

<400> 463  
 tggcttaaac cttatttgta gttgtcaata aatatgaaat tccttagcaa cttgtttaaa 60  
 tagacgtata aacaagtttg aaaaaggaag gttatccatc ttg aaa aag cat gtg 115  
 Leu Lys Lys His Val  
 1 5  
 acc tca gcc gtt acc gcc gtg gtg acg gct ttt tca acg gct gcg ctt 163  
 Thr Ser Ala Val Thr Ala Val Val Thr Ala Phe Ser Thr Ala Ala Leu  
 10 15 20  
 ggt tta agt att gcc gtt tct cct gct gtt gcc caa gtg gct aat cca 211  
 Gly Leu Ser Ile Ala Val Ser Pro Ala Val Ala Gln Val Ala Asn Pro  
 25 30 35  
 gct cca gat ctt tct gcg ccg tat aca tgg gtg gaa gag ttt gat tcc 259  
 Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val Glu Glu Phe Asp Ser  
 40 45 50  
 gag gat gct ctc aaa ggg tgg aac att ttc cgc cag cca gat tat ggc 307  
 Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg Gln Pro Asp Tyr Gly

55	60	65	
agc gac aaa gtt ctc tat Ser Asp Lys Val Leu Tyr 70	acc gaa gat gct tta agt atc Thr Glu Asp Ala Leu Ser Ile 75	gaa gat ggc Glu Asp Gly 80	355
aag ctc acc atc acc act Lys Leu Thr Ile Thr Thr 90	cag cgc cac tgc gtt gac Gln Arg His Cys Val Asp 95	gaa gac ttc gcg Glu Asp Phe Ala 100	403
atc agt gat cct gtc aac cgc Ile Ser Asp Pro Val Asn Arg 105	gga aag ctc aat gac agc Gly Lys Leu Asn Asp 110	acc gcg caa Ser Thr Ala Gln 115	451
gtt gaa cct tgt gct cca ggt Val Glu Pro Cys Ala Pro Gly 120	cag ttt gaa aag ttc acc Gln Phe Glu Lys Phe Thr 125	agc gcg cgc Ser Ala Arg 130	499
atc gtc act ccg aaa att gct Ile Val Thr Pro Lys Ile Ala 135	cgt gga gag ttc gac ctt Ala Arg Gly Glu Phe Asp 140	tct gtc act Leu Ser Val Thr 145	547
gca act ctt aac acc ggt ggc Ala Thr Leu Asn Thr Gly Gly 150	gtc gaa ggt gtc cga agt Val Glu Gly Val Arg Ser 155	gcc att tgg Ala Ile Trp 160	595
atg caa aac ggt gaa cag gcg Met Gln Asn Gly Glu Gln Ala 170	tgt tcc tca gca acc aac Cys Ser Ser Ala Thr Asn 175	aat ggc ctc Asn Asn Gly Leu 180	643
tac gga gaa cta gac ctg gta Tyr Gly Glu Leu Asp Leu Val 185	gag cac ttt tct tac gat Glu His Phe Ser Tyr Asp 190	ctt cgc tcg Leu Arg Ser 195	691
cca tgg tct cca tca aac acc Pro Trp Ser Pro Ser Asn Thr 200	cac ttg ggt tgt gat cct His Leu Gly Cys Asp Pro 205	gaa agt gtc Glu Ser Val 210	739
aac ggc acc aac cgt gca cct Asn Gly Thr Asn Arg Ala Pro 215	cgt gaa ctt aaa cta gat Arg Glu Leu Lys Leu Asp 220	gag tca ctc Glu Ser Leu 225	787
gat ggc gtg gag cac acc tgg Asp Gly Val Glu His Thr Trp 230	act gtg agc acc acc cgc Thr Val Ser Thr Thr Arg 235	gac ggc gtt Asp Gly Val 240	835
gag tac ttc att gat gat gag Glu Tyr Phe Ile Asp Asp 250	gcg att aac cgc cag tca Ala Ile Asn Arg Gln Ser 255	tgg cgc aac Trp Arg Asn 260	883
gat gtc act ttg ggg cat gcc Asp Val Thr Leu Gly His Ala 265	gaa att gat gat ttc ggg Glu Ile Asp Asp Phe Gly 270	atc tcc gcg Ile Ser Ala 275	931
cag acg ttt gat gag atc gtc Gln Thr Phe Asp Glu Ile Val 280	gac cgc gaa tgg act ctc Asp Arg Glu Trp Thr Leu 285	act ctt aat Thr Leu Asn 290	979
caa aag gta gaa agc gcc gac Gln Lys Val Glu Ser Ala Asp 295	tgg gca aaa cca cgt tcc Trp Ala Lys Pro Arg Ser 300	tct gag gaa Ser Ser Glu Glu 305	1027

gat ttc cca gtc cgg tcc atg gtg att gac cgc atc gag gtc acc gga	1075
Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg Ile Glu Val Thr Gly	
310 315 320 325	
tct ccc gca gta tct gaa gac acc ccc atg cca gat acc acc cag ctt	1123
Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro Asp Thr Thr Gln Leu	
330 335 340	
ttg acc caa gac act ctg gaa tac ctc ggt cgc atg cca gtg ctg gaa	1171
Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg Met Pro Val Leu Glu	
345 350 355	
cgc tac gag cca gca agt gct gat ttt gcc gat ggc cgc agg cct tcc	1219
Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp Gly Arg Arg Pro Ser	
360 365 370	
tgg aac tac ttc aat ttg aag gaa tcg tgg cag aat cca gaa ctc gag	1267
Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln Asn Pro Glu Leu Glu	
375 380 385	
caa cgc cca gaa gct gtc gaa ttc gtt gat gga cgc atg gat atc gtg	1315
Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly Arg Met Asp Ile Val	
390 395 400 405	
acc cgt cgc cac tgt ctg gcc acc act gat gac atc gcc act ccg gaa	1363
Thr Arg Arg His Cys Leu Ala Thr Thr Asp Ile Ala Thr Pro Glu	
410 415 420	
aac gca cag gag gaa ccg tgc gcg ccg ggt gag gtg aca cgc tac agc	1411
Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu Val Thr Arg Tyr Ser	
425 430 435	
tca gcg cgt gtc cac ctt cca gag atc ccc gcc ggc aac ttc cgg ctc	1459
Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala Gly Asn Phe Arg Leu	
440 445 450	
acc gtg cgc gca cgg gcg cag tcc gaa gag ctt gtc gac ggc gtc cgc	1507
Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu Val Asp Gly Val Arg	
455 460 465	
ccc gct atc tgg atg cag aac aat acc aac ttc tgt gct gac aac gat	1555
Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe Cys Ala Asp Asn Asp	
470 475 480 485	
gga cgc cct tat ggt gaa ctg gat att act gag ttc tac agc tct cgt	1603
Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu Phe Tyr Ser Ser Arg	
490 495 500	
gtg aac acc cag tac tcg gca gta cac ctt gga tgt gct ggc aac cgc	1651
Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly Cys Ala Gly Asn Arg	
505 510 515	
cca gag atg aag ctt cgc caa atg gaa atg gaa gag tcc atg ttt ggg	1699
Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu Glu Ser Met Phe Gly	
520 525 530	
gat tgg cat gac tgg ggc gtc gaa gtc ttc gac ggc cag atc gta ttc	1747
Asp Trp His Asp Trp Gly Val Glu Val Phe Asp Gly Gln Ile Val Phe	
535 540 545	

acc att gac ggc aag gca gta act tcc tct ggc aaa gat gtc ttt ggc 1795  
 Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly Lys Asp Val Phe Gly  
 550 555 560 565  
  
 aac tct gtt acc cca gcc gct gca cct ctt cgc ccc gcg cac ttc aag 1843  
 Asn Ser Val Thr Pro Ala Ala Pro Leu Arg Pro Ala His Phe Lys  
 570 575 580  
  
 ttg tcg gaa gag gaa tac cgt gaa gtc atc ggg cag cct tgg cac ctt 1891  
 Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly Gln Pro Trp His Leu  
 585 590 595  
  
 att ttg aac acc atg gtg gag cag tct ggc aaa gac agc tgg att aca 1939  
 Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys Asp Ser Trp Ile Thr  
 600 605 610  
  
 gcg gtc gac aat aac gag gcg ttc cca gaa cac cgc ttc caa att gac 1987  
 Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His Arg Phe Gln Ile Asp  
 615 620 625  
  
 cat gtg gca gta gat atc gag tct gac tct gtg gac aat gta tgg cct 2035  
 His Val Ala Val Asp Ile Glu Ser Asp Ser Val Asp Asn Val Trp Pro  
 630 635 640 645  
  
 gac gct gcg aat gaa atc cca gac aat gtt ggt att gaa gac tct gat 2083  
 Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly Ile Glu Asp Ser Asp  
 650 655 660  
  
 gat ggc agc gac ctg gag gtt ggt tcg acc gga agc tct aca gct gag 2131  
 Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly Ser Ser Thr Ala Glu  
 665 670 675  
  
 acc gtg agc tgg atc tcg ttg ttc acc gcg ttg agc tcg ctg gtc ttc 2179  
 Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu Ser Ser Leu Val Phe  
 680 685 690  
  
 aca ctg gct ctc aat caa gaa gca ttg cag aat ttg att aat cag ttc 2227  
 Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn Leu Ile Asn Gln Phe  
 695 700 705  
  
 atg aga cag ttc aag taatccttgt gggcgctttg tct 2265  
 Met Arg Gln Phe Lys  
 710

&lt;210&gt; 464

&lt;211&gt; 714

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 464

Leu Lys Lys His Val Thr Ser Ala Val Thr Ala Val Val Thr Ala Phe  
 1 5 10 15

Ser Thr Ala Ala Leu Gly Leu Ser Ile Ala Val Ser Pro Ala Val Ala  
 20 25 30

Gln Val Ala Asn Pro Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val  
 35 40 45

Glu Glu Phe Asp Ser Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg

50	55	60
Gln Pro Asp Tyr Gly Ser Asp Lys Val Leu Tyr Thr Glu Asp Ala Leu		
65	70	75 80
Ser Ile Glu Asp Gly Lys Leu Thr Ile Thr Thr Gln Arg His Cys Val		
	85	90 95
Asp Glu Asp Phe Ala Ile Ser Asp Pro Val Asn Arg Gly Lys Leu Asn		
	100	105 110
Asp Ser Thr Ala Gln Val Glu Pro Cys Ala Pro Gly Gln Phe Glu Lys		
	115	120 125
Phe Thr Ser Ala Arg Ile Val Thr Pro Lys Ile Ala Arg Gly Glu Phe		
	130	135 140
Asp Leu Ser Val Thr Ala Thr Leu Asn Thr Gly Gly Val Glu Gly Val		
	145	150 155 160
Arg Ser Ala Ile Trp Met Gln Asn Gly Glu Gln Ala Cys Ser Ser Ala		
	165	170 175
Thr Asn Asn Gly Leu Tyr Gly Glu Leu Asp Leu Val Glu His Phe Ser		
	180	185 190
Tyr Asp Leu Arg Ser Pro Trp Ser Pro Ser Asn Thr His Leu Gly Cys		
	195	200 205
Asp Pro Glu Ser Val Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys		
	210	215 220
Leu Asp Glu Ser Leu Asp Gly Val Glu His Thr Trp Thr Val Ser Thr		
	225	230 235 240
Thr Arg Asp Gly Val Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg		
	245	250 255
Gln Ser Trp Arg Asn Asp Val Thr Leu Gly His Ala Glu Ile Asp Asp		
	260	265 270
Phe Gly Ile Ser Ala Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp		
	275	280 285
Thr Leu Thr Leu Asn Gln Lys Val Glu Ser Ala Asp Trp Ala Lys Pro		
	290	295 300
Arg Ser Ser Glu Glu Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg		
	305	310 315 320
Ile Glu Val Thr Gly Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro		
	325	330 335
Asp Thr Thr Gln Leu Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg		
	340	345 350
Met Pro Val Leu Glu Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp		
	355	360 365
Gly Arg Arg Pro Ser Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln		
	370	375 380

Asn Pro Glu Leu Glu Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly  
 385 390 395 400  
 Arg Met Asp Ile Val Thr Arg Arg His Cys Leu Ala Thr Thr Asp Asp  
 405 410 415  
 Ile Ala Thr Pro Glu Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu  
 420 425 430  
 Val Thr Arg Tyr Ser Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala  
 435 440 445  
 Gly Asn Phe Arg Leu Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu  
 450 455 460  
 Val Asp Gly Val Arg Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe  
 465 470 475 480  
 Cys Ala Asp Asn Asp Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu  
 485 490 495  
 Phe Tyr Ser Ser Arg Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly  
 500 505 510  
 Cys Ala Gly Asn Arg Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu  
 515 520 525  
 Glu Ser Met Phe Gly Asp Trp His Asp Trp Gly Val Glu Val Phe Asp  
 530 535 540  
 Gly Gln Ile Val Phe Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly  
 545 550 555 560  
 Lys Asp Val Phe Gly Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg  
 565 570 575  
 Pro Ala His Phe Lys Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly  
 580 585 590  
 Gln Pro Trp His Leu Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys  
 595 600 605  
 Asp Ser Trp Ile Thr Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His  
 610 615 620  
 Arg Phe Gln Ile Asp His Val Ala Val Asp Ile Glu Ser Asp Ser Val  
 625 630 635 640  
 Asp Asn Val Trp Pro Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly  
 645 650 655  
 Ile Glu Asp Ser Asp Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly  
 660 665 670  
 Ser Ser Thr Ala Glu Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu  
 675 680 685  
 Ser Ser Leu Val Phe Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn  
 690 695 700



Leu Ile Asn Gln Phe Met Arg Gln Phe Lys  
705 710

<210> 465  
<211> 389  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(382)  
<223> RXN03015

<400> 465  
ccgggtttgc ctgaggtttt ggagcgcaat ctggaaaatg gtcgcctgaa cttcactact 60  
gattatgcgg aggctgcggc tttcgcgcag gtgcattttct ttg ggc gtg ggt act . 115  
Leu Gly Val Gly Thr  
1 5  
cct cag cag aag ggt act tat gcg gcg gat ctg acg tat gtt cgt cag 163  
Pro Gln Gln Lys Gly Thr Tyr Ala Ala Asp Leu Thr Tyr Val Arg Gln  
10 15 20  
gtt gtt gag gat ttg gtg ccg ctg ctt gag ggc gag cac att att ttc 211  
Val Val Glu Asp Leu Val Pro Leu Leu Glu Gly Glu His Ile Ile Phe  
25 30 35  
ggc aag tct acg gtt ccg gtt ggt act gct gag cag ttg cag gag ctt 259  
Gly Lys Ser Thr Val Pro Val Gly Thr Ala Glu Gln Leu Gln Glu Leu  
40 45 50  
gct gat tct ctg gtc aag cct ggt tcg cac gtg gag atc gcg tgg aat 307  
Ala Asp Ser Leu Val Lys Pro Gly Ser His Val Glu Ile Ala Trp Asn  
55 60 65  
ccg gag ttc ttg cgt gag ggc tac gcg gtc aaa gac acc atc act ccg 355  
Pro Glu Phe Leu Arg Glu Gly Tyr Ala Val Lys Asp Thr Ile Thr Pro  
70 75 80 85  
gac cgc atc gtg gtg ggt gtg cgt gaa taagaca 389  
Asp Arg Ile Val Val Gly Val Arg Glu  
90

<210> 466  
<211> 94  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 466  
Leu Gly Val Gly Thr Pro Gln Gln Lys Gly Thr Tyr Ala Ala Asp Leu  
1 5 10 15  
Thr Tyr Val Arg Gln Val Val Glu Asp Leu Val Pro Leu Leu Glu Gly  
20 25 30  
Glu His Ile Ile Phe Gly Lys Ser Thr Val Pro Val Gly Thr Ala Glu  
35 40 45

Gln Leu Gln Glu Leu Ala Asp Ser Leu Val Lys Pro Gly Ser His Val  
50 55 60

Glu Ile Ala Trp Asn Pro Glu Phe Leu Arg Glu Gly Tyr Ala Val Lys  
65 70 75 80

Asp Thr Ile Thr Pro Asp Arg Ile Val Val Gly Val Arg Glu  
85 90

<210> 467

<211> 801

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(778)

<223> RXN03056

<400> 467

ttactatcac tgggttttgca gatgagatcg cacatgatct cgacgaacag atttccttac 60

ttaataaaact gaagaacagc tcgcggaagc taaagccaaa ttg gat gcc gca gga 115  
Leu Asp Ala Ala Gly  
1 5

att tca ctt tca gcc gtt gga tcc gac ttc ggc aag atc aac atc acc 163  
Ile Ser Leu Ser Ala Val Gly Ser Asp Phe Gly Lys Ile Asn Ile Thr  
10 15 20

gat cct ttt gaa gat cac ttg gag cgc gca cgc cac ggt gtt gag gtc 211  
Asp Pro Phe Glu Asp His Leu Glu Arg Ala Arg His Gly Val Glu Val  
25 30 35

gct aag ctc ttc ggc gcg aaa tac atc cgc atg ttc tcc ttc ttt att 259  
Ala Lys Leu Phe Gly Ala Lys Tyr Ile Arg Met Phe Ser Phe Phe Ile  
40 45 50

gca gaa ggc gac aac cct gaa agc ttc cgc aaa gaa gta ctc tcc cgc 307  
Ala Glu Gly Asp Asn Pro Glu Ser Phe Arg Lys Glu Val Leu Ser Arg  
55 60 65

acc cac gca atg gtc gaa ctc gca gaa gcc ggc ggc atc acc ctc ctc 355  
Thr His Ala Met Val Glu Leu Ala Glu Ala Gly Gly Ile Thr Leu Leu  
70 75 80 85

cac gaa aat gaa aag gga atc tat ggc gac tcc ccg cag cgc gtg aag 403  
His Glu Asn Glu Lys Gly Ile Tyr Gly Asp Ser Pro Gln Arg Val Lys  
90 95 100

gat tta atc acc agc atc gac tcc cct aac tac cgc gca atc tac gac 451  
Asp Leu Ile Thr Ser Ile Asp Ser Pro Asn Tyr Arg Ala Ile Tyr Asp  
105 110 115

gca gct aac tac gtg caa acc gga ttc aag cct ttt gat gag gca tgg 499  
Ala Ala Asn Tyr Val Gln Thr Gly Phe Lys Pro Phe Asp Glu Ala Trp  
120 125 130

ccg atc gtt aag gac tac gtc gac tac gtc cac atc aag gac gcg acc 547  
Pro Ile Val Lys Asp Tyr Val Asp Tyr Val His Ile Lys Asp Ala Thr

135	140	145	
att cca gat gca gag cac	ccc atc gga atc atc	aag cca gca gga caa	595
Ile Pro Asp Ala Glu His	Pro Ile Gly Ile Ile Lys	Pro Ala Gly Gln	
150	155	160 165	
ggc gac ggc caa tac cca	gag ctc ctt gcc gcg cta	aac gcc gac ggt	643
Gly Asp Gly Gln Tyr Pro	Glu Leu Leu Ala Ala Leu	Asn Ala Asp Gly	
170	175	180	
tac aac gga ttc gtc tcc	atc gag cct cac ctg ggt	gac ttc gat gaa	691
Tyr Asn Gly Phe Val Ser	Ile Glu Pro His Leu Gly	Asp Phe Asp Glu	
185	190	195	
ttc ggc gga ctc tgc gga	cct gac ctg tgg acc agc	gca tgc gac gct	739
Phe Gly Gly Leu Cys Gly	Pro Asp Leu Trp Thr Ser	Ala Cys Asp Ala	
200	205	210	
ctc gca gga atc ctg aac	aac atc aac gcc gag tac	aac taaggacaac	788
Leu Ala Gly Ile Leu Asn	Asn Ile Asn Ala Glu Tyr	Asn	
215	220	225	
tgataatgac aaa			801
<210> 468			
<211> 226			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 468			
Leu Asp Ala Ala Gly Ile	Ser Leu Ser Ala Val Gly	Ser Asp Phe Gly	
1	5	10 15	
Lys Ile Asn Ile Thr Asp	Pro Phe Glu Asp His Leu	Glu Arg Ala Arg	
20	25	30	
His Gly Val Glu Val Ala	Lys Leu Phe Gly Ala Lys	Tyr Ile Arg Met	
35	40	45	
Phe Ser Phe Phe Ile Ala	Glu Gly Asp Asn Pro Glu	Ser Phe Arg Lys	
50	55	60	
Glu Val Leu Ser Arg Thr	His Ala Met Val Glu Leu	Ala Glu Ala Gly	
65	70	75 80	
Gly Ile Thr Leu Leu His	Glu Asn Glu Lys Gly Ile	Tyr Gly Asp Ser	
85	90	95	
Pro Gln Arg Val Lys Asp	Leu Ile Thr Ser Ile Asp	Ser Pro Asn Tyr	
100	105	110	
Arg Ala Ile Tyr Asp Ala	Ala Asn Tyr Val Gln Thr	Gly Phe Lys Pro	
115	120	125	
Phe Asp Glu Ala Trp Pro	Ile Val Lys Asp Tyr Val	Asp Tyr Val His	
130	135	140	
Ile Lys Asp Ala Thr Ile	Pro Asp Ala Glu His Pro	Ile Gly Ile Ile	
145	150	155 160	

Lys Pro Ala Gly Gln Gly Asp Gly Gln Tyr Pro Glu Leu Leu Ala Ala  
                   165                                  170                                  175  
 Leu Asn Ala Asp Gly Tyr Asn Gly Phe Val Ser Ile Glu Pro His Leu  
                   180                                  185                                  190  
 Gly Asp Phe Asp Glu Phe Gly Gly Leu Cys Gly Pro Asp Leu Trp Thr  
                   195                                  200                                  205  
 Ser Ala Cys Asp Ala Leu Ala Gly Ile Leu Asn Asn Ile Asn Ala Glu  
                   210                                  215                                  220  
 Tyr Asn  
 225

&lt;210&gt; 469

&lt;211&gt; 687

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(664)

&lt;223&gt; RXN03030

&lt;400&gt; 469

gaagatgaag cagaaaagat cattggtgcg ccagagggtt ctgcattggg caacaaagca 60

cagcttgatt ccgtcacctt gctgcgtaac aaccccatcc gtg ctg cca ctg gat 115  
   Val Leu Pro Leu Asp  
   1                                  5

cct gca gca agc ctg aag atc tac cca ttg gtt act ggc cgt acc aag 163  
 Pro Ala Ala Ser Leu Lys Ile Tyr Pro Leu Val Thr Gly Arg Thr Lys  
                                   10                                  15                                  20

atc gac gag gtt caa cta cag ctg gaa gca gcc att cgc gca gaa ctc 211  
 Ile Asp Glu Val Gln Leu Gln Leu Glu Ala Ala Ile Arg Ala Glu Leu  
                                   25                                  30                                  35

cca ggg gta acc ttg gtg tct tcc gag tca gaa gca gat ctt gca atc 259  
 Pro Gly Val Thr Leu Val Ser Ser Glu Ser Glu Ala Asp Leu Ala Ile  
                                   40                                  45                                  50

gtg tgg gct cgc cct gaa att gca ctg ttt gaa gat gac ctc gaa ggt 307  
 Val Trp Ala Arg Pro Glu Ile Ala Leu Phe Glu Asp Asp Leu Glu Gly  
                   55                                  60                                  65

gtt tcc ctc tct gtt gac cct cgt gcc aat ggt gtc gat gtg gaa cgc 355  
 Val Ser Leu Ser Val Asp Pro Arg Ala Asn Gly Val Asp Val Glu Arg  
                   70                                  75                                  80                                  85

gtt cag gct gtg gaa gct gca gtc cca acc atc ttg gct gtg aac ttc 403  
 Val Gln Ala Val Glu Ala Ala Val Pro Thr Ile Leu Ala Val Asn Phe  
                                   90                                  95                                  100

acc aac cct tgg gtg ctg tct gag atc gag cct ggt gcc gct gcc gtg 451  
 Thr Asn Pro Trp Val Leu Ser Glu Ile Glu Pro Gly Ala Ala Val  
                   105                                  110                                  115

gtg ggc act ttt gag atc aag cca gag ttc ctt ctc aag gct ttg act 499  
 Val Gly Thr Phe Glu Ile Lys Pro Glu Phe Leu Leu Lys Ala Leu Thr  
           120                          125                          130

ggt caa gag gga gga cca aag ggc aag ctg cca ttg act gtt cct gct 547  
 Gly Gln Glu Gly Gly Pro Lys Gly Lys Leu Pro Leu Thr Val Pro Ala  
           135                          140                          145

tcc atg cag gcg att gct gat tcc cct cgc gat atc cca ggc aag ttc 595  
 Ser Met Gln Ala Ile Ala Asp Ser Pro Arg Asp Ile Pro Gly Lys Phe  
           150                          155                          160                          165

ctc gat gag tct tac acc tac gtg gac tcc gca ggg atg gcc tac aag 643  
 Leu Asp Glu Ser Tyr Thr Tyr Val Asp Ser Ala Gly Met Ala Tyr Lys  
                           170                          175                          180

tac ggt cac gga ctt aat ttc tagattgtag gtagtctcgt ggg 687  
 Tyr Gly His Gly Leu Asn Phe  
                           185

<210> 470  
 <211> 188  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 470  
 Val Leu Pro Leu Asp Pro Ala Ala Ser Leu Lys Ile Tyr Pro Leu Val  
   1                          5                          10                          15

Thr Gly Arg Thr Lys Ile Asp Glu Val Gln Leu Gln Leu Glu Ala Ala  
           20                          25                          30

Ile Arg Ala Glu Leu Pro Gly Val Thr Leu Val Ser Ser Glu Ser Glu  
           35                          40                          45

Ala Asp Leu Ala Ile Val Trp Ala Arg Pro Glu Ile Ala Leu Phe Glu  
           50                          55                          60

Asp Asp Leu Glu Gly Val Ser Leu Ser Val Asp Pro Arg Ala Asn Gly  
   65                          70                          75                          80

Val Asp Val Glu Arg Val Gln Ala Val Glu Ala Ala Val Pro Thr Ile  
                           85                          90                          95

Leu Ala Val Asn Phe Thr Asn Pro Trp Val Leu Ser Glu Ile Glu Pro  
           100                          105                          110

Gly Ala Ala Ala Val Val Gly Thr Phe Glu Ile Lys Pro Glu Phe Leu  
           115                          120                          125

Leu Lys Ala Leu Thr Gly Gln Glu Gly Gly Pro Lys Gly Lys Leu Pro  
           130                          135                          140

Leu Thr Val Pro Ala Ser Met Gln Ala Ile Ala Asp Ser Pro Arg Asp  
   145                          150                          155                          160

Ile Pro Gly Lys Phe Leu Asp Glu Ser Tyr Thr Tyr Val Asp Ser Ala  
           165                          170                          175

Gly Met Ala Tyr Lys Tyr Gly His Gly Leu Asn Phe



Phe Ile Gly Phe Lys Asp Gly Thr Gly Asn Ile Glu His Leu Ala Lys  
 170 175 180  
 atc acc acg cta tgc gga gat cgc ctg ttc tac ctc ggt gga ctt ccc 691  
 Ile Thr Thr Leu Cys Gly Asp Arg Leu Phe Tyr Leu Gly Gly Leu Pro  
 185 190 195  
 acc gct gag acc ttt gca cta cca ctg ctt cag atg ggc atg agc acc 739  
 Thr Ala Glu Thr Phe Ala Leu Pro Leu Leu Gln Met Gly Met Ser Thr  
 200 205 210  
 tac tcc tct gca atg ttc aac ttc att cca gat ttc gca ctg agc ttc 787  
 Tyr Ser Ser Ala Met Phe Asn Phe Ile Pro Asp Phe Ala Leu Ser Phe  
 215 220 225  
 tac gcc gat gtt cgt gcg cag gac agc gca gca gta aag cag aag ctg 835  
 Tyr Ala Asp Val Arg Ala Gln Asp Ser Ala Ala Val Lys Gln Lys Leu  
 230 235 240 245  
 agc gat ttt gtg ctc ccc tac ttg gat atc cgc gat cgc gca caa ggc 883  
 Ser Asp Phe Val Leu Pro Tyr Leu Asp Ile Arg Asp Arg Ala Gln Gly  
 250 255 260  
 tac ggt gtc tcc att ggt aag ggc gga ctc aag gct gtt ggc cgc aac 931  
 Tyr Gly Val Ser Ile Gly Lys Gly Gly Leu Lys Ala Val Gly Arg Asn  
 265 270 275  
 gct ggc ggc gtt cgc cca cca ctg cgt aac ctt tcc gag caa gat atc 979  
 Ala Gly Gly Val Arg Pro Pro Leu Arg Asn Leu Ser Glu Gln Asp Ile  
 280 285 290  
 gcg gac ctg tcg gat ttg ctt gcc acc tct ggc gca ggt tcc tac cgc 1027  
 Ala Asp Leu Ser Asp Leu Leu Ala Thr Ser Gly Ala Gly Ser Tyr Arg  
 295 300 305  
 ctt cag ttg agg tgaaagcatg atcaccgcaa ccg 1062  
 Leu Gln Leu Arg  
 310

&lt;210&gt; 472

&lt;211&gt; 313

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 472

Met Ala Arg Phe Ser Pro Gln Asp Leu Ala Asp His Leu Lys Asp Gly  
 1 5 10 15  
 Leu Leu Ser Phe Pro Ala Thr Ala Phe Gln Asp Asp Leu Glu Val Asp  
 20 25 30  
 Glu Ala Ala Tyr Val Glu His Ile Glu Trp Gln Ser Ser Tyr Pro Val  
 35 40 45  
 Ala Gly Leu Phe Ala Ala Gly Gly Thr Gly Glu Gly Phe Ser Leu Thr  
 50 55 60  
 Val Glu Glu Asn His Arg Val Thr Gln Leu Ala Val Gln Ala Ser Ser  
 65 70 75 80

```
<210> 473
<211> 924
<212> DNA
<213> Corynebacterium glutamicum
```

```

<400> 473
gacctaaaat tcatcacctc accgttttta aggcttagaa aaatagcagt gttgggatgt 60
gaatatccat ttatgctgct gtagtcggct atgtggacgc atg gtg gca acc tct 115
Met Val Ala Thr Ser

```



	1	5	
cag ttt atc gat gac agc gag gct gcc cag gcg gta cgc gca gct att			163
Gln Phe Ile Asp Asp Ser Glu Ala Ala Gln Ala Val Arg Ala Ala Ile			
	10	15	20
gtt gca gga tac cga aac att gat act gcc cta gcg tat gga aac gag			211
Val Ala Gly Tyr Arg Asn Ile Asp Thr Ala Leu Ala Tyr Gly Asn Glu			
	25	30	35
cgc ggc gtt ggc gaa ggc att cgc acc gct gga gtg ccc cgc gag gag			259
Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly Val Pro Arg Glu Glu			
	40	45	50
ctc ttt att tcc acc aag cta gct gca gaa atc aaa gat tac gat gga			307
Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile Lys Asp Tyr Asp Gly			
	55	60	65
gca gtc gcc gcg att gat gag tct ttg gcg aaa att ggc ttg gat tat			355
Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys Ile Gly Leu Asp Tyr			
	70	75	80
gtc gat ctg atg ctc att cac tcc cca caa cca tgg agt gat ttc cgt			403
Val Asp Leu Met Leu Ile His Ser Pro Gln Pro Trp Ser Asp Phe Arg			
	90	95	100
ggt ggg gac tat tca gag gga aac cgt gaa gcg tgg cgc gcg ctg gaa			451
Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala Trp Arg Ala Leu Glu			
	105	110	115
gat gcc tac aaa gcc gga aag att cga tcc att ggt gtc tcg aac ttc			499
Asp Ala Tyr Lys Ala Gly Lys Ile Arg Ser Ile Gly Val Ser Asn Phe			
	120	125	130
ctg gag gcc gat ctg gag aat atc tta gac tcc gcg acg gtt gct cct			547
Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser Ala Thr Val Ala Pro			
	135	140	145
cac gtt aat cag ctt ctt gtg cat gtt gga aac acc cca agc gag tta			595
His Val Asn Gln Leu Leu Val His Val Gly Asn Thr Pro Ser Glu Leu			
	150	155	160
atc agt ttc tgc gat tcc aag ggc att ctg gtc gaa gca tat tca ccc			643
Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val Glu Ala Tyr Ser Pro			
	170	175	180
atc gcc cac gga gag atg ctg aag aac cag cag gtc aag gcg att gct			691
Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln Val Lys Ala Ile Ala			
	185	190	195
gac aag tac aac gtg agc att ccg cag cta tgc att cgg tac aca att			739
Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys Ile Arg Tyr Thr Ile			
	200	205	210
caa ctg gga acg gtg tct ttg cca aag act gcc aac cca gat cat atg			787
Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala Asn Pro Asp His Met			
	215	220	225
agc tcc aat gcg cag atc gac ttt gaa att tcc gag gaa gac atg gcg			835
Ser Ser Asn Ala Gln Ile Asp Phe Glu Ile Ser Glu Glu Asp Met Ala			
	230	235	240
			245

gca ctt caa gaa gtg acc gcc cgc gat tat ggc gag cac agc ggt ttt 883  
 Ala Leu Gln Glu Val Thr Ala Arg Asp Tyr Gly Glu His Ser Gly Phe  
                   250                  255                  260

cct gtg tat tcc ggc aag tagaaagatt tttatcatgg gac 924  
 Pro Val Tyr Ser Gly Lys  
                   265

<210> 474

<211> 267

<212> PRT

<213> Corynebacterium glutamicum

<400> 474

Met Val Ala Thr Ser Gln Phe Ile Asp Asp Ser Glu Ala Ala Gln Ala  
   1                  5                  10                  15

Val Arg Ala Ala Ile Val Ala Gly Tyr Arg Asn Ile Asp Thr Ala Leu  
                   20                  25                  30

Ala Tyr Gly Asn Glu Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly  
                   35                  40                  45

Val Pro Arg Glu Glu Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile  
                   50                  55                  60

Lys Asp Tyr Asp Gly Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys  
   65                  70                  75                  80

Ile Gly Leu Asp Tyr Val Asp Leu Met Leu Ile His Ser Pro Gln Pro  
                   85                  90                  95

Trp Ser Asp Phe Arg Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala  
                   100                  105                  110

Trp Arg Ala Leu Glu Asp Ala Tyr Lys Ala Gly Lys Ile Arg Ser Ile  
                   115                  120                  125

Gly Val Ser Asn Phe Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser  
                   130                  135                  140

Ala Thr Val Ala Pro His Val Asn Gln Leu Leu Val His Val Gly Asn  
   145                  150                  155                  160

Thr Pro Ser Glu Leu Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val  
                   165                  170                  175

Glu Ala Tyr Ser Pro Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln  
                   180                  185                  190

Val Lys Ala Ile Ala Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys  
                   195                  200                  205

Ile Arg Tyr Thr Ile Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala  
                   210                  215                  220

Asn Pro Asp His Met Ser Ser Asn Ala Gln Ile Asp Phe Glu Ile Ser  
   225                  230                  235                  240



Leu Ser Pro Thr Glu Val Asn Arg Leu Pro Asp Asp Ala Ile Leu Glu 150 155 160 165	
att tcc tcc acc gag gaa acc acc agc gcg gaa atc acc ggc acg gca Ile Ser Ser Thr Glu Glu Thr Thr Ser Ala Glu Ile Thr Gly Thr Ala 170 175 180	643
ttc agc ggc gag acc gaa ggc gat gag cgg cct cag gtc acc ggc gtt Phe Ser Gly Glu Thr Glu Gly Asp Glu Arg Pro Gln Val Thr Gly Val 185 190 195	691
tac acc gag ctt gtc gac gac ccc tcc acc gca tcg gcc ctg gcc tca Tyr Thr Glu Leu Val Asp Asp Pro Ser Thr Ala Ser Ala Leu Ala Ser 200 205 210	739
gcg ggc tta aac gtt gat att gag atc aac tcc cgc ttc act tca tcc Ala Gly Leu Asn Val Asp Ile Glu Ile Asn Ser Arg Phe Thr Ser Ser 215 220 225	787
ccc agc ctt cta aag tac gca gcc atc ttc att ggc ctt gcg tct gtg Pro Ser Leu Leu Lys Tyr Ala Ala Ile Phe Ile Gly Leu Ala Ser Val 230 235 240 245	835
ttg gtc tcc ctg tgg aca ctg cac cgc atg gat att ttg gat ggt cga Leu Val Ser Leu Trp Thr Leu His Arg Met Asp Ile Leu Asp Gly Arg 250 255 260	883
aaa gca cac cgc ttc ctg cct gcc aac tgg tac aag ctg aag cca ctt Lys Ala His Arg Phe Leu Pro Ala Asn Trp Tyr Lys Leu Lys Pro Leu 265 270 275	931
gat ggt gtt gtc gta gcg att ttg gtg ttc tgg cac ttc ctt ggc gcc Asp Gly Val Val Val Ala Ile Leu Val Phe Trp His Phe Leu Gly Ala 280 285 290	979
aac acc tct gac gac ggc ttc atc atg acc atg gcc cgc gtg tcc cag Asn Thr Ser Asp Asp Gly Phe Ile Met Thr Met Ala Arg Val Ser Gln 295 300 305	1027
aac gcg gat tat atg gcc aac tac tac cgc tgg ttc ggt gtc cca gaa Asn Ala Asp Tyr Met Ala Asn Tyr Tyr Arg Trp Phe Gly Val Pro Glu 310 315 320 325	1075
tca cca ttc ggc gca cca tat tac gac ttg ctg gct ctg atg gcc tac Ser Pro Phe Gly Ala Pro Tyr Tyr Asp Leu Leu Ala Leu Met Ala Tyr 330 335 340	1123
atc tca acc tca tca atc tgg ctt cgt cta ccc gca ttg ctc gct gga Ile Ser Thr Ser Ser Ile Trp Leu Arg Leu Pro Ala Leu Leu Ala Gly 345 350 355	1171
ctg atc atg tgg ttc gtg atc acc aga gag gtc atg cca cgg ttt ggc Leu Ile Met Trp Phe Val Ile Thr Arg Glu Val Met Pro Arg Phe Gly 360 365 370	1219
tca ttg gtt aac ggt cgc cgc gtt gcg cac tgg tct gca gcc atg gtg Ser Leu Val Asn Gly Arg Arg Val Ala His Trp Ser Ala Ala Met Val 375 380 385	1267
ttc ctg gcg ttc tgg ctt cca tac aac aac ggc act cgc cca gag cca Phe Leu Ala Phe Trp Leu Pro Tyr Asn Asn Gly Thr Arg Pro Glu Pro	1315

390	395	400	405	
atc atc gcg atg gga gct cta ctt gcg tgg gtt tcc ttc gag cgc gct				1363
Ile Ile Ala Met Gly Ala Leu Leu Ala Trp Val Ser Phe Glu Arg Ala	410	415	420	
atc gct acc tcc agg ttg ttg ccc gct gcc att ggt gtc att atc gcc				1411
Ile Ala Thr Ser Arg Leu Leu Pro Ala Ala Ile Gly Val Ile Ile Ala	425	430	435	
acc att tcc ctg gca tca ggc ccc acc ggt cta atg gca gtt gct gcg				1459
Thr Ile Ser Leu Ala Ser Gly Thr Gly Leu Met Ala Val Ala Ala	440	445	450	
ttg ctg gtc agt ttg tcc gcg ttg att cgc att ctt tat agg cgc ttg				1507
Leu Leu Val Ser Leu Ser Ala Leu Ile Arg Ile Leu Tyr Arg Arg Leu	455	460	465	
ccg ctt att ggg gcg tcg agg ggg gcg tcg aaa agc aaa gtc ttt ggc				1555
Pro Leu Ile Gly Ala Ser Arg Gly Ala Ser Lys Ser Lys Val Phe Gly	470	475	480	485
gct tcg atg gct atg ctt gcc cca ttc ctt gcg tct ggc acc gcg att				1603
Ala Ser Met Ala Met Leu Ala Pro Phe Leu Ala Ser Gly Thr Ala Ile	490	495	500	
ctc atc gcc gtt ttt ggc gat cag act ctg tca acc gtc atg gaa tcc				1651
Leu Ile Ala Val Phe Gly Asp Gln Thr Leu Ser Thr Val Met Glu Ser	505	510	515	
atc agc gtg cgc tcc gcg aag ggc ccg gca ctg acc tgg tac cac gaa				1699
Ile Ser Val Arg Ser Ala Lys Gly Pro Ala Leu Thr Trp Tyr His Glu	520	525	530	
tat gtg cgc tac caa acc gtc atg gaa caa acc gtt gat ggt tcc ttc				1747
Tyr Val Arg Tyr Gln Thr Val Met Glu Gln Thr Val Asp Gly Ser Phe	535	540	545	
acc cgc cgt ttt gct gtg ctg atg ctc atg gcg tgt ctg gct att gtg				1795
Thr Arg Arg Phe Ala Val Leu Met Leu Met Ala Cys Leu Ala Ile Val	550	555	560	565
gtc atc gcg atc ctg cgt tac ggc cgc att cca ggc gct gcg aag gga				1843
Val Ile Ala Ile Leu Arg Tyr Gly Arg Ile Pro Gly Ala Ala Lys Gly	570	575	580	
cca tca ctg cgt ttg atg atg gtc att ttc ggc acc atg ttc ttc atg				1891
Pro Ser Leu Arg Leu Met Met Val Ile Phe Gly Thr Met Phe Phe Met	585	590	595	
atg ttc acc cca acc aag tgg act cac cac ttc ggt gtc tac gca gga				1939
Met Phe Thr Pro Thr Lys Trp Thr His His Phe Gly Val Tyr Ala Gly	600	605	610	
ctt gcc ggc gca ttg gcc gga ctt gct gcc gtg ggg ctg tcc tat gtt				1987
Leu Ala Gly Ala Leu Ala Gly Leu Ala Ala Val Gly Leu Ser Tyr Val	615	620	625	
gcg gtg aaa tca cca cgc atg cgc acc att tcc atc ggt gcg ttc ctc				2035
Ala Val Lys Ser Pro Arg Met Arg Thr Ile Ser Ile Gly Ala Phe Leu	630	635	640	645

ttc ctg ctg gcg ctg gct ctc gca ggc gtg aac gga ttc tgg tac acc	2083
Phe Leu Leu Ala Leu Ala Leu Ala Gly Val Asn Gly Phe Trp Tyr Thr	
650 655 660	
tcc agc tac gcc gtg cca tgg tgg gat aaa acc atc cag atc aag ggc	2131
Ser Ser Tyr Ala Val Pro Trp Trp Asp Lys Thr Ile Gln Ile Lys Gly	
665 670 675	
atc gaa gca tcc acc gta gtg ctc gtg atc gcc gtg atc gtg ctg atc	2179
Ile Glu Ala Ser Thr Val Val Leu Val Ile Ala Val Ile Val Leu Ile	
680 685 690	
atc ggt gtt att caa tcc ttt gtc cac gat gtg aaa acc gcg caa gcc	2227
Ile Gly Val Ile Gln Ser Phe Val His Asp Val Lys Thr Ala Gln Ala	
695 700 705	
gaa acc aat cac tcc atg ggc gaa ctc gtg gcg gaa gat gaa gca aag	2275
Glu Thr Asn His Ser Met Gly Glu Leu Val Ala Glu Asp Glu Ala Lys	
710 715 720 725	
cgc gag cgt gcc tcc agg ttc acc ggc ctt gcg gcc tcc cct atc gca	2323
Arg Glu Arg Ala Ser Arg Phe Thr Gly Leu Ala Ala Ser Pro Ile Ala	
730 735 740	
gga gtg tcc gcc ctc gtt gtg ctg att acc tgc gca tcc atg ggc aaa	2371
Gly Val Ser Ala Leu Val Val Leu Ile Thr Cys Ala Ser Met Gly Lys	
745 750 755	
ggc ttt gtg gac caa tac ccc gcg tac tcc gtg ggt ctt ggc aac ctc	2419
Gly Phe Val Asp Gln Tyr Pro Ala Tyr Ser Val Gly Leu Gly Asn Leu	
760 765 770	
cgc tcc ctg acc ggc aac aca tgt ggc ctt gcc tcc gac gcc atg ctg	2467
Arg Ser Leu Thr Gly Asn Thr Cys Gly Leu Ala Ser Asp Ala Met Leu	
775 780 785	
gaa acc aac tcc aac gat tcc ttc ctc act cca gtg aac tcc aca ctt	2515
Glu Thr Asn Ser Asn Asp Ser Phe Leu Thr Pro Val Asn Ser Thr Leu	
790 795 800 805	
ggc gag tcc ctg gaa tcc gaa gat att cgc ggc ttt agt gct gcc ggc	2563
Gly Glu Ser Leu Glu Ser Glu Asp Ile Arg Gly Phe Ser Ala Ala Gly	
810 815 820	
atc cca cca tca atc agc cag gac caa gca gac ctg tct gct gtt ggt	2611
Ile Pro Pro Ser Ile Ser Gln Asp Gln Ala Asp Leu Ser Ala Val Gly	
825 830 835	
gcc att gcc aac act gac gac tcc acc gaa acc ggc gga tcc gac gaa	2659
Ala Ile Ala Asn Thr Asp Asp Ser Thr Glu Thr Gly Gly Ser Asp Glu	
840 845 850	
tca tcc gga caa tcc acc ggc aac acc ggc ggt gtc cga ggc tcc gaa	2707
Ser Ser Gly Gln Ser Thr Gly Asn Thr Gly Gly Val Arg Gly Ser Glu	
855 860 865	
ggc atc aac ggc tcc aac gcc cgc ctg cca ttc aac ctg gac tac acc	2755
Gly Ile Asn Gly Ser Asn Ala Arg Leu Pro Phe Asn Leu Asp Tyr Thr	
870 875 880 885	

caa gtt cca gtc gtc ggc tcc tgg tcc gct ggc acc caa aac cca gca	2803
Gln Val Pro Val Val Gly Ser Trp Ser Ala Gly Thr Gln Asn Pro Ala	
890 895 900	
aac atc acc acc gac tgg tac gaa atc cca gaa gcc acc gaa gaa gca	2851
Asn Ile Thr Thr Asp Trp Tyr Glu Ile Pro Glu Ala Thr Glu Glu Ala	
905 910 915	
ccc atc atc gtg gta tct gca gca ggt cgc atc gaa cac tac gac atc	2899
Pro Ile Ile Val Val Ser Ala Ala Gly Arg Ile Glu His Tyr Asp Ile	
920 925 930	
aac ggc gtc cgc caa tcc gga caa tcc gtc atg ctc gaa tac ggt cgc	2947
Asn Gly Val Arg Gln Ser Gly Gln Ser Val Met Leu Glu Tyr Gly Arg	
935 940 945	
ctt cgc gat aac ggc gac gtt gaa gac ctc ggc gaa gcc atg atg tac	2995
Leu Arg Asp Asn Gly Asp Val Glu Asp Leu Gly Glu Ala Met Met Tyr	
950 955 960 965	
gac atc ggc ccc gag cca tcc tgg cgc aac ctc cgc tac cca ctt gac	3043
Asp Ile Gly Pro Glu Pro Ser Trp Arg Asn Leu Arg Tyr Pro Leu Asp	
970 975 980	
caa ctc cca gaa gaa gcg gac gtc gtg cgc atc gtc gcc acc gac gtc	3091
Gln Leu Pro Glu Glu Ala Asp Val Val Arg Ile Val Ala Thr Asp Val	
985 990 995	
aac ctc gac gaa gac caa tgg gta gca ctg acg cca cca cgc gta cct	3139
Asn Leu Asp Glu Asp Gln Trp Val Ala Leu Thr Pro Pro Arg Val Pro	
1000 1005 1010	
aac cta gat tct ctg aac aac gtc atc gga tcc gaa acc cca gga ctc	3187
Asn Leu Asp Ser Leu Asn Asn Val Ile Gly Ser Glu Thr Pro Gly Leu	
1015 1020 1025	
ctc gac tgg gca gtt ggc ctg caa ttc cca tgc caa cgc acc ttc gac	3235
Leu Asp Trp Ala Val Gly Leu Gln Phe Pro Cys Gln Arg Thr Phe Asp	
1030 1035 1040 1045	
cac tac gcc gga gtc acc gag att cct gaa tac cga atc tcc cca gac	3283
His Tyr Ala Gly Val Thr Glu Ile Pro Glu Tyr Arg Ile Ser Pro Asp	
1050 1055 1060	
cac ggc gga aaa tcc acc ctc tcc cca ttc caa gac tgg gca ggc ggc	3331
His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln Asp Trp Ala Gly Gly	
1065 1070 1075	
gga tcc atg ggc acg gcc gaa gca gta aac aac gcc tac gaa atc ccg	3379
Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn Ala Tyr Glu Ile Pro	
1080 1085 1090	
tcc tac ctc cgc aac gac tgg ggc cgc gac tgg ggt tcc atc gaa cgc	3427
Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp Gly Ser Ile Glu Arg	
1095 1100 1105	
tac tcg ctg cgc acc aac tcc aac ggc gat gca cct aag gtt gca gac	3475
Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala Pro Lys Val Ala Asp	
1110 1115 1120 1125	
atc aac ctt gaa acc atc caa cgt tcc gga ctc tgg aat cca ggg cat	3523

Ile Asn Leu Glu Thr Ile Gln Arg Ser Gly Leu Trp Asn Pro Gly His  
 1130 1135 1140

atg aag gta gat gaa taagaccttc agtactggaa gtt 3561  
 Met Lys Val Asp Glu  
 1145

<210> 476

<211> 1146

<212> PRT

<213> Corynebacterium glutamicum

<400> 476

Met Arg Gln Val Gly Gly Asn Gly Gly His Gln Leu Asp Ser Ile Asn  
 1 5 10 15

Val Ser Asp Val Val Glu Ser Lys Lys Leu Lys Gly Ser Ala Gln Glu  
 20 25 30

Pro Pro Gln Val Ala Pro Gly Trp Leu Lys Lys Leu Ala Ile Ser Ser  
 35 40 45

Gly Leu Leu Gly Leu Leu Met Phe Val Leu Leu Pro Phe Leu Pro Val  
 50 55 60

Asn Gln Val Gln Ser Ser Leu Ser Trp Pro Gln Asn Gly Glu Leu Ser  
 65 70 75 80

Ser Val Asn Ala Pro Leu Ile Ser Tyr Ala Pro Gln Ser Met Asp Ala  
 85 90 95

Ser Ile Pro Val Ser Ala Leu Asp Ser Leu Asn Asp Asn Gln Ser Leu  
 100 105 110

Val Met Gly Thr Leu Pro Leu Asp Ser Thr Asp Ala Thr Asn Arg Gly  
 115 120 125

Leu Phe Val Arg Thr Ile Asp Gly Asn Leu Asp Val Ile Val Arg Gly  
 130 135 140

Glu Val Leu Leu Asp Leu Ser Pro Thr Glu Val Asn Arg Leu Pro Asp  
 145 150 155 160

Asp Ala Ile Leu Glu Ile Ser Ser Thr Glu Glu Thr Thr Ser Ala Glu  
 165 170 175

Ile Thr Gly Thr Ala Phe Ser Gly Glu Thr Glu Gly Asp Glu Arg Pro  
 180 185 190

Gln Val Thr Gly Val Tyr Thr Glu Leu Val Asp Asp Pro Ser Thr Ala  
 195 200 205

Ser Ala Leu Ala Ser Ala Gly Leu Asn Val Asp Ile Glu Ile Asn Ser  
 210 215 220

Arg Phe Thr Ser Ser Pro Ser Leu Leu Lys Tyr Ala Ala Ile Phe Ile  
 225 230 235 240

Gly Leu Ala Ser Val Leu Val Ser Leu Trp Thr Leu His Arg Met Asp  
 245 250 255



Ile Leu Asp Gly Arg Lys Ala His Arg Phe Leu Pro Ala Asn Trp Tyr  
 260 265 270  
 Lys Leu Lys Pro Leu Asp Gly Val Val Val Ala Ile Leu Val Phe Trp  
 275 280 285  
 His Phe Leu Gly Ala Asn Thr Ser Asp Asp Gly Phe Ile Met Thr Met  
 290 295 300  
 Ala Arg Val Ser Gln Asn Ala Asp Tyr Met Ala Asn Tyr Tyr Arg Trp  
 305 310 315 320  
 Phe Gly Val Pro Glu Ser Pro Phe Gly Ala Pro Tyr Tyr Asp Leu Leu  
 325 330 335  
 Ala Leu Met Ala Tyr Ile Ser Thr Ser Ser Ile Trp Leu Arg Leu Pro  
 340 345 350  
 Ala Leu Leu Ala Gly Leu Ile Met Trp Phe Val Ile Thr Arg Glu Val  
 355 360 365  
 Met Pro Arg Phe Gly Ser Leu Val Asn Gly Arg Arg Val Ala His Trp  
 370 375 380  
 Ser Ala Ala Met Val Phe Leu Ala Phe Trp Leu Pro Tyr Asn Asn Gly  
 385 390 395 400  
 Thr Arg Pro Glu Pro Ile Ile Ala Met Gly Ala Leu Leu Ala Trp Val  
 405 410 415  
 Ser Phe Glu Arg Ala Ile Ala Thr Ser Arg Leu Leu Pro Ala Ala Ile  
 420 425 430  
 Gly Val Ile Ile Ala Thr Ile Ser Leu Ala Ser Gly Pro Thr Gly Leu  
 435 440 445  
 Met Ala Val Ala Ala Leu Leu Val Ser Leu Ser Ala Leu Ile Arg Ile  
 450 455 460  
 Leu Tyr Arg Arg Leu Pro Leu Ile Gly Ala Ser Arg Gly Ala Ser Lys  
 465 470 475 480  
 Ser Lys Val Phe Gly Ala Ser Met Ala Met Leu Ala Pro Phe Leu Ala  
 485 490 495  
 Ser Gly Thr Ala Ile Leu Ile Ala Val Phe Gly Asp Gln Thr Leu Ser  
 500 505 510  
 Thr Val Met Glu Ser Ile Ser Val Arg Ser Ala Lys Gly Pro Ala Leu  
 515 520 525  
 Thr Trp Tyr His Glu Tyr Val Arg Tyr Gln Thr Val Met Glu Gln Thr  
 530 535 540  
 Val Asp Gly Ser Phe Thr Arg Arg Phe Ala Val Leu Met Leu Met Ala  
 545 550 555 560  
 Cys Leu Ala Ile Val Val Ile Ala Ile Leu Arg Tyr Gly Arg Ile Pro  
 565 570 575

Gly Ala Ala Lys Gly Pro Ser Leu Arg Leu Met Met Val Ile Phe Gly  
 580 585 590  
 Thr Met Phe Phe Met Met Phe Thr Pro Thr Lys Trp Thr His His Phe  
 595 600 605  
 Gly Val Tyr Ala Gly Leu Ala Gly Ala Leu Ala Gly Leu Ala Ala Val  
 610 615 620  
 Gly Leu Ser Tyr Val Ala Val Lys Ser Pro Arg Met Arg Thr Ile Ser  
 625 630 635 640  
 Ile Gly Ala Phe Leu Phe Leu Leu Ala Leu Ala Leu Ala Gly Val Asn  
 645 650 655  
 Gly Phe Trp Tyr Thr Ser Ser Tyr Ala Val Pro Trp Trp Asp Lys Thr  
 660 665 670  
 Ile Gln Ile Lys Gly Ile Glu Ala Ser Thr Val Val Leu Val Ile Ala  
 675 680 685  
 Val Ile Val Leu Ile Ile Gly Val Ile Gln Ser Phe Val His Asp Val  
 690 695 700  
 Lys Thr Ala Gln Ala Glu Thr Asn His Ser Met Gly Glu Leu Val Ala  
 705 710 715 720  
 Glu Asp Glu Ala Lys Arg Glu Arg Ala Ser Arg Phe Thr Gly Leu Ala  
 725 730 735  
 Ala Ser Pro Ile Ala Gly Val Ser Ala Leu Val Val Leu Ile Thr Cys  
 740 745 750  
 Ala Ser Met Gly Lys Gly Phe Val Asp Gln Tyr Pro Ala Tyr Ser Val  
 755 760 765  
 Gly Leu Gly Asn Leu Arg Ser Leu Thr Gly Asn Thr Cys Gly Leu Ala  
 770 775 780  
 Ser Asp Ala Met Leu Glu Thr Asn Ser Asn Asp Ser Phe Leu Thr Pro  
 785 790 795 800  
 Val Asn Ser Thr Leu Gly Glu Ser Leu Glu Ser Glu Asp Ile Arg Gly  
 805 810 815  
 Phe Ser Ala Ala Gly Ile Pro Pro Ser Ile Ser Gln Asp Gln Ala Asp  
 820 825 830  
 Leu Ser Ala Val Gly Ala Ile Ala Asn Thr Asp Asp Ser Thr Glu Thr  
 835 840 845  
 Gly Gly Ser Asp Glu Ser Ser Gly Gln Ser Thr Gly Asn Thr Gly Gly  
 850 855 860  
 Val Arg Gly Ser Glu Gly Ile Asn Gly Ser Asn Ala Arg Leu Pro Phe  
 865 870 875 880  
 Asn Leu Asp Tyr Thr Gln Val Pro Val Val Gly Ser Trp Ser Ala Gly  
 885 890 895  
 Thr Gln Asn Pro Ala Asn Ile Thr Thr Asp Trp Tyr Glu Ile Pro Glu

```
<210> 477
<211> 1509
<212> DNA
<213> Corynebacterium glutamicum
```

<400> 477  
tcgcgtctct tagtcgatct gctcccatc cataggttgg gagaaaactt aactgttatt 60

ccatttcctta aaacaccgat atcgtgctat gaataggggt	gtg agt tgg aca gtt	115
	Val Ser Trp Thr Val	5
	1	
gat atc cct aaa gaa gtt ctc cct gat ttg cca cca ttg cca gaa ggc		163
Asp Ile Pro Lys Glu Val Leu Pro Asp Leu Pro Pro Leu Pro Glu Gly		
	10 15 20	
atg cag cag cag ttc gag gac acc att tcc cgt gac gct aag cag caa		211
Met Gln Gln Gln Phe Glu Asp Thr Ile Ser Arg Asp Ala Lys Gln Gln		
	25 30 35	
cct acg tgg gat cgt gca cag gca gaa aac gtg cgc aag atc ctt gag		259
Pro Thr Trp Asp Arg Ala Gln Ala Glu Asn Val Arg Lys Ile Leu Glu		
	40 45 50	
tcg gtt cct cca atc gtt gtt gcc cct gag gta ctt gag ctg aag cag		307
Ser Val Pro Pro Ile Val Val Ala Pro Glu Val Leu Glu Leu Lys Gln		
	55 60 65	
aag ctt gct gat gtt gcc aac ggt aag gcc ttc ctc ttg cag ggt ggt		355
Lys Leu Ala Asp Val Ala Asn Gly Lys Ala Phe Leu Leu Gln Gly Gly		
	70 75 80 85	
gac tgt gcg gaa act ttc gag tca aac act gag ccg cac att cgc gcc		403
Asp Cys Ala Glu Thr Phe Glu Ser Asn Thr Glu Pro His Ile Arg Ala		
	90 95 100	
aac gta aag act ctg ctg cag atg gca gtt gtt ttg acc tac ggt gca		451
Asn Val Lys Thr Leu Leu Gln Met Ala Val Val Leu Thr Tyr Gly Ala		
	105 110 115	
tcc act cct gtg atc aag atg gct cgt att gct ggt cag tac gca aag		499
Ser Thr Pro Val Ile Lys Met Ala Arg Ile Ala Gly Gln Tyr Ala Lys		
	120 125 130	
cct cgc tct tct gat ctg gat gga aat ggt ctg cca aac tac cgt ggc		547
Pro Arg Ser Ser Asp Leu Asp Gly Asn Gly Leu Pro Asn Tyr Arg Gly		
	135 140 145	
gat atc gtc aac ggt gtg gag gca acc cca gag gct cgt cgc cac gat		595
Asp Ile Val Asn Gly Val Glu Ala Thr Pro Glu Ala Arg Arg His Asp		
	150 155 160 165	
cct gcc cgc atg atc cgt gct tac gct aac gct tct gct gcg atg aac		643
Pro Ala Arg Met Ile Arg Ala Tyr Ala Asn Ala Ser Ala Ala Met Asn		
	170 175 180	
ttg gtg cgc gcg ctc acc agc tct ggc acc gct gat ctt tac cgt ctc		691
Leu Val Arg Ala Leu Thr Ser Ser Gly Thr Ala Asp Leu Tyr Arg Leu		
	185 190 195	
agc gag tgg aac cgc gag ttc gtt gcg aac tcc cca gct ggt gca cgc		739
Ser Glu Trp Asn Arg Glu Phe Val Ala Asn Ser Pro Ala Gly Ala Arg		
	200 205 210	
tac gag gct ctt gct cgt gag atc gac tcc ggt ctg cgc ttc atg gaa		787
Tyr Glu Ala Leu Ala Arg Glu Ile Asp Ser Gly Leu Arg Phe Met Glu		
	215 220 225	
gca tgt ggc gtg tcc gat gag tcc ctg cgt gct gca gat atc tac tgc		835

Ala Cys Gly Val Ser Asp Glu Ser Leu Arg Ala Ala Asp Ile Tyr Cys	
230 235 240 245	
tcc cac gag gct ttg ctg gtg gat tac gag cgt tcc atg ctg cgt ctt	883
Ser His Glu Ala Leu Leu Val Asp Tyr Glu Arg Ser Met Leu Arg Leu	
250 255 260	
gca acc gat gag gaa ggc aac gag gaa ctt tac gat ctt tca gct cac	931
Ala Thr Asp Glu Glu Gly Asn Glu Glu Leu Tyr Asp Leu Ser Ala His	
265 270 275	
cag ctg tgg atc ggc gag cgc acc cgt ggc atg gat gat ttc cat gtg	979
Gln Leu Trp Ile Gly Glu Arg Thr Arg Gly Met Asp Asp Phe His Val	
280 285 290	
aac ttc gca tcc atg atc tct aac cca atc ggc atc aag att ggt cct	1027
Asn Phe Ala Ser Met Ile Ser Asn Pro Ile Gly Ile Lys Ile Gly Pro	
295 300 305	
ggt atc acc cct gaa gag gct gtt gca tac gct gac aag ctc gat ccg	1075
Gly Ile Thr Pro Glu Glu Ala Val Ala Tyr Ala Asp Lys Leu Asp Pro	
310 315 320 325	
aac ttc gag cct ggc cgt ttg acc atc gtt gct cgc atg ggc cac gac	1123
Asn Phe Glu Pro Gly Arg Leu Thr Ile Val Ala Arg Met Gly His Asp	
330 335 340	
aag gtt cgc tcc gta ctt cct ggt gtt atc cag gct gtt gag gca tcc	1171
Lys Val Arg Ser Val Leu Pro Gly Val Ile Gln Ala Val Glu Ala Ser	
345 350 355	
gga cac aag gtt att tgg cag tcc gat ccg atg cac ggc aac act ttc	1219
Gly His Lys Val Ile Trp Gln Ser Asp Pro Met His Gly Asn Thr Phe	
360 365 370	
acc gca tcc aat ggc tac aag acc cgt cac ttc gac aag gtt atc gat	1267
Thr Ala Ser Asn Gly Tyr Lys Thr Arg His Phe Asp Lys Val Ile Asp	
375 380 385	
gag gtc cag ggc ttc ttc gag gtc cac cgc gca ttg ggc acc cac cca	1315
Glu Val Gln Gly Phe Phe Glu Val His Arg Ala Leu Gly Thr His Pro	
390 395 400 405	
ggc gga atc cac att gag ttc act ggt gaa gat gtc acc gag tgc ctc	1363
Gly Gly Ile His Ile Glu Phe Thr Gly Glu Asp Val Thr Glu Cys Leu	
410 415 420	
ggt ggc gct gaa gac atc acc gat gtt gat ctg cca ggc cgc tac gag	1411
Gly Gly Ala Glu Asp Ile Thr Asp Val Asp Leu Pro Gly Arg Tyr Glu	
425 430 435	
tcc gca tgc gat cct cgc ctg aac act cag cag tct ttg gag ttg gct	1459
Ser Ala Cys Asp Pro Arg Leu Asn Thr Gln Gln Ser Leu Glu Leu Ala	
440 445 450	
ttc ctc gtt gca gaa atg ctg cgt aac taagctttta gaccaactct	1506
Phe Leu Val Ala Glu Met Leu Arg Asn	
455 460	
aaa	1509

&lt;210&gt; 478

&lt;211&gt; 462

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 478

```

Val Ser Trp Thr Val Asp Ile Pro Lys Glu Val Leu Pro Asp Leu Pro
 1              5              10              15

Pro Leu Pro Glu Gly Met Gln Gln Gln Phe Glu Asp Thr Ile Ser Arg
          20          25          30

Asp Ala Lys Gln Gln Pro Thr Trp Asp Arg Ala Gln Ala Glu Asn Val
      35          40          45

Arg Lys Ile Leu Glu Ser Val Pro Pro Ile Val Val Ala Pro Glu Val
      50          55          60

Leu Glu Leu Lys Gln Lys Leu Ala Asp Val Ala Asn Gly Lys Ala Phe
 65          70          75          80

Leu Leu Gln Gly Gly Asp Cys Ala Glu Thr Phe Glu Ser Asn Thr Glu
          85          90          95

Pro His Ile Arg Ala Asn Val Lys Thr Leu Leu Gln Met Ala Val Val
          100          105          110

Leu Thr Tyr Gly Ala Ser Thr Pro Val Ile Lys Met Ala Arg Ile Ala
      115          120          125

Gly Gln Tyr Ala Lys Pro Arg Ser Ser Asp Leu Asp Gly Asn Gly Leu
      130          135          140

Pro Asn Tyr Arg Gly Asp Ile Val Asn Gly Val Glu Ala Thr Pro Glu
      145          150          155          160

Ala Arg Arg His Asp Pro Ala Arg Met Ile Arg Ala Tyr Ala Asn Ala
          165          170          175

Ser Ala Ala Met Asn Leu Val Arg Ala Leu Thr Ser Ser Gly Thr Ala
          180          185          190

Asp Leu Tyr Arg Leu Ser Glu Trp Asn Arg Glu Phe Val Ala Asn Ser
      195          200          205

Pro Ala Gly Ala Arg Tyr Glu Ala Leu Ala Arg Glu Ile Asp Ser Gly
      210          215          220

Leu Arg Phe Met Glu Ala Cys Gly Val Ser Asp Glu Ser Leu Arg Ala
      225          230          235          240

Ala Asp Ile Tyr Cys Ser His Glu Ala Leu Leu Val Asp Tyr Glu Arg
          245          250          255

Ser Met Leu Arg Leu Ala Thr Asp Glu Glu Gly Asn Glu Glu Leu Tyr
          260          265          270

Asp Leu Ser Ala His Gln Leu Trp Ile Gly Glu Arg Thr Arg Gly Met
      275          280          285

```

Asp Asp Phe His Val Asn Phe Ala Ser Met Ile Ser Asn Pro Ile Gly  
 290 295 300  
 Ile Lys Ile Gly Pro Gly Ile Thr Pro Glu Glu Ala Val Ala Tyr Ala  
 305 310 315 320  
 Asp Lys Leu Asp Pro Asn Phe Glu Pro Gly Arg Leu Thr Ile Val Ala  
 325 330 335  
 Arg Met Gly His Asp Lys Val Arg Ser Val Leu Pro Gly Val Ile Gln  
 340 345 350  
 Ala Val Glu Ala Ser Gly His Lys Val Ile Trp Gln Ser Asp Pro Met  
 355 360 365  
 His Gly Asn Thr Phe Thr Ala Ser Asn Gly Tyr Lys Thr Arg His Phe  
 370 375 380  
 Asp Lys Val Ile Asp Glu Val Gln Gly Phe Phe Glu Val His Arg Ala  
 385 390 395 400  
 Leu Gly Thr His Pro Gly Gly Ile His Ile Glu Phe Thr Gly Glu Asp  
 405 410 415  
 Val Thr Glu Cys Leu Gly Gly Ala Glu Asp Ile Thr Asp Val Asp Leu  
 420 425 430  
 Pro Gly Arg Tyr Glu Ser Ala Cys Asp Pro Arg Leu Asn Thr Gln Gln  
 435 440 445  
 Ser Leu Glu Leu Ala Phe Leu Val Ala Glu Met Leu Arg Asn  
 450 455 460

<210> 479  
 <211> 984  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(961)  
 <223> RXN01376

<400> 479  
 tcctcatcgg ttatcgggag tggcggatcac ttcttgcaaa cttaaaccac tatgctttcg 60  
 cttcgtgagt actttgaaat ccccatcgc tgtgatcaca gtg acc tat tca cca 115  
 Val Thr Tyr Ser Pro  
 1 5  
 ggt aaa tac ttg gcg tcg ttc ctg gat tct ttg cct ggt gcg act tca 163  
 Gly Lys Tyr Leu Ala Ser Phe Leu Asp Ser Leu Pro Gly Ala Thr Ser  
 10 15 20  
 cga gac acc cac gtt gtg atg gca gac aat ggt tct gtg gac ggt gtt 211  
 Arg Asp Thr His Val Val Met Ala Asp Asn Gly Ser Val Asp Gly Val  
 25 30 35  
 cct gag cag gca gca gcc tca cgc agc aac gtg gag ttc ctc tca act 259  
 Pro Glu Gln Ala Ala Ala Ser Arg Ser Asn Val Glu Phe Leu Ser Thr

40	45	50	
ggc ggc aac tta ggc tac gga acg gct att aat att gcc gcc cga tcg Gly Gly Asn Leu Gly Tyr Gly Thr Ala Ile Asn Ile Ala Ala Arg Ser 55 60 65			307
ttg cgt gcg cgc cgg gag gca gga gag atc gat ggg gag ttc ttc ctc Leu Arg Ala Arg Arg Glu Ala Gly Glu Ile Asp Gly Glu Phe Phe Leu 70 75 80 85			355
gtc tca aac cct gat gtt gtt ttt gac gaa gac tct att gat caa ttg Val Ser Asn Pro Asp Val Val Phe Asp Glu Asp Ser Ile Asp Gln Leu 90 95 100			403
ctt gaa tgt gcg aaa cgt cac cct gaa gca gga gcg gtt ggc ccg ttg Leu Glu Cys Ala Lys Arg His Pro Glu Ala Gly Ala Val Gly Pro Leu 105 110 115			451
atc cgt gag gcg gac ggt tcg gcg tat ccg tcg gct cgg gcg gta ccc Ile Arg Glu Ala Asp Gly Ser Ala Tyr Pro Ser Ala Arg Ala Val Pro 120 125 130			499
act ttg gcg aat ggc att ggt cac gct ttg ttg ggt gct gtg tgg aaa Thr Leu Ala Asn Gly Ile Gly His Ala Leu Leu Gly Ala Val Trp Lys 135 140 145			547
tcc aat ccg tgg tcg gcg gct tac cgt gac gat gaa gat atg gac act Ser Asn Pro Trp Ser Ala Ala Tyr Arg Asp Asp Glu Asp Met Asp Thr 150 155 160 165			595
gag cgc act gct ggc tgg ctg tcg gga tcg tgc ctg tta tta agg tgg Glu Arg Thr Ala Gly Trp Leu Ser Gly Ser Cys Leu Leu Leu Arg Trp 170 175 180			643
gat gcg ttt gat cga gtt ggt ggt ttt gat gag cgc tac ttc atg tac Asp Ala Phe Asp Arg Val Gly Gly Phe Asp Glu Arg Tyr Phe Met Tyr 185 190 195			691
atg gaa gac gtt gac ctg gga gat cgg ctg gtt cgc gcc ggt ttc acc Met Glu Asp Val Asp Leu Gly Asp Arg Leu Val Arg Ala Gly Phe Thr 200 205 210			739
aac gtc ttt tgc cca agt gcg cag atc atc cac gcg aaa ggt cat gtt Asn Val Phe Cys Pro Ser Ala Gln Ile Ile His Ala Lys Gly His Val 215 220 225			787
gcg ggt aaa aac cca gag aac atg ttg ccc gca cac cac gag agc gcg Ala Gly Lys Asn Pro Glu Asn Met Leu Pro Ala His His Glu Ser Ala 230 235 240 245			835
tat cgc ttc cag gct gat cgc ctc gcg aag ccg tgg caa gcc cca att Tyr Arg Phe Gln Ala Asp Arg Leu Ala Lys Pro Trp Gln Ala Pro Ile 250 255 260			883
cgg ttg gct ctg cga att ggt ttg aaa tta cga gcc gga gtc gcg gtt Arg Leu Ala Leu Arg Ile Gly Leu Lys Leu Arg Ala Gly Val Ala Val 265 270 275			931
ggt gtc tct aag atg aga acg aaa gcc tct tagaccgtcg acgaccaccg Gly Val Ser Lys Met Arg Thr Lys Ala Ser 280 285			981



gac

984

&lt;210&gt; 480

&lt;211&gt; 287

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 480

Val Thr Tyr Ser Pro Gly Lys Tyr Leu Ala Ser Phe Leu Asp Ser Leu  
 1 5 10 15

Pro Gly Ala Thr Ser Arg Asp Thr His Val Val Met Ala Asp Asn Gly  
 20 25 30

Ser Val Asp Gly Val Pro Glu Gln Ala Ala Ala Ser Arg Ser Asn Val  
 35 40 45

Glu Phe Leu Ser Thr Gly Gly Asn Leu Gly Tyr Gly Thr Ala Ile Asn  
 50 55 60

Ile Ala Ala Arg Ser Leu Arg Ala Arg Arg Glu Ala Gly Glu Ile Asp  
 65 70 75 80

Gly Glu Phe Phe Leu Val Ser Asn Pro Asp Val Val Phe Asp Glu Asp  
 85 90 95

Ser Ile Asp Gln Leu Leu Glu Cys Ala Lys Arg His Pro Glu Ala Gly  
 100 105 110

Ala Val Gly Pro Leu Ile Arg Glu Ala Asp Gly Ser Ala Tyr Pro Ser  
 115 120 125

Ala Arg Ala Val Pro Thr Leu Ala Asn Gly Ile Gly His Ala Leu Leu  
 130 135 140

Gly Ala Val Trp Lys Ser Asn Pro Trp Ser Ala Ala Tyr Arg Asp Asp  
 145 150 155 160

Glu Asp Met Asp Thr Glu Arg Thr Ala Gly Trp Leu Ser Gly Ser Cys  
 165 170 175

Leu Leu Leu Arg Trp Asp Ala Phe Asp Arg Val Gly Gly Phe Asp Glu  
 180 185 190

Arg Tyr Phe Met Tyr Met Glu Asp Val Asp Leu Gly Asp Arg Leu Val  
 195 200 205

Arg Ala Gly Phe Thr Asn Val Phe Cys Pro Ser Ala Gln Ile Ile His  
 210 215 220

Ala Lys Gly His Val Ala Gly Lys Asn Pro Glu Asn Met Leu Pro Ala  
 225 230 235 240

His His Glu Ser Ala Tyr Arg Phe Gln Ala Asp Arg Leu Ala Lys Pro  
 245 250 255

Trp Gln Ala Pro Ile Arg Leu Ala Leu Arg Ile Gly Leu Lys Leu Arg  
 260 265 270

Ala Gly Val Ala Val Gly Val Ser Lys Met Arg Thr Lys Ala Ser  
 275 280 285

<210> 481  
 <211> 1002  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(979)  
 <223> RXN01631

<400> 481  
 gccagttgag gatgctctca cagtcgctcg cattgtcagt gcatgctacg aatccgacaa 60  
 caaccagggc atttccgtaa acatctaaga ggagcactcc atg aaa cca caa ctt 115  
 Met Lys Pro Gln Leu  
 1 5  
 att gca tct tgc tgg acc agc gcg gga gac gcc gca ccc gat cgt gac 163  
 Ile Ala Ser Cys Trp Thr Ser Ala Gly Asp Ala Ala Pro Asp Arg Asp  
 10 15 20  
 gat ctc agc agc cca gta gca atc gat gag cgc atc gct cta gtc gct 211  
 Asp Leu Ser Ser Pro Val Ala Ile Asp Glu Arg Ile Ala Leu Val Ala  
 25 30 35  
 gaa acc ggt tgg gca ggc att ggg ctt gtt cac gcc gat ctc atc aaa 259  
 Glu Thr Gly Trp Ala Gly Ile Gly Leu Val His Ala Asp Leu Ile Lys  
 40 45 50  
 gca cgc gac acc att ggc tac gag gaa ttg cgc cga cgc atc cac gct 307  
 Ala Arg Asp Thr Ile Gly Tyr Glu Glu Leu Arg Arg Arg Ile His Ala  
 55 60 65  
 gca gga att gaa atc att gag gtg gag ttc ctc aat ggt tgg tgg gcg 355  
 Ala Gly Ile Glu Ile Ile Glu Val Glu Phe Leu Asn Gly Trp Trp Ala  
 70 75 80 85  
 act ggt gcg gaa cgc caa gag tcc gat gcc gtt cgt gcg gat ctg ttt 403  
 Thr Gly Ala Glu Arg Gln Glu Ser Asp Ala Val Arg Ala Asp Leu Phe  
 90 95 100  
 gct gcg gcg caa gct ctt ggt tcc cca cac att aag gtc gga gca gga 451  
 Ala Ala Ala Gln Ala Leu Gly Ser Pro His Ile Lys Val Gly Ala Gly  
 105 110 115  
 gag ggc acc aat ggt gtg gtt ccc att gct cac atg gcc agt gcg ttt 499  
 Glu Gly Thr Asn Gly Val Val Pro Ile Ala His Met Ala Ser Ala Phe  
 120 125 130  
 act gat ctc gct gcg gaa gct gaa gct cat ggc gtc aag ctc gcg ttg 547  
 Thr Asp Leu Ala Ala Glu Ala Glu Ala His Gly Val Lys Leu Ala Leu  
 135 140 145  
 gaa gca act ccg ttt tct cac ctg aag acc atc tac gac gcg ctg gaa 595  
 Glu Ala Thr Pro Phe Ser His Leu Lys Thr Ile Tyr Asp Ala Leu Glu  
 150 155 160 165

gtt gtc agc cat tcc gat agc cca tcg gct gga ctc atg gtt gat atc 643  
 Val Val Ser His Ser Asp Ser Pro Ser Ala Gly Leu Met Val Asp Ile  
 170 175 180  
  
 tgg cac acc gcg aaa atc gga atc ccc aac gat gaa ctg tgg cgc aac 691  
 Trp His Thr Ala Lys Ile Gly Ile Pro Asn Asp Glu Leu Trp Arg Asn  
 185 190 195  
  
 att cca ctg tcc aag gtc aac gca gtg gag gtt gat gat ggt ttc att 739  
 Ile Pro Leu Ser Lys Val Asn Ala Val Glu Val Asp Asp Gly Phe Ile  
 200 205 210  
  
 gac acc cca att gat ctt ttc gat gac tcc acc aac cgt cgc gcg tac 787  
 Asp Thr Pro Ile Asp Leu Phe Asp Asp Ser Thr Asn Arg Arg Ala Tyr  
 215 220 225  
  
 tgc ggt gaa ggc gaa ttt gat ccc gca agc ttc atc cgt ggc gcc atc 835  
 Cys Gly Glu Gly Glu Phe Asp Pro Ala Ser Phe Ile Arg Gly Ala Ile  
 230 235 240 245  
  
 gac gcc ggt tgg acg ggc gca tat ggt gtg gaa att att tcc gca gag 883  
 Asp Ala Gly Trp Thr Gly Ala Tyr Gly Val Glu Ile Ile Ser Ala Glu  
 250 255 260  
  
 cac cga agc ctc ccg gtg aaa gaa ggg ctg caa cgt gct ttc gac acc 931  
 His Arg Ser Leu Pro Val Lys Glu Gly Leu Gln Arg Ala Phe Asp Thr  
 265 270 275  
  
 acc atc gca gcg ttt gaa caa gct gct cgt ctc gcc ccc tcc act aac 979  
 Thr Ile Ala Ala Phe Glu Gln Ala Ala Arg Leu Ala Pro Ser Thr Asn  
 280 285 290  
  
 tgatctttga aaggctgaaa aaa 1002

&lt;210&gt; 482

&lt;211&gt; 293

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 482

Met Lys Pro Gln Leu Ile Ala Ser Cys Trp Thr Ser Ala Gly Asp Ala  
 1 5 10 15  
  
 Ala Pro Asp Arg Asp Asp Leu Ser Ser Pro Val Ala Ile Asp Glu Arg  
 20 25 30  
  
 Ile Ala Leu Val Ala Glu Thr Gly Trp Ala Gly Ile Gly Leu Val His  
 35 40 45  
  
 Ala Asp Leu Ile Lys Ala Arg Asp Thr Ile Gly Tyr Glu Glu Leu Arg  
 50 55 60  
  
 Arg Arg Ile His Ala Ala Gly Ile Glu Ile Ile Glu Val Glu Phe Leu  
 65 70 75 80  
  
 Asn Gly Trp Trp Ala Thr Gly Ala Glu Arg Gln Glu Ser Asp Ala Val  
 85 90 95  
  
 Arg Ala Asp Leu Phe Ala Ala Ala Gln Ala Leu Gly Ser Pro His Ile  
 100 105 110

Lys Val Gly Ala Gly Glu Gly Thr Asn Gly Val Val Pro Ile Ala His  
 115 120 125  
 Met Ala Ser Ala Phe Thr Asp Leu Ala Ala Glu Ala Glu Ala His Gly  
 130 135 140  
 Val Lys Leu Ala Leu Glu Ala Thr Pro Phe Ser His Leu Lys Thr Ile  
 145 150 155 160  
 Tyr Asp Ala Leu Glu Val Val Ser His Ser Asp Ser Pro Ser Ala Gly  
 165 170 175  
 Leu Met Val Asp Ile Trp His Thr Ala Lys Ile Gly Ile Pro Asn Asp  
 180 185 190  
 Glu Leu Trp Arg Asn Ile Pro Leu Ser Lys Val Asn Ala Val Glu Val  
 195 200 205  
 Asp Asp Gly Phe Ile Asp Thr Pro Ile Asp Leu Phe Asp Asp Ser Thr  
 210 215 220  
 Asn Arg Arg Ala Tyr Cys Gly Glu Gly Glu Phe Asp Pro Ala Ser Phe  
 225 230 235 240  
 Ile Arg Gly Ala Ile Asp Ala Gly Trp Thr Gly Ala Tyr Gly Val Glu  
 245 250 255  
 Ile Ile Ser Ala Glu His Arg Ser Leu Pro Val Lys Glu Gly Leu Gln  
 260 265 270  
 Arg Ala Phe Asp Thr Thr Ile Ala Ala Phe Glu Gln Ala Ala Arg Leu  
 275 280 285  
 Ala Pro Ser Thr Asn  
 290

<210> 483  
 <211> 990  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(967)  
 <223> RXN01593

<400> 483  
 atatgacagc cttcttcttg atctagatgg aaccgtctac gagggcggcc gagccattga 60  
 gcacgtagtt tctgcgctct ctggcgccgg cctaccgctc atg tat gtc acc aat 115  
 Met Tyr Val Thr Asn  
 1 5  
 aat gcc tcc cgt gct ccg gag gtg gtg gct gcg caa ctc cgt gag att 163  
 Asn Ala Ser Arg Ala Pro Glu Val Val Ala Ala Gln Leu Arg Glu Ile  
 10 15 20  
 ggc ctt gcc gac acc act gcg gac aat gtg atg aca tct gct caa gct 211  
 Gly Leu Ala Asp Thr Thr Ala Asp Asn Val Met Thr Ser Ala Gln Ala

25										30					35					
gcc	tgc	aag	atg	gcg	gcg	gag	aag	att	ccc	gct	gga	tcc	aag	gtg	tat	259				
Ala	Cys	Lys	Met	Ala	Ala	Glu	Lys	Ile	Pro	Ala	Gly	Ser	Lys	Val	Tyr					
		40				45						50								
gtt	ttg	ggt	tca	gaa	tcc	ttc	cgc	gag	cta	gct	act	gaa	gct	ggt	ttt	307				
Val	Leu	Gly	Ser	Glu	Ser	Phe	Arg	Glu	Leu	Ala	Thr	Glu	Ala	Gly	Phe					
		55				60						65								
gtg	gtg	gtt	gat	tcg	gct	gat	gat	aaa	cct	gtg	gct	gtg	ctt	cac	ggc	355				
Val	Val	Val	Asp	Ser	Ala	Asp	Asp	Lys	Pro	Val	Ala	Val	Leu	His	Gly					
		70				75						80		85						
cac	aac	cct	gag	acc	ggt	tgg	gct	cag	ttg	agc	gag	gct	gcg	ctg	tca	403				
His	Asn	Pro	Glu	Thr	Gly	Trp	Ala	Gln	Leu	Ser	Glu	Ala	Ala	Leu	Ser					
				90				95						100						
att	aat	gct	ggc	gcg	cag	tat	ttt	gca	tca	aat	ttg	gat	tcc	acc	ctt	451				
Ile	Asn	Ala	Gly	Ala	Gln	Tyr	Phe	Ala	Ser	Asn	Leu	Asp	Ser	Thr	Leu					
		105						110						115						
ccc	atg	gaa	cgc	ggt	cgt	cac	att	ggc	aac	ggt	tcc	atg	gtg	gct	gcc	499				
Pro	Met	Glu	Arg	Gly	Arg	His	Ile	Gly	Asn	Gly	Ser	Met	Val	Ala	Ala					
		120				125						130								
gtg	gtc	aac	gcg	act	ggc	gta	aag	cct	ctt	tcc	gca	ggt	aag	cca	ggc	547				
Val	Val	Asn	Ala	Thr	Gly	Val	Lys	Pro	Leu	Ser	Ala	Gly	Lys	Pro	Gly					
		135				140						145								
ccc	gcg	atg	ttc	tat	gcg	ggg	gct	gaa	act	ctt	aat	tct	tca	aag	cct	595				
Pro	Ala	Met	Phe	Tyr	Ala	Gly	Ala	Glu	Thr	Leu	Asn	Ser	Ser	Lys	Pro					
		150				155						160		165						
ttg	gct	gtc	ggc	gat	cgt	ctc	gat	acc	gat	atc	gcc	ggc	gga	aac	gct	643				
Leu	Ala	Val	Gly	Asp	Arg	Leu	Asp	Thr	Asp	Ile	Ala	Gly	Gly	Asn	Ala					
				170				175						180						
gca	ggc	atg	gac	aca	ttc	cag	gtc	ctg	acc	ggc	gtc	agc	ggc	tac	tac	691				
Ala	Gly	Met	Asp	Thr	Phe	Gln	Val	Leu	Thr	Gly	Val	Ser	Gly	Tyr	Tyr					
		185						190						195						
gat	ttg	gtg	cgc	gcc	att	ccc	aga	gca	gcg	ccc	cac	cta	tat	cgc	cac	739				
Asp	Leu	Val	Arg	Ala	Ile	Pro	Arg	Ala	Ala	Pro	His	Leu	Tyr	Arg	His					
		200				205						210								
ctc	gat	gca	gga	tct	cta	cag	cga	tcc	ggg	cga	gct	caa	gcc	agg	tgc	787				
Leu	Asp	Ala	Gly	Ser	Leu	Gln	Arg	Ser	Gly	Arg	Ala	Gln	Ala	Arg	Cys					
		215				220						225								
cca	ggg	cgg	ttt	ttc	agc	gct	tat	cga	cgg	cga	cac	cct	ggt	cat	ttc	835				
Pro	Gly	Arg	Phe	Phe	Ser	Ala	Tyr	Arg	Arg	Arg	His	Pro	Gly	His	Phe					
		230				235				240				245						
cgg	cgg	cga	tgc	cgg	cgc	aac	tcc	ggt	tgc	agc	act	ccg	cac	tgc	gtt	883				
Arg	Arg	Arg	Cys	Arg	Arg	Asn	Ser	Gly	Cys	Ser	Thr	Pro	His	Cys	Val					
				250				255						260						
gga	tgt	ggc	ctg	ggc	ggc	cac	aga	gca	gtc	acc	gag	gta	cgc	gct	gat	931				
Gly	Cys	Gly	Leu	Gly	Gly	His	Arg	Ala	Val	Thr	Glu	Val	Arg	Ala	Asp					
		265						270						275						

tca gag gta gct gct act gca ttg cag agc tgg tgg taaacggtga 977  
 Ser Glu Val Ala Ala Thr Ala Leu Gln Ser Trp Trp  
           280                          285

attcaccaaa gcc 990

<210> 484  
 <211> 289  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 484  
 Met Tyr Val Thr Asn Asn Ala Ser Arg Ala Pro Glu Val Val Ala Ala  
   1                  5                  10                  15

Gln Leu Arg Glu Ile Gly Leu Ala Asp Thr Thr Ala Asp Asn Val Met  
           20                  25                  30

Thr Ser Ala Gln Ala Ala Cys Lys Met Ala Ala Glu Lys Ile Pro Ala  
           35                  40                  45

Gly Ser Lys Val Tyr Val Leu Gly Ser Glu Ser Phe Arg Glu Leu Ala  
           50                  55                  60

Thr Glu Ala Gly Phe Val Val Val Asp Ser Ala Asp Asp Lys Pro Val  
           65                  70                  75                  80

Ala Val Leu His Gly His Asn Pro Glu Thr Gly Trp Ala Gln Leu Ser  
                   85                  90                  95

Glu Ala Ala Leu Ser Ile Asn Ala Gly Ala Gln Tyr Phe Ala Ser Asn  
                   100                  105                  110

Leu Asp Ser Thr Leu Pro Met Glu Arg Gly Arg His Ile Gly Asn Gly  
           115                  120                  125

Ser Met Val Ala Ala Val Val Asn Ala Thr Gly Val Lys Pro Leu Ser  
           130                  135                  140

Ala Gly Lys Pro Gly Pro Ala Met Phe Tyr Ala Gly Ala Glu Thr Leu  
   145                  150                  155                  160

Asn Ser Ser Lys Pro Leu Ala Val Gly Asp Arg Leu Asp Thr Asp Ile  
                   165                  170                  175

Ala Gly Gly Asn Ala Ala Gly Met Asp Thr Phe Gln Val Leu Thr Gly  
                   180                  185                  190

Val Ser Gly Tyr Tyr Asp Leu Val Arg Ala Ile Pro Arg Ala Ala Pro  
           195                  200                  205

His Leu Tyr Arg His Leu Asp Ala Gly Ser Leu Gln Arg Ser Gly Arg  
           210                  215                  220

Ala Gln Ala Arg Cys Pro Gly Arg Phe Phe Ser Ala Tyr Arg Arg Arg  
   225                  230                  235                  240

His Pro Gly His Phe Arg Arg Arg Cys Arg Arg Asn Ser Gly Cys Ser  
                   245                  250                  255

Thr Pro His Cys Val Gly Cys Gly Leu Gly Gly His Arg Ala Val Thr  
 260 265 270

Glu Val Arg Ala Asp Ser Glu Val Ala Ala Thr Ala Leu Gln Ser Trp  
 275 280 285

Trp

<210> 485

<211> 1173

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1150)

<223> RXN00337

<400> 485

ggacgccttat tggtagcat tcggattacg ccggtggtgt ggtgctggcg gctaatacgca 60

attgccggac tgcggctgcc gtcaataaag aaccgcgacg atg ttg tta acg tat 115  
 Met Leu Leu Thr Tyr  
 1 5

gcg ttt gtg gat gtg gag gga ggc gtc gaa aag cat tct tta agc act 163  
 Ala Phe Val Asp Val Glu Gly Gly Val Glu Lys His Ser Leu Ser Thr  
 10 15 20

gcg gac att gca gct cgc gca cac gcc cat atg aaa tcc cat gat gtt 211  
 Ala Asp Ile Ala Ala Arg Ala His Ala His Met Lys Ser His Asp Val  
 25 30 35

ttg ggg cgg cag act acg ccg cct cag ccg gag ggc ggc gtt gct gcc 259  
 Leu Gly Arg Gln Thr Thr Pro Pro Gln Pro Glu Gly Gly Val Ala Ala  
 40 45 50

cgg ttg ggc ggg att gcg tgg aca atg atc cat aag caa atg ctt tcg 307  
 Arg Leu Gly Gly Ile Ala Trp Thr Met Ile His Lys Gln Met Leu Ser  
 55 60 65

cgt gac aca aaa ggc ctg gat atc acc gtg ttg agc acc att cct gag 355  
 Arg Asp Thr Lys Gly Leu Asp Ile Thr Val Leu Ser Thr Ile Pro Glu  
 70 75 80 85

ggg gtg ggc ctg ggt gaa aat tcc gcc atg gat gtg gcg ctc gca ttg 403  
 Gly Val Gly Leu Gly Glu Asn Ser Ala Met Asp Val Ala Leu Ala Leu  
 90 95 100

gcg ctg tat cgg gaa aat att gag gaa gcc ccc acg aag gcg cgc att 451  
 Ala Leu Tyr Arg Glu Asn Ile Glu Glu Ala Pro Thr Lys Ala Arg Ile  
 105 110 115

gcg gag att tgt tcg cag tcc gca ttc atg ttc agt gag act tca gtg 499  
 Ala Glu Ile Cys Ser Gln Ser Ala Phe Met Phe Ser Glu Thr Ser Val  
 120 125 130

ttg cgt gcg cgg cac acc gtg gcg ttg cgg ggt gaa act gga cag att 547

```

Leu Arg Ala Arg His Thr Val Ala Leu Arg Gly Glu Thr Gly Gln Ile
 135                               140                               145

tcg gtg gtt gat tac gcc gat ggt tcg gtc act cag gcg cca cat ccg 595
Ser Val Val Asp Tyr Ala Asp Gly Ser Val Thr Gln Ala Pro His Pro
150                               155                               160                               165

gtg agt cgt tcc gct ggt ttg tcg gca ttt gtt gtt gct gcg caa act 643
Val Ser Arg Ser Ala Gly Leu Ser Ala Phe Val Val Ala Ala Gln Thr
170                               175                               180

gaa act gat ccg agc att tac cgc gag atc tat gct cga cat gcg ttt 691
Glu Thr Asp Pro Ser Ile Tyr Arg Glu Ile Tyr Ala Arg His Ala Phe
185                               190                               195

atc gat gaa gct gcg cgc gct ttc agt gtg gaa tct ttg cgg ttg ctt 739
Ile Asp Glu Ala Ala Arg Ala Phe Ser Val Glu Ser Leu Arg Leu Leu
200                               205                               210

ccc gac gct tcc act cgt gtt gtg gat tgg ttg cag gcc gtg att gag 787
Pro Asp Ala Ser Thr Arg Val Val Asp Trp Leu Gln Ala Val Ile Glu
215                               220                               225

gtg act ggt cga gag gat ctg ccc tcg att gaa caa gcc cag cgc tgg 835
Val Thr Gly Arg Glu Asp Leu Pro Ser Ile Glu Gln Ala Gln Arg Trp
230                               235                               240                               245

ttg aat ctg tgg gaa aac gaa acc cgg cgc gct cag agg aca gcc aat 883
Leu Asn Leu Trp Glu Asn Glu Thr Arg Arg Ala Gln Arg Thr Ala Asn
250                               255                               260

gcc ctg cgt tcg aga agg ctg agt gag ttt tct gag ctg ctg atg gaa 931
Ala Leu Arg Ser Arg Arg Leu Ser Glu Phe Ser Glu Leu Leu Met Glu
265                               270                               275

tcc caa gat gat ttg agc gac acc ttc gat ttc ccc cct gct gat ttg 979
Ser Gln Asp Asp Leu Ser Asp Thr Phe Asp Phe Pro Pro Ala Asp Leu
280                               285                               290

gcg ctt gct cgt ttg tgc gtc gag cgg ggt gcc aca gct gct cgg tcc 1027
Ala Leu Ala Arg Leu Cys Val Glu Arg Gly Ala Thr Ala Ala Arg Ser
295                               300                               305

acg tca gcg cgc ggt gtg att gcg ttg gtt gat gcc cat cat gcg cac 1075
Thr Ser Ala Arg Gly Val Ile Ala Leu Val Asp Ala His His Ala His
310                               315                               320                               325

aat ttt gct gcg gat ctc agc gag gat ggc ttg ttg gtg gtt cct ctc 1123
Asn Phe Ala Ala Asp Leu Ser Glu Asp Gly Leu Leu Val Val Pro Leu
330                               335                               340

ggg cac ggg gac gtc gcg gaa cag ggc tagcacgcct acttaaccag 1170
Gly His Gly Asp Val Ala Glu Gln Gly
345                               350

cct 1173

<210> 486
<211> 350
<212> PRT

```



&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 486

Met Leu Leu Thr Tyr Ala Phe Val Asp Val Glu Gly Gly Val Glu Lys  
 1 5 10 15  
 His Ser Leu Ser Thr Ala Asp Ile Ala Ala Arg Ala His Ala His Met  
 20 25 30  
 Lys Ser His Asp Val Leu Gly Arg Gln Thr Thr Pro Pro Gln Pro Glu  
 35 40 45  
 Gly Gly Val Ala Ala Arg Leu Gly Gly Ile Ala Trp Thr Met Ile His  
 50 55 60  
 Lys Gln Met Leu Ser Arg Asp Thr Lys Gly Leu Asp Ile Thr Val Leu  
 65 70 75 80  
 Ser Thr Ile Pro Glu Gly Val Gly Leu Gly Glu Asn Ser Ala Met Asp  
 85 90 95  
 Val Ala Leu Ala Leu Ala Leu Tyr Arg Glu Asn Ile Glu Glu Ala Pro  
 100 105 110  
 Thr Lys Ala Arg Ile Ala Glu Ile Cys Ser Gln Ser Ala Phe Met Phe  
 115 120 125  
 Ser Glu Thr Ser Val Leu Arg Ala Arg His Thr Val Ala Leu Arg Gly  
 130 135 140  
 Glu Thr Gly Gln Ile Ser Val Val Asp Tyr Ala Asp Gly Ser Val Thr  
 145 150 155 160  
 Gln Ala Pro His Pro Val Ser Arg Ser Ala Gly Leu Ser Ala Phe Val  
 165 170 175  
 Val Ala Ala Gln Thr Glu Thr Asp Pro Ser Ile Tyr Arg Glu Ile Tyr  
 180 185 190  
 Ala Arg His Ala Phe Ile Asp Glu Ala Ala Arg Ala Phe Ser Val Glu  
 195 200 205  
 Ser Leu Arg Leu Leu Pro Asp Ala Ser Thr Arg Val Val Asp Trp Leu  
 210 215 220  
 Gln Ala Val Ile Glu Val Thr Gly Arg Glu Asp Leu Pro Ser Ile Glu  
 225 230 235 240  
 Gln Ala Gln Arg Trp Leu Asn Leu Trp Glu Asn Glu Thr Arg Arg Ala  
 245 250 255  
 Gln Arg Thr Ala Asn Ala Leu Arg Ser Arg Arg Leu Ser Glu Phe Ser  
 260 265 270  
 Glu Leu Leu Met Glu Ser Gln Asp Asp Leu Ser Asp Thr Phe Asp Phe  
 275 280 285  
 Pro Pro Ala Asp Leu Ala Leu Ala Arg Leu Cys Val Glu Arg Gly Ala  
 290 295 300  
 Thr Ala Ala Arg Ser Thr Ser Ala Arg Gly Val Ile Ala Leu Val Asp

697

gtt gtg aac ctt gat ctc cca gtc ggc tgc gaa ttc ctc gaa cca aac	595
Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu Phe Leu Glu Pro Asn	
150 155 160 165	
agc cct cag tac tac gcc gac act gtc gca tgg gga gca atc ggc gct	643
Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp Gly Ala Ile Gly Ala	
170 175 180	
cgt acc acc gaa tct cag gtg cac cgc cag ctg gct tct ggg atg tct	691
Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu Ala Ser Gly Met Ser	
185 190 195	
atg cca att ggt ttc aag aac gga act gac gga aac atc cag gtt gca	739
Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly Asn Ile Gln Val Ala	
200 205 210	
gtc gac gcg gta cag gct gcc cag aac cca cac ttc ttc ttc gga acc	787
Val Asp Ala Val Gln Ala Ala Gln Asn Pro His Phe Phe Phe Gly Thr	
215 220 225	
tcc gac gac ggc gcg ctg agc gtc gtg gag acc gca ggc aac agc aac	835
Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr Ala Gly Asn Ser Asn	
230 235 240 245	
tcc cac atc att ttg cgc ggc ggt acc tcc ggc ccg aat cat gat gca	883
Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly Pro Asn His Asp Ala	
250 255 260	
gct tcg gtg gag gcc gtc gtc gag aag ctt ggt gaa aac gct cgt ctc	931
Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly Glu Asn Ala Arg Leu	
265 270 275	
atg atc gat gct tcc cat gct aac tcc ggc aag gat cat atc cga cag	979
Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys Asp His Ile Arg Gln	
280 285 290	
gtt gag gtt gtt cgt gaa atc gca gag cag att tct ggc ggt tct gaa	1027
Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile Ser Gly Gly Ser Glu	
295 300 305	
gct gtg gct gga atc atg att gag tcc ttc ctc gtt ggt ggc gca cag	1075
Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu Val Gly Gly Ala Gln	
310 315 320 325	
aac ctt gat cct gcg aaa ttg cgc atc aat ggc ggt gaa ggc ctg gtg	1123
Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly Gly Glu Gly Leu Val	
330 335 340	
tac gga cag tct gtg acc gat aag tgc atc gat att gac acc acc atc	1171
Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp Ile Asp Thr Thr Ile	
345 350 355	
gat ttg ctc gct gag ctg gcc gca gca gta agg gaa cgc cga gca gca	1219
Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg Glu Arg Arg Ala Ala	
360 365 370	
gcc aag taattaaggg cgctagactg tta	1248
Ala Lys	
375	

<210> 488  
 <211> 375  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 488  
 Met His Ser Pro Glu Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu  
     1                    5                    10                    15  
 Glu Asn Ala Ala Ser Thr Ser Asn Lys Arg Val Val Ala Phe His Glu  
                     20                    25                    30  
 Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys  
                     35                    40                    45  
 Gln Ala Ser Lys Val Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe  
                     50                    55                    60  
 Ala Gly Asp Asp Asp Arg Leu Val Val Val Val Gly Pro Cys Ser Val  
                     65                    70                    75                    80  
 His Asp Pro Glu Ala Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu  
                     85                    90                    95  
 Ala Lys Arg Leu Asp Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe  
                     100                    105                    110  
 Glu Lys Pro Arg Thr Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro  
                     115                    120                    125  
 His Leu Asn Glu Thr Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg  
                     130                    135                    140  
 Lys Val Leu Ile Asp Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu  
                     145                    150                    155                    160  
 Phe Leu Glu Pro Asn Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp  
                     165                    170                    175  
 Gly Ala Ile Gly Ala Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu  
                     180                    185                    190  
 Ala Ser Gly Met Ser Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly  
                     195                    200                    205  
 Asn Ile Gln Val Ala Val Asp Ala Val Gln Ala Ala Gln Asn Pro His  
                     210                    215                    220  
 Phe Phe Phe Gly Thr Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr  
                     225                    230                    235                    240  
 Ala Gly Asn Ser Asn Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly  
                     245                    250                    255  
 Pro Asn His Asp Ala Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly  
                     260                    265                    270  
 Glu Asn Ala Arg Leu Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys  
                     275                    280                    285

Asp His Ile Arg Gln Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile  
 290 295 300

Ser Gly Gly Ser Glu Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu  
 305 310 315 320

Val Gly Gly Ala Gln Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly  
 325 330 335

Gly Glu Gly Leu Val Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp  
 340 345 350

Ile Asp Thr Thr Ile Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg  
 355 360 365

Glu Arg Arg Ala Ala Ala Lys  
 370 375

<210> 489  
 <211> 1131  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1108)  
 <223> RXS02574

<400> 489  
 tgtgtctcctt gcgggctgcg cagaagagcc ggaacagcaa aaagcaataa gccgcttattc 60

gacgtccccc tccaccctc ccgcaccgac cgcgaggat ttg gcg cgc gcg caa 115  
 Leu Ala Arg Ala Gln  
 1 5

atc cct gaa cag caa cgc gac caa gtc gcg tcg ctg atg atg gtt gga 163  
 Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser Leu Met Met Val Gly  
 10 15 20

gtt gcg aat tat gat cag gca ttg gat gcg ctc aat cag ggg gtg ggt 211  
 Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu Asn Gln Gly Val Gly  
 25 30 35

ggc atc ttt att ggt tcc tgg aca gat gaa aat ctg ctc acg gaa cct 259  
 Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn Leu Leu Thr Glu Pro  
 40 45 50

ggc cgt aat att gag gcg ctc cgc gaa gcc gtc ggc agg gat ttc tcc 307  
 Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val Gly Arg Asp Phe Ser  
 55 60 65

gtc agc atc gac ttc gaa ggc ggc cgc gtc cag cgt gcc acc aat att 355  
 Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln Arg Ala Thr Asn Ile  
 70 75 80 85

ctt ggt gat ttc ccc tca ccg cgc gtg atg gcg caa acc atg acg ccg 403  
 Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala Gln Thr Met Thr Pro  
 90 95 100

gaa caa gta gaa gat ctc gca gaa atc cta ggc act ggt tta gct gca 451

Glu Gln Val	Glu Asp Leu Ala	Glu Ile Leu Gly Thr Gly	Leu Ala Ala	
105		110	115	
cat ggt gtg aca gtt aac ttt gca cct gtt gta gat gta gat gct tgg	499			
His Gly Val Thr Val Asn Phe Ala Pro Val Val Asp Val Asp Ala Trp		120	125	130
ggt ctc ccc gtc gtt ggc gat cgt tcc ttt tcc aac gac cca gcc gta	547			
Gly Leu Pro Val Val Gly Asp Arg Ser Phe Ser Asn Asp Pro Ala Val		135	140	145
gca gct act tat gcc aca gct ttt gca aag ggc tta agc aaa gta gga	595			
Ala Ala Thr Tyr Ala Thr Ala Phe Ala Lys Gly Leu Ser Lys Val Gly		150	155	160
att acc cca gta ttc aaa cat ttc cca ggt cac ggt cgt gca agt ggc	643			
Ile Thr Pro Val Phe Lys His Phe Pro Gly His Gly Arg Ala Ser Gly		170	175	180
gat tcg cac acc caa gat gtg gtg acc ccc gca ctt gat gag ctt aaa	691			
Asp Ser His Thr Gln Asp Val Val Thr Pro Ala Leu Asp Glu Leu Lys		185	190	195
act tac gac ctc atc cct tat ggt caa gca ctt tct gaa act gac gga	739			
Thr Tyr Asp Leu Ile Pro Tyr Gly Gln Ala Leu Ser Glu Thr Asp Gly		200	205	210
gcc gtc atg gtg ggc cac atg att gtt cca ggt ctt ggc acc gac gga	787			
Ala Val Met Val Gly His Met Ile Val Pro Gly Leu Gly Thr Asp Gly		215	220	225
gtt cca tcc tct atc gac ccc gcc acc tat caa ctg ctc cgc agt ggc	835			
Val Pro Ser Ser Ile Asp Pro Ala Thr Tyr Gln Leu Leu Arg Ser Gly		230	235	240
gat tac cca ggt ggc gtg cct ttc gat ggc gtg atc tac acc gac gat	883			
Asp Tyr Pro Gly Gly Val Pro Phe Asp Gly Val Ile Tyr Thr Asp Asp		250	255	260
ctc tct gga atg agt gcc att tcc gcc acc cat tca ccc gca gaa gca	931			
Leu Ser Gly Met Ser Ala Ile Ser Ala Thr His Ser Pro Ala Glu Ala		265	270	275
gtg ctt gcc tcc ctc aaa gca ggc gca gac caa gca cta tgg atc gac	979			
Val Leu Ala Ser Leu Lys Ala Gly Ala Asp Gln Ala Leu Trp Ile Asp		280	285	290
tat ggg tcg ttg ggc tcc gcg att gat cgc gtt gat gct gcc gtt agc	1027			
Tyr Gly Ser Leu Gly Ser Ala Ile Asp Arg Val Asp Ala Ala Val Ser		295	300	305
agc ggt gaa tac cct caa gaa caa atg ctg gca tct gcg tta aga gtc	1075			
Ser Gly Glu Tyr Pro Gln Glu Gln Met Leu Ala Ser Ala Leu Arg Val		310	315	320
caa ttg ctc tac atc aca cgt ctc gaa caa aag tgaagttacc agtccgtaac	1128			
Gln Leu Leu Tyr Ile Thr Arg Leu Glu Gln Lys		330	335	
ccc	1131			

&lt;210&gt; 490

&lt;211&gt; 336

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 490

Leu Ala Arg Ala Gln Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser  
 1 5 10 15

Leu Met Met Val Gly Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu  
 20 25 30

Asn Gln Gly Val Gly Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn  
 35 40 45

Leu Leu Thr Glu Pro Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val  
 50 55 60

Gly Arg Asp Phe Ser Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln  
 65 70 75 80

Arg Ala Thr Asn Ile Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala  
 85 90 95

Gln Thr Met Thr Pro Glu Gln Val Glu Asp Leu Ala Glu Ile Leu Gly  
 100 105 110

Thr Gly Leu Ala Ala His Gly Val Thr Val Asn Phe Ala Pro Val Val  
 115 120 125

Asp Val Asp Ala Trp Gly Leu Pro Val Val Gly Asp Arg Ser Phe Ser  
 130 135 140

Asn Asp Pro Ala Val Ala Ala Thr Tyr Ala Thr Ala Phe Ala Lys Gly  
 145 150 155 160

Leu Ser Lys Val Gly Ile Thr Pro Val Phe Lys His Phe Pro Gly His  
 165 170 175

Gly Arg Ala Ser Gly Asp Ser His Thr Gln Asp Val Val Thr Pro Ala  
 180 185 190

Leu Asp Glu Leu Lys Thr Tyr Asp Leu Ile Pro Tyr Gly Gln Ala Leu  
 195 200 205

Ser Glu Thr Asp Gly Ala Val Met Val Gly His Met Ile Val Pro Gly  
 210 215 220

Leu Gly Thr Asp Gly Val Pro Ser Ser Ile Asp Pro Ala Thr Tyr Gln  
 225 230 235 240

Leu Leu Arg Ser Gly Asp Tyr Pro Gly Gly Val Pro Phe Asp Gly Val  
 245 250 255

Ile Tyr Thr Asp Asp Leu Ser Gly Met Ser Ala Ile Ser Ala Thr His  
 260 265 270

Ser Pro Ala Glu Ala Val Leu Ala Ser Leu Lys Ala Gly Ala Asp Gln  
 275 280 285

Ala Leu Trp Ile Asp Tyr Gly Ser Leu Gly Ser Ala Ile Asp Arg Val  
 290 295 300

Asp Ala Ala Val Ser Ser Gly Glu Tyr Pro Gln Glu Gln Met Leu Ala  
 305 310 315 320

Ser Ala Leu Arg Val Gln Leu Leu Tyr Ile Thr Arg Leu Glu Gln Lys  
 325 330 335

<210> 491

<211> 1038

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1008)

<223> RXS03215

<400> 491

atc gat gtt gtc agc gtc gtg gtg gct aac ttc ctg cac cgc gaa atc	48
Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile	
1 5 10 15	
gtg gaa gca ctt ctg gca tcc ggc aag cat gtg ctg tgc gag aag cca	96
Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro	
20 25 30	
ctg tca gac acc atc gaa gat gca gaa gcc atg att gag gca gcc ggc	144
Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly	
35 40 45	
cgt gca gca aca aat ggc acc atc gcc cgc atc gga ctg acc tac cgc	192
Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg	
50 55 60	
cgt tcc cca ggc gtg gca cac atc cgt gat ctc gtg cag tcc ggc gag	240
Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu	
65 70 75 80	
ctt ggc aag gtt cta cac gtc acc ggc cac tac tgg acc gac tac gga	288
Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly	
85 90 95	
tcc aat gca cag gca cca atc agc tgg cgt tac aag ggg cca aac ggc	336
Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly	
100 105 110	
tcc ggc gca ctg gca gat gtg gga agc cac ctc acc tac ctg gca gaa	384
Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu	
115 120 125	
ttc gtt gca gga tct gac ttc gcc gcc gtc cgt ggt ggc cag ttg tcc	432
Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser	
130 135 140	
acc gtg atc acc gag cgc ccc aag cca ctc ggc gcg att gtc ggc cac	480



Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His  
 145 150 155 160  
 gaa ggc ggc gca gtt tcc gat gaa tac gaa gca gtg gaa aat gat gac 528  
 Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp  
 165 170 175  
 att gca tca ttc tcc gga tcc ttc atc ggt ggc gga acc gca acc ctc 576  
 Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu  
 180 185 190  
 cag gtc agc cgc att tcc cag gga cac cca aac acc cta ggt ttt gaa 624  
 Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu  
 195 200 205  
 gtg ttc tgt gaa aag ggc tcc gtg ctc ttt gat ttc cgc aac tca ggc 672  
 Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly  
 210 215 220  
 gaa ttc aaa atc ttc acc cca gca acc tcc ggt gac atc agc caa gaa 720  
 Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu  
 225 230 235 240  
 gcc ggc tac cgc acc atc acc atc gga cca aag cac cca tac tgg cgc 768  
 Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg  
 245 250 255  
 ggc ggc ctt gca atg gat gca cca ggc gtg gga att ggc caa aac gaa 816  
 Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu  
 260 265 270  
 ggc ttc gtt ttc cag gcg cgc gca ttc ctc gaa gaa atc gca gga atc 864  
 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile  
 275 280 285  
 tcc gaa gct gaa agc ctg cca cgc tgc gca act ttg gaa gaa ggg cta 912  
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu  
 290 295 300  
 cac aat atg cag ctc att gat gct gta tca cag tca gct gca gca ggt 960  
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly  
 305 310 315 320  
 ggc gaa acc gtt gcg gtc cca gcg gct gct ctg atc cct gca aac aac 1008  
 Gly Glu Thr Val Ala Val Pro Ala Ala Leu Ile Pro Ala Asn Asn  
 325 330 335  
 tagaaactat tcagaaagca tcaccatgaa 1038

&lt;210&gt; 492

&lt;211&gt; 336

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 492

Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile  
 1 5 10 15

Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro  
 20 25 30

Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly  
           35                          40                          45  
 Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg  
           50                          55                          60  
 Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu  
           65                          70                          75                          80  
 Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly  
                           85                          90                          95  
 Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly  
                           100                          105                          110  
 Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu  
           115                          120                          125  
 Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser  
           130                          135                          140  
 Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His  
           145                          150                          155                          160  
 Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp  
                           165                          170                          175  
 Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu  
                           180                          185                          190  
 Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu  
           195                          200                          205  
 Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly  
           210                          215                          220  
 Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu  
           225                          230                          235                          240  
 Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg  
                           245                          250                          255  
 Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu  
                           260                          265                          270  
 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile  
           275                          280                          285  
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu  
           290                          295                          300  
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly  
           305                          310                          315                          320  
 Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn  
                           325                          330                          335

<210> 493  
 <211> 1031  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1008)  
 <223> FRXA01915

<400> 493  
 atc gat gtt gtc agc gtc gtg gtg gct aac ttc ctg cac cgc gaa atc 48  
 Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile  
 1 5 10 15  
 gtg gaa gca ctt ctg gca tcc ggc aag cat gtg ctg tgc gag aag cca 96  
 Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro  
 20 25 30  
 ctg tca gac acc atc gaa gat gca gaa gcc atg att gag gca gcc ggc 144  
 Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly  
 35 40 45  
 cgt gca gca aca aat ggc acc atc gcc cgc atc gga ctg acc tac cgc 192  
 Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg  
 50 55 60  
 cgt tcc cca ggc gtg gca cac atc cgt gat ctc gtg cag tcc ggc gag 240  
 Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu  
 65 70 75 80  
 ctt ggc aag gtt cta cac gtc acc ggc cac tac tgg acc gac tac gga 288  
 Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly  
 85 90 95  
 tcc aat gca cag gca cca atc agc tgg cgt tac aag ggc cca aac ggc 336  
 Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly  
 100 105 110  
 tcc ggc gca ctg gca gat gtg gga agc cac ctc acc tac ctg gca gaa 384  
 Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu  
 115 120 125  
 ttc gtt gca gga tct gac ttc gcc gcc gtc cgt ggt ggc cag ttg tcc 432  
 Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser  
 130 135 140  
 acc gtg atc acc gag cgc ccc aag cca ctc ggc gcg att gtc ggc cac 480  
 Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His  
 145 150 155 160  
 gaa ggc ggc gca gtt tcc gat gaa tac gaa gca gtg gaa aat gat gac 528  
 Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp  
 165 170 175  
 att gca tca ttc tcc gga tcc ttc atc ggt ggc gga acc gca acc ctc 576  
 Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu  
 180 185 190  
 cag gtc agc cgc att tcc cag gga cac cca aac acc cta ggt ttt gaa 624

Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu  
 195 200 205

gtg ttc tgt gaa aag ggc tcc gtg ctc ttt gat ttc cgc aac tca ggc 672  
 Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly  
 210 215 220

gaa ttc aaa atc ttc acc cca gca acc tcc ggt gac atc agc caa gaa 720  
 Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu  
 225 230 235 240

gcc ggc tac cgc acc atc acc atc gga cca aag cac cca tac tgg cgc 768  
 Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg  
 245 250 255

ggc ggc ctt gca atg gat gca cca ggc gtg gga att ggc caa aac gaa 816  
 Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu  
 260 265 270

ggc ttc gtt ttc cag gcg cgc gca ttc ctc gaa gaa atc gca gga atc 864  
 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile  
 275 280 285

tcc gaa gct gaa agc ctg cca cgc tgc gca act ttg gaa gaa ggg cta 912  
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu  
 290 295 300

cac aat atg cag ctc att gat gct gta tca cag tca gct gca gca ggt 960  
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly  
 305 310 315 320

ggc gaa acc gtt gcg gtc cca gcg gct gct ctg atc cct gca aac aac 1008  
 Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn  
 325 330 335

tagaaactat tcagaaagca tca 1031

&lt;210&gt; 494

&lt;211&gt; 336

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 494

Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile  
 1 5 10 15

Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro  
 20 25 30

Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly  
 35 40 45

Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg  
 50 55 60

Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu  
 65 70 75 80

Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly  
 85 90 95

Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly  
 100 105 110  
 Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu  
 115 120 125  
 Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser  
 130 135 140  
 Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His  
 145 150 155 160  
 Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp  
 165 170 175  
 Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu  
 180 185 190  
 Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu  
 195 200 205  
 Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly  
 210 215 220  
 Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu  
 225 230 235 240  
 Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg  
 245 250 255  
 Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu  
 260 265 270  
 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile  
 275 280 285  
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu  
 290 295 300  
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly  
 305 310 315 320  
 Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn  
 325 330 335

<210> 495  
 <211> 1288  
 <212> DNA  
 <213> Corynebacterium glutamicum  
  
 <220>  
 <221> CDS  
 <222> (101)..(1258)  
 <223> RXS03224  
  
 <400> 495

```

acgattgtgc tgcgtttgc gttggtgaat agttctggac cgggtatttt gcggcgacaca 60

tggaactcat tgaacgccgc gcccggtctaa ggtgggaggc atg agt ttt gct gaa 115
                                         Met Ser Phe Ala Glu
                                         1           5

cat gcg atc atc tgg cac gtc tac ccc ctg ggc gct ttg ggt gct ccc 163
His Ala Ile Ile Trp His Val Tyr Pro Leu Gly Ala Leu Gly Ala Pro
          10                15                20

atc cgg cct gaa gcc ccc gca cct gtc aca cat cgg ctc ccc aat cta 211
Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His Arg Leu Pro Asn Leu
          25                30                35

att ggg tgg ctg gat tat gtt gtc gaa cta ggc tgc aac gcc ctc atg 259
Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly Cys Asn Ala Leu Met
          40                45                50

ctg gga ccg gta ttc gag tcc gtc agc cac ggc tac gac acc ctc gat 307
Leu Gly Pro Val Phe Glu Ser Val Ser His Gly Tyr Asp Thr Leu Asp
          55                60                65

ttc tac cgc atc gac ccg cgc ctc ggc acc gag gaa gac atg gac gcg 355
Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu Glu Asp Met Asp Ala
          70                75                80                85

ctg ctg gag gct gcg aat cag cgg ggc att gga gtg ctt ttc gac ggc 403
Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly Val Leu Phe Asp Gly
          90                95                100

gtc ttc aat cat gtt tcc agt tcc tct aaa tat ctc gac ctg acc acc 451
Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr Leu Asp Leu Thr Thr
          105                110                115

ggg gcg tca ttt gaa ggc cac gac atc ctg gcg gaa ctc gac cac acg 499
Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala Glu Leu Asp His Thr
          120                125                130

aat ccc gcc gta gtg gat ctg gtt gtc gat gtc atg aac cac tgg ctc 547
Asn Pro Ala Val Val Asp Leu Val Val Asp Val Met Asn His Trp Leu
          135                140                145

gac cgc gga atc gca ggc tgg cga ctc gac gct gtc tac gcc atc gcc 595
Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala Val Tyr Ala Ile Ala
          150                155                160                165

cct gaa ttt tgg gaa aaa gtc ctg cca gaa gtg cga cga aaa cac cca 643
Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val Arg Arg Lys His Pro
          170                175                180

cac gca tgg atc gtg ggg gag atg atc cat gga gat tac tcc gac tac 691
His Ala Trp Ile Val Gly Glu Met Ile His Gly Asp Tyr Ser Asp Tyr
          185                190                195

gtg aaa agc tcc ggc att gat tcc gtt acc gaa tac gaa ctg tgg aaa 739
Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu Tyr Glu Leu Trp Lys
          200                205                210

gcc att tgg agc agc atc aaa gag cgc aat ttc ttt gaa ctc gaa tgg 787
Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe Phe Glu Leu Glu Trp
          215                220                225

```

act ttg agt cgc cac aat gaa ttc ctc gat act ttc gta ccg cag aca 835  
 Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr Phe Val Pro Gln Thr  
 230 235 240 245  
  
 ttc att ggt aac cat gac gtc acc cgc att gcc acc cga atc ggt caa 883  
 Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala Thr Arg Ile Gly Gln  
 250 255 260  
  
 tca aat gcg atc ctg gcc gca gcg atc ctc ttc acg gtc gga gga acc 931  
 Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe Thr Val Gly Gly Thr  
 265 270 275  
  
 cca agc att tac tac ggc gat gag cag ggc ttt acg gga ttg aaa gag 979  
 Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe Thr Gly Leu Lys Glu  
 280 285 290  
  
 gat aac gtt ttc ggt gac gat gcc att agg cca cct ctt cct gcc gag 1027  
 Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro Pro Leu Pro Ala Glu  
 295 300 305  
  
 ttt tct cca ctg ggc acc tgg att gaa aac att tat aag gct ctg atc 1075  
 Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile Tyr Lys Ala Leu Ile  
 310 315 320 325  
  
 gcg ctg cgc agg caa cac ccg tgg ttg tat cag gcg cac acc gaa gtc 1123  
 Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln Ala His Thr Glu Val  
 330 335 340  
  
 ctt gag att gct aat gaa gcg atg acc tat aag tcc gtc ggt ctt gga 1171  
 Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys Ser Val Gly Leu Gly  
 345 350 355  
  
 ggt gaa gag ctg aca gtg cat ctt gat ttg gaa gag gtg tct gtt cgg 1219  
 Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu Glu Val Ser Val Arg  
 360 365 370  
  
 atc ctt gat ggc gag aag gtg ctg ttt cag tac agc gct tagttgtcgg 1268  
 Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr Ser Ala  
 375 380 385  
  
 ttcaagggtg ggggaacaaa 1288

&lt;210&gt; 496

&lt;211&gt; 386

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 496

Met Ser Phe Ala Glu His Ala Ile Ile Trp His Val Tyr Pro Leu Gly  
 1 5 10 15

Ala Leu Gly Ala Pro Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His  
 20 25 30

Arg Leu Pro Asn Leu Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly  
 35 40 45

Cys Asn Ala Leu Met Leu Gly Pro Val Phe Glu Ser Val Ser His Gly  
 50 55 60

Tyr Asp Thr Leu Asp Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu  
 65 70 75 80  
 Glu Asp Met Asp Ala Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly  
 85 90 95  
 Val Leu Phe Asp Gly Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr  
 100 105 110  
 Leu Asp Leu Thr Thr Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala  
 115 120 125  
 Glu Leu Asp His Thr Asn Pro Ala Val Val Asp Leu Val Val Asp Val  
 130 135 140  
 Met Asn His Trp Leu Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala  
 145 150 155 160  
 Val Tyr Ala Ile Ala Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val  
 165 170 175  
 Arg Arg Lys His Pro His Ala Trp Ile Val Gly Glu Met Ile His Gly  
 180 185 190  
 Asp Tyr Ser Asp Tyr Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu  
 195 200 205  
 Tyr Glu Leu Trp Lys Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe  
 210 215 220  
 Phe Glu Leu Glu Trp Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr  
 225 230 235 240  
 Phe Val Pro Gln Thr Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala  
 245 250 255  
 Thr Arg Ile Gly Gln Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe  
 260 265 270  
 Thr Val Gly Gly Thr Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe  
 275 280 285  
 Thr Gly Leu Lys Glu Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro  
 290 295 300  
 Pro Leu Pro Ala Glu Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile  
 305 310 315 320  
 Tyr Lys Ala Leu Ile Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln  
 325 330 335  
 Ala His Thr Glu Val Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys  
 340 345 350  
 Ser Val Gly Leu Gly Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu  
 355 360 365  
 Glu Val Ser Val Arg Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr  
 370 375 380



Ser Ala  
385

<210> 497  
<211> 1281  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1258)  
<223> FRXA00038

<400> 497  
acgattgtgc tgtcgtttgc gttggtgaat agttctggac cgggtatttt gcggcgacaca 60  
  
tggaactcat tgaacgccgc gcccggctaa ggtgggaggc atg agt ttt gct gaa 115  
Met Ser Phe Ala Glu  
1 5  
  
cat gcg atc atc tgg cac gtc tac ccc ctg ggc gct ttg ggt gct ccc 163  
His Ala Ile Ile Trp His Val Tyr Pro Leu Gly Ala Leu Gly Ala Pro  
10 15 20  
  
atc cgg cct gaa gcc ccc gca cct gtc aca cat cgg ctc ccc aat cta 211  
Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His Arg Leu Pro Asn Leu  
25 30 35  
  
att ggg tgg ctg gat tat gtt gtc gaa cta ggc tgc aac gcc ctc atg 259  
Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly Cys Asn Ala Leu Met  
40 45 50  
  
ctg gga ccg gta ttc gag tcc gtc agc cac ggc tac gac acc ctc gat 307  
Leu Gly Pro Val Phe Glu Ser Val Ser His Gly Tyr Asp Thr Leu Asp  
55 60 65  
  
ttc tac cgc atc gac ccg cgc ctc ggc acc gag gaa gac atg gac gcg 355  
Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu Glu Asp Met Asp Ala  
70 75 80 85  
  
ctg ctg gag gct gcg aat cag cgg ggc att gga gtg ctt ttc gac ggc 403  
Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly Val Leu Phe Asp Gly  
90 95 100  
  
gtc ttc aat cat gtt tcc agt tcc tct aaa tat ctc gac ctg acc acc 451  
Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr Leu Asp Leu Thr Thr  
105 110 115  
  
ggg gcg tca ttt gaa ggc cac gac atc ctg gcg gaa ctc gac cac acg 499  
Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala Glu Leu Asp His Thr  
120 125 130  
  
aat ccc gcc gta gtg gat ctg gtt gtc gat gtc atg aac cac tgg ctc 547  
Asn Pro Ala Val Val Asp Leu Val Val Asp Val Met Asn His Trp Leu  
135 140 145  
  
gac cgc gga atc gca ggc tgg cga ctc gac gct gtc tac gcc atc gcc 595  
Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala Val Tyr Ala Ile Ala  
150 155 160 165

cct gaa ttt tgg gaa aaa gtc ctg cca gaa gtg cga cga aaa cac cca 643  
 Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val Arg Arg Lys His Pro  
 170 175 180

cac gca tgg atc gtg ggg gag atg atc cat gga gat tac tcc gac tac 691  
 His Ala Trp Ile Val Gly Glu Met Ile His Gly Asp Tyr Ser Asp Tyr  
 185 190 195

gtg aaa agc tcc ggc att gat tcc gtt acc gaa tac gaa ctg tgg aaa 739  
 Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu Tyr Glu Leu Trp Lys  
 200 205 210

gcc att tgg agc agc atc aaa gag cgc aat ttc ttt gaa ctc gaa tgg 787  
 Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe Phe Glu Leu Glu Trp  
 215 220 225

act ttg agt cgc cac aat gaa ttc ctc gat act ttc gta ccg cag aca 835  
 Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr Phe Val Pro Gln Thr  
 230 235 240 245

ttc att ggt aac cat gac gtc acc cgc att gcc acc cga atc ggt caa 883  
 Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala Thr Arg Ile Gly Gln  
 250 255 260

tca aat gcg atc ctg gcc gca gcg atc ctc ttc acg gtc gga gga acc 931  
 Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe Thr Val Gly Gly Thr  
 265 270 275

cca agc att tac tac ggc gat gag cag ggc ttt acg gga ttg aaa gag 979  
 Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe Thr Gly Leu Lys Glu  
 280 285 290

gat aac gtt ttc ggt gac gat gcc att agg cca cct ctt cct gcc gag 1027  
 Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro Pro Leu Pro Ala Glu  
 295 300 305

ttt tct cca ctg ggc acc tgg att gaa aac att tat aag gct ctg atc 1075  
 Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile Tyr Lys Ala Leu Ile  
 310 315 320 325

gcg ctg cgc agg caa cac ccg tgg ttg tat cag gcg cac acc gaa gtc 1123  
 Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln Ala His Thr Glu Val  
 330 335 340

ctt gag att gct aat gaa gcg atg acc tat aag tcc gtc ggt ctt gga 1171  
 Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys Ser Val Gly Leu Gly  
 345 350 355

ggt gaa gag ctg aca gtg cat ctt gat ttg gaa gag gtg tct gtt cgg 1219  
 Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu Glu Val Ser Val Arg  
 360 365 370

atc ctt gat ggc gag aag gtg ctg ttt cag tac agc gct tagttgtcgg 1268  
 Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr Ser Ala  
 375 380 385

ttcaagggtgta ggg 1281

&lt;210&gt; 498

&lt;211&gt; 386

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 498

```

Met Ser Phe Ala Glu His Ala Ile Ile Trp His Val Tyr Pro Leu Gly
 1           5           10           15

Ala Leu Gly Ala Pro Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His
      20           25           30

Arg Leu Pro Asn Leu Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly
      35           40           45

Cys Asn Ala Leu Met Leu Gly Pro Val Phe Glu Ser Val Ser His Gly
      50           55           60

Tyr Asp Thr Leu Asp Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu
      65           70           75           80

Glu Asp Met Asp Ala Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly
      85           90           95

Val Leu Phe Asp Gly Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr
      100          105          110

Leu Asp Leu Thr Thr Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala
      115          120          125

Glu Leu Asp His Thr Asn Pro Ala Val Val Asp Leu Val Val Asp Val
      130          135          140

Met Asn His Trp Leu Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala
      145          150          155          160

Val Tyr Ala Ile Ala Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val
      165          170          175

Arg Arg Lys His Pro His Ala Trp Ile Val Gly Glu Met Ile His Gly
      180          185          190

Asp Tyr Ser Asp Tyr Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu
      195          200          205

Tyr Glu Leu Trp Lys Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe
      210          215          220

Phe Glu Leu Glu Trp Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr
      225          230          235          240

Phe Val Pro Gln Thr Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala
      245          250          255

Thr Arg Ile Gly Gln Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe
      260          265          270

Thr Val Gly Gly Thr Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe
      275          280          285

Thr Gly Leu Lys Glu Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro
      290          295          300

```

Pro Leu Pro Ala Glu Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile  
 305 310 315 320

Tyr Lys Ala Leu Ile Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln  
 325 330 335

Ala His Thr Glu Val Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys  
 340 345 350

Ser Val Gly Leu Gly Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu  
 355 360 365

Glu Val Ser Val Arg Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr  
 370 375 380

Ser Ala  
 385

<210> 499  
 <211> 517  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(517)  
 <223> RXC00233

<400> 499  
 cgcctccagc agttgaggga gaagttccaa cacttgacc, aactgaggaa gcaactgtgc 60

aatagcgctt tagacacaga ctcattgacag aatagaagac atg agt gtg aat gaa 115  
 Met Ser Val Asn Glu  
 1 5

gca gat ctg aac gct gtc gaa gag caa ttg gga agg gcc cca cga ggt 163  
 Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly Arg Ala Pro Arg Gly  
 10 15 20

gtc ctc gat att tct tac cgc agc cct gat gga gta ccc ggt gtg gtg 211  
 Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly Val Pro Gly Val Val  
 25 30 35

atg acc gca cca aaa ctg gat gac gga acc cca ttc cca acc ctg tac 259  
 Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro Phe Pro Thr Leu Tyr  
 40 45 50

tac ttg aca gat cca cgc ctg acc acc gag gca tcc cgc ctc gag gtc 307  
 Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala Ser Arg Leu Glu Val  
 55 60 65

gca ttg gta atg aag tgg atg act gat cgc ctt tcc acc gac gaa gag 355  
 Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu Ser Thr Asp Glu Glu  
 70 75 80 85

ctt cgt gcc gac tac cag cgc gcc cac gag cac ttc ctg gca aag cgc 403  
 Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His Phe Leu Ala Lys Arg  
 90 95 100

aac gca att gaa gat ctc ggc acg gat ttt tcc ggc ggt ggc atg cct 451

Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser Gly Gly Gly Met Pro  
 105 110 115  
 gac cga gtg aag tgc ctt cac gtc ctc att gac tat gca ctg gca gaa 499  
 Asp Arg Val Lys Cys Leu His Val Leu Ile Asp Tyr Ala Leu Ala Glu  
 120 125 130  
 ggc cca cac cat ttc ctt 517  
 Gly Pro His His Phe Leu  
 135

<210> 500  
 <211> 139  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 500  
 Met Ser Val Asn Glu Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly  
 1 5 10 15  
 Arg Ala Pro Arg Gly Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly  
 20 25 30  
 Val Pro Gly Val Val Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro  
 35 40 45  
 Phe Pro Thr Leu Tyr Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala  
 50 55 60  
 Ser Arg Leu Glu Val Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu  
 65 70 75 80  
 Ser Thr Asp Glu Glu Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His  
 85 90 95  
 Phe Leu Ala Lys Arg Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser  
 100 105 110  
 Gly Gly Gly Met Pro Asp Arg Val Lys Cys Leu His Val Leu Ile Asp  
 115 120 125  
 Tyr Ala Leu Ala Glu Gly Pro His His Phe Leu  
 130 135

<210> 501  
 <211> 849  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(826)  
 <223> RXC00236

<400> 501  
 aatgcgagag ttctaaaacg agccggtaac atcgaccccc atgagttcag gggtagaaa 60  
 agcaatggga tttggatgcg gttcgggtttt ggccgtcatc atg gtg atc tca ttt 115  
 Met Val Ile Ser Phe

														1	5	
gtt gga tgg gcg ctc agc ttc atg gat gga acg gca cct att cgc caa	163															
Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr Ala Pro Ile Arg Gln																
	10 15 20															
ctc cag caa atc cct gaa gat gtt ccg ccg gcg cgt ggt gta gaa gtt	211															
Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala Arg Gly Val Glu Val																
	25 30 35															
ccg caa att gat aca gag gca gat gga cgc aca tcc aac cat ttg cgt	259															
Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr Ser Asn His Leu Arg																
	40 45 50															
ttt tgg gcg gaa cca att gct caa gat act ggt gtg tcc gct caa gcg	307															
Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly Val Ser Ala Gln Ala																
	55 60 65															
att gcg gct tat gga aac gca gag ctc atc gcg agt act gcg tgg cct	355															
Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala Ser Thr Ala Trp Pro																
	70 75 80 85															
ggc tgc aat ctg ggg tgg aat acc ttg gca ggt atc ggc cag gtg gaa	403															
Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly Ile Gly Gln Val Glu																
	90 95 100															
acc cgt cac ggt acc tac aac ggc aaa atg ttc ggg ggc agt tcc ctg	451															
Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe Gly Gly Ser Ser Leu																
	105 110 115															
gat gaa aat gga gtt gca acc cct cca atc atc ggc gtt cca ctt gat	499															
Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile Gly Val Pro Leu Asp																
	120 125 130															
ggt tca ccg ggg ttt gcg gaa att ccc gac act gat ggt ggg gaa tta	547															
Gly Ser Pro Gly Phe Ala Ile Pro Asp Thr Asp Gly Gly Glu Leu																
	135 140 145															
gat ggc gat act gaa tat gat cgc gcg gta ggt ccc atg cag ttc att	595															
Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly Pro Met Gln Phe Ile																
	150 155 160 165															
ccg gaa acg tgg cga ctt atg gga ttg gat gca aac ggt gat ggg gta	643															
Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala Asn Gly Asp Gly Val																
	170 175 180															
gcg gac ccc aac caa att gat gac gca gca ttg agt gcc gca aac ctg	691															
Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu Ser Ala Ala Asn Leu																
	185 190 195															
ttg tgt tcc aac gat cgt gac ttg tcc act cct gaa gga tgg acc gca	739															
Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro Glu Gly Trp Thr Ala																
	200 205 210															
gct gtt cat tct tac aac atg tct aat cag tat ttg atg gac gtt cga	787															
Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr Leu Met Asp Val Arg																
	215 220 225															
gat gct gcc gcg tcc tac gct tta cga cag ccg gcg atc taaaacttaa	836															
Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro Ala Ile																
	230 235 240															

caagcgcaac ccc

849

&lt;210&gt; 502

&lt;211&gt; 242

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 502

Met Val Ile Ser Phe Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr  
 1 5 10 15

Ala Pro Ile Arg Gln Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala  
 20 25 30

Arg Gly Val Glu Val Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr  
 35 40 45

Ser Asn His Leu Arg Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly  
 50 55 60

Val Ser Ala Gln Ala Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala  
 65 70 75 80

Ser Thr Ala Trp Pro Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly  
 85 90 95

Ile Gly Gln Val Glu Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe  
 100 105 110

Gly Gly Ser Ser Leu Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile  
 115 120 125

Gly Val Pro Leu Asp Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr  
 130 135 140

Asp Gly Gly Glu Leu Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly  
 145 150 155 160

Pro Met Gln Phe Ile Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala  
 165 170 175

Asn Gly Asp Gly Val Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu  
 180 185 190

Ser Ala Ala Asn Leu Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro  
 195 200 205

Glu Gly Trp Thr Ala Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr  
 210 215 220

Leu Met Asp Val Arg Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro  
 225 230 235 240

Ala Ile

&lt;210&gt; 503

&lt;211&gt; 1113

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1090)

&lt;223&gt; RXC00271

&lt;400&gt; 503

```

tagttttaa at catgagacat ttcacatatg gttctttatc cgagacatgt gttgacgctg 60

tctgccccctt tttgaaaata acactttaag gagatgtgcc atg ttt tct tcc cgt 115
                                     Met Phe Ser Ser Arg
                                     1 5

tcg aag gta ctc gca agc atc ttt act gtt ggc gcc ttg gcg ttg gct 163
Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly Ala Leu Ala Leu Ala
          10                      15                      20

tcg tgc tca agc gat tcc agt gac agc tcc acc tcc act gat gct gca 211
Ser Cys Ser Ser Ser Asp Ser Ser Asp Ser Ser Thr Ser Thr Asp Ala Ala
          25                      30                      35

ggg ggc gac tct tac cga gtt ggc atc aac cag ctt gtt cag cac cct 259
Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln Leu Val Gln His Pro
          40                      45                      50

gca ctt gat gca gcg acc act ggt ttc aag gaa gct ttt gaa gag gca 307
Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu Ala Phe Glu Glu Ala
          55                      60                      65

ggc gtt gac gtc acc ttt gat gag caa aac gct aac ggc gag cag ggc 355
Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala Asn Gly Glu Gln Gly
          70                      75                      80                      85

act gca ctg act att tct cag cag ttc gct tct gac aat ttg gat ctc 403
Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser Asp Asn Leu Asp Leu
          90                      95                      100

gtg ttg gct gtt gca act cca gca gca cag gca act gcg cag aat atc 451
Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala Thr Ala Gln Asn Ile
          105                      110                      115

act gat atc cca gtc ctg ttc acc gca gtt acc gat gca gtg tcg gca 499
Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr Asp Ala Val Ser Ala
          120                      125                      130

gag ctg gtg gat tct aat gaa gca cct ggc gga aac gtc acc ggt act 547
Glu Leu Val Asp Ser Asn Glu Ala Pro Gly Gly Asn Val Thr Gly Thr
          135                      140                      145

tct gat atc gca ccg att gag cag cag ttg gag ctt ttg cag cag ctg 595
Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu Leu Leu Gln Gln Leu
          150                      155                      160                      165

gtt cct gac gca aag tcc atc ggc atc gtc tac gcg tct ggt gag gtc 643
Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr Ala Ser Gly Glu Val
          170                      175                      180

aac tct cag gtg cag gtc gat gag gtc acc aag gct gct gag cca ctg 691
Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys Ala Ala Glu Pro Leu

```



185	190	195	
ggg ctg tcc gtt aat act cag act gtc act acc gtg aac gag att cag			739
Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr Val Asn Glu Ile Gln			
200	205	210	
cag gct gtt gaa gct ctc ggc gat gtt gat gtc atc tac gtt cca act			787
Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val Ile Tyr Val Pro Thr			
215	220	225	
gac aac atg gtt gtt tcc ggt att tct tct ctg gtt cag gtt gct gag			835
Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu Val Gln Val Ala Glu			
230	235	240	245
cag aag cag atc cct gtg atc ggc gct gag tcc ggc act gtt gag ggt			883
Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser Gly Thr Val Glu Gly			
250	255	260	
ggc gca ctg gca acc ctg ggt atc gat tac acc gag ctt ggc cgc cag			931
Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr Glu Leu Gly Arg Gln			
265	270	275	
act ggt gag atg gct ctg cgt att ctg cag gac ggc gaa gac cca gca			979
Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp Gly Glu Asp Pro Ala			
280	285	290	
acc atg cct gtg gag act gca act gag ttc acc tac gtg atc aac gaa			1027
Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr Tyr Val Ile Asn Glu			
295	300	305	
gat gca gca gag cgc cag ggc gtg gag atc cct caa gag att ttg gat			1075
Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro Gln Glu Ile Leu Asp			
310	315	320	325
aag gcc gaa cgc gta tgatcggcgc ttttgagttc gga			1113
Lys Ala Glu Arg Val			
330			

&lt;210&gt; 504

&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 504

Met Phe Ser Ser Arg Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly			
1	5	10	15
Ala Leu Ala Leu Ala Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr			
20	25	30	
Ser Thr Asp Ala Ala Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln			
35	40	45	
Leu Val Gln His Pro Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu			
50	55	60	
Ala Phe Glu Glu Ala Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala			
65	70	75	80
Asn Gly Glu Gln Gly Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser			

85										90					95				
Asp	Asn	Leu	Asp	Leu	Val	Leu	Ala	Val	Ala	Thr	Pro	Ala	Ala	Gln	Ala				
			100						105					110					
Thr	Ala	Gln	Asn	Ile	Thr	Asp	Ile	Pro	Val	Leu	Phe	Thr	Ala	Val	Thr				
		115					120					125							
Asp	Ala	Val	Ser	Ala	Glu	Leu	Val	Asp	Ser	Asn	Glu	Ala	Pro	Gly	Gly				
		130				135					140								
Asn	Val	Thr	Gly	Thr	Ser	Asp	Ile	Ala	Pro	Ile	Glu	Gln	Gln	Leu	Glu				
145					150					155					160				
Leu	Leu	Gln	Gln	Leu	Val	Pro	Asp	Ala	Lys	Ser	Ile	Gly	Ile	Val	Tyr				
				165					170						175				
Ala	Ser	Gly	Glu	Val	Asn	Ser	Gln	Val	Gln	Val	Asp	Glu	Val	Thr	Lys				
			180					185						190					
Ala	Ala	Glu	Pro	Leu	Gly	Leu	Ser	Val	Asn	Thr	Gln	Thr	Val	Thr	Thr				
		195					200						205						
Val	Asn	Glu	Ile	Gln	Gln	Ala	Val	Glu	Ala	Leu	Gly	Asp	Val	Asp	Val				
		210				215						220							
Ile	Tyr	Val	Pro	Thr	Asp	Asn	Met	Val	Val	Ser	Gly	Ile	Ser	Ser	Leu				
225					230					235					240				
Val	Gln	Val	Ala	Glu	Gln	Lys	Gln	Ile	Pro	Val	Ile	Gly	Ala	Glu	Ser				
				245					250						255				
Gly	Thr	Val	Glu	Gly	Gly	Ala	Leu	Ala	Thr	Leu	Gly	Ile	Asp	Tyr	Thr				
		260						265						270					
Glu	Leu	Gly	Arg	Gln	Thr	Gly	Glu	Met	Ala	Leu	Arg	Ile	Leu	Gln	Asp				
		275						280					285						
Gly	Glu	Asp	Pro	Ala	Thr	Met	Pro	Val	Glu	Thr	Ala	Thr	Glu	Phe	Thr				
		290				295					300								
Tyr	Val	Ile	Asn	Glu	Asp	Ala	Ala	Glu	Arg	Gln	Gly	Val	Glu	Ile	Pro				
305					310					315					320				
Gln	Glu	Ile	Leu	Asp	Lys	Ala	Glu	Arg	Val										
				325					330										

&lt;210&gt; 505

&lt;211&gt; 1263

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1240)

&lt;223&gt; RXC00338

&lt;400&gt; 505

tcttagaagg cgtagtcaca ccattaacct tgccagaatt tttcaaggct tggctagact 60

tgggaaacga	acatg	cggtta	ccaaccaggg	gag	tta	atgc	gtg	agt	gat	gta	acc	115
							Val	Ser	Asp	Val	Thr	5
							1					
ggt	ggc	gat	att	cgc	cgc	att	ttg	gat	gag	gct	tat	163
Val	Gly	Asp	Ile	Arg	Arg	Ile	Leu	Asp	Glu	Ala	Tyr	20
			10						15			
gcg	gaa	agc	tgg	gac	aaa	gtg	ggg	ctg	atc	tgc	ggg	211
Ala	Glu	Ser	Trp	Asp	Lys	Val	Gly	Leu	Ile	Cys	Gly	35
			25					30				
tcg	gtg	aag	cgt	gtc	ggg	tta	gca	ctc	gat	tgc	acc	259
Ser	Val	Lys	Arg	Val	Gly	Leu	Ala	Leu	Asp	Cys	Thr	50
		40					45					
gac	aag	gct	gtg	gac	atg	ggg	ttg	gac	atg	ctg	atc	307
Asp	Lys	Ala	Val	Asp	Met	Gly	Leu	Asp	Met	Leu	Ile	65
	55					60						
ttg	ctg	ctg	cgt	ggg	gtg	acg	tct	gtt	gct	gcg	gat	355
Leu	Leu	Leu	Arg	Gly	Val	Thr	Ser	Val	Ala	Ala	Asp	85
	70					75				80		
aag	gtc	att	cac	acc	cta	att	cgc	ggc	ggg	gtg	gca	403
Lys	Val	Ile	His	Thr	Leu	Ile	Arg	Gly	Gly	Val	Ala	100
			90						95			
cac	act	aat	gcg	gat	tcc	gcg	cgc	cca	ggg	gtc	aac	451
His	Thr	Asn	Ala	Asp	Ser	Ala	Arg	Pro	Gly	Val	Asn	115
			105					110				
gag	ctc	gtc	ggc	atc	acg	gcc	ggg	cga	ccc	atc	gcg	499
Glu	Leu	Val	Gly	Ile	Thr	Ala	Gly	Arg	Pro	Ile	Ala	130
		120					125					
ggc	ggc	atg	gac	aaa	tgg	ggc	gtg	cac	gtt	ctg	ccc	547
Gly	Gly	Met	Asp	Lys	Trp	Gly	Val	His	Val	Leu	Pro	145
	135					140						
tac	cta	aag	aag	atg	ctt	ttc	gac	gca	ggg	gac	ggg	595
Tyr	Leu	Lys	Lys	Met	Leu	Phe	Asp	Ala	Gly	Ala	Gly	165
	150				155					160		
tac	cga	gag	tgt	gcc	ttt	gag	atc	gaa	gga	acc	ggg	643
Tyr	Arg	Glu	Cys	Ala	Phe	Glu	Ile	Glu	Gly	Thr	Gly	180
			170						175			
gtg	gag	ggg	gcg	aat	ccg	gca	gag	ggg	gac	gtc	gat	691
Val	Glu	Gly	Ala	Asn	Pro	Ala	Glu	Gly	Asp	Val	Asp	195
		185						190				
tcc	ctt	gag	ctg	cgc	atc	gag	ttt	gtt	gca	ccg	cgc	739
Ser	Leu	Glu	Leu	Arg	Ile	Glu	Phe	Val	Ala	Pro	Arg	210
		200					205					
cgg	ctc	acg	tcg	gtg	ctg	cgg	gag	gct	cat	ccg	tat	787
Arg	Leu	Thr	Ser	Val	Leu	Arg	Glu	Ala	His	Pro	Tyr	225
	215					220						
ttc	gat	att	gtt	gaa	atg	cac	agc	gct	gag	agt	tta	835

Phe Asp Ile Val Glu Met His Ser Ala Glu Ser Leu Glu Asn Ala Thr  
 230 235 240 245  
 gga ttg ggt cgt gtg ggt gaa ttg ccg gag ccg atg cgc ctc gcg gat 883  
 Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro Met Arg Leu Ala Asp  
 250 255 260  
 ttc gtg caa caa gtg gcc aac aac ctg cct gtc acc gaa tgg ggc gtg 931  
 Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val Thr Glu Trp Gly Val  
 265 270 275  
 cgc gct acc ggc gat cct gaa caa atg gtg tcc cgt gtg gcg gtt tca 979  
 Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser Arg Val Ala Val Ser  
 280 285 290  
 tca ggg tcg ggt gac agt ttc tta aac gat gtg att aag ctc gga gtg 1027  
 Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val Ile Lys Leu Gly Val  
 295 300 305  
 gac gtt tat gtc act tct gat ctg cgc cac cat cca gtt gat gaa tat 1075  
 Asp Val Tyr Val Thr Ser Asp Leu Arg His His Pro Val Asp Glu Tyr  
 310 315 320 325  
 ctc cga gaa ggt ggc cct gca gta atc gat act gca cac tgg gcc agc 1123  
 Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr Ala His Trp Ala Ser  
 330 335 340  
 gaa ttt cca tgg act tcc caa gcc caa gaa att ttg cag gac aaa gcc 1171  
 Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile Leu Gln Asp Lys Ala  
 345 350 355  
 cca cag gtt gaa gtt gat gtg att tcg atc cgc aca gac ccc tgg acc 1219  
 Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg Thr Asp Pro Trp Thr  
 360 365 370  
 atg tct gcg cga gca gtg aac taaattcttg agaactaaaa aag 1263  
 Met Ser Ala Arg Ala Val Asn  
 375 380

&lt;210&gt; 506

&lt;211&gt; 380

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 506

Val Ser Asp Val Thr Val Gly Asp Ile Arg Arg Ile Leu Asp Glu Ala  
 1 5 10 15

Tyr Pro Pro Ala Leu Ala Glu Ser Trp Asp Lys Val Gly Leu Ile Cys  
 20 25 30

Gly Asp Pro Thr Glu Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys  
 35 40 45

Thr Gln Ala Val Ala Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu  
 50 55 60

Ile Ile His His Pro Leu Leu Arg Gly Val Thr Ser Val Ala Ala  
 65 70 75 80

Asp Glu Pro Lys Gly Lys Val Ile His Thr Leu Ile Arg Gly Gly Val  
                     85                    90                    95  
 Ala Leu Phe Ser Ala His Thr Asn Ala Asp Ser Ala Arg Pro Gly Val  
                     100                    105                    110  
 Asn Asp Lys Leu Ala Glu Leu Val Gly Ile Thr Ala Gly Arg Pro Ile  
                     115                    120                    125  
 Ala Thr Arg Leu Leu Gly Gly Met Asp Lys Trp Gly Val His Val Leu  
                     130                    135                    140  
 Pro Lys Asp Ala Ala Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Ala  
                     145                    150                    155                    160  
 Gly Ala Ile Gly Asp Tyr Arg Glu Cys Ala Phe Glu Ile Glu Gly Thr  
                     165                    170                    175  
 Gly Gln Phe Arg Pro Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val  
                     180                    185                    190  
 Asp Lys Leu Phe Lys Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro  
                     195                    200                    205  
 Arg Asn Leu Arg Ala Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro  
                     210                    215                    220  
 Tyr Glu Glu Pro Ala Phe Asp Ile Val Glu Met His Ser Ala Glu Ser  
                     225                    230                    235                    240  
 Leu Glu Asn Ala Thr Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro  
                     245                    250                    255  
 Met Arg Leu Ala Asp Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val  
                     260                    265                    270  
 Thr Glu Trp Gly Val Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser  
                     275                    280                    285  
 Arg Val Ala Val Ser Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val  
                     290                    295                    300  
 Ile Lys Leu Gly Val Asp Val Tyr Val Thr Ser Asp Leu Arg His His  
                     305                    310                    315                    320  
 Pro Val Asp Glu Tyr Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr  
                     325                    330                    335  
 Ala His Trp Ala Ser Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile  
                     340                    345                    350  
 Leu Gln Asp Lys Ala Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg  
                     355                    360                    365  
 Thr Asp Pro Trp Thr Met Ser Ala Arg Ala Val Asn  
                     370                    375                    380

&lt;210&gt; 507

&lt;211&gt; 1470

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1447)

&lt;223&gt; RXC00362

&lt;400&gt; 507

cacttttttggtgtgaaaatttcacggaagttaatgccgcttt aagtcaattc aatcacatgt 60

aacatgctac ggtttttttcgtgcacttaaa ggaggcgctt atg gga atc att gct 115  
 Met Gly Ile Ile Ala  
 1 5

ctg ctc gtt ttt atc gca att gcc gtg ata ttg aat gtg ttt ttg aaa 163  
 Leu Leu Val Phe Ile Ala Ile Ala Val Ile Leu Asn Val Phe Leu Lys  
 10 15 20

cga gat att tca gaa gca ttg cta gtt gga tta gta gga act gcg ctt 211  
 Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu Val Gly Thr Ala Leu  
 25 30 35

gtc ggc ggt gta aat gca ccg aca tta ctg att gat gct gta gtg gat 259  
 Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile Asp Ala Val Val Asp  
 40 45 50

gct gct cag tcg gaa gtt act ttc gca ggt atg gcc ttt gtt ttc atg 307  
 Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met Ala Phe Val Phe Met  
 55 60 65

ggc atc gtt gtg caa tca act gga ttg att gat cga tta atc gca atc 355  
 Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp Arg Leu Ile Ala Ile  
 70 75 80 85

ctt aac tcg att ttt ggt cgg ctt cga ggt ggc gca ggt tat gtt tcc 403  
 Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly Ala Gly Tyr Val Ser  
 90 95 100

act ctt gga tct gcg ctc att gga ctc atc gct gga tca acg gct gga 451  
 Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala Gly Ser Thr Ala Gly  
 105 110 115

aac tcc gcg acg gtt ggc tca gtg acg atc cct tgg atg aaa aag acg 499  
 Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro Trp Met Lys Lys Thr  
 120 125 130

gga tgg act gct gaa agg tcc gca acg tta gtc gcg ggc aac tct ggc 547  
 Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val Ala Gly Asn Ser Gly  
 135 140 145

ctt ggt gtt gcg ttg cct ccc aat tca aca atg ttc atc att ttg gca 595  
 Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met Phe Ile Ile Leu Ala  
 150 155 160 165

ttg cca gct gca gca gct tct tcg gcc tct cag gtg tac att gct ttg 643  
 Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln Val Tyr Ile Ala Leu  
 170 175 180

gct tgt ggt ggt gcg tat gca gtg ctc tac cgc tta gcg gtc gtc ttt 691  
 Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg Leu Ala Val Val Phe  
 185 190 195

tac tgg aca cgt aaa gat aaa att cct gcc acc cct gat gat caa cgg	739
Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr Pro Asp Asp Gln Arg	
200 205 210	
gtg tca ttc ggt gag gca atg aag act gga tgg cgt tca ccg ttg atc	787
Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp Arg Ser Pro Leu Ile	
215 220 225	
ttc ctt gga att ttg atc ccc gta atc ctc aca atc ggc cca ttg tct	835
Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr Ile Gly Pro Leu Ser	
230 235 240 245	
gaa tgg tta aag aca cat gga gtt ggg gag tct ggt gtt aaa tcg atg	883
Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser Gly Val Lys Ser Met	
250 255 260	
tcg atc atc gtg tgg gtg cca att ctg att acg gca att gct ctg att	931
Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr Ala Ile Ala Leu Ile	
265 270 275	
gaa ggg cgt aaa cga att gct aac aac atg gca cac ttt agg gtt cag	979
Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala His Phe Arg Val Gln	
280 285 290	
atc tcc aag gac ttg cca caa ttt gcc acc gta gga att tcg ttg ttt	1027
Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val Gly Ile Ser Leu Phe	
295 300 305	
tct gcg ctt gca gca gcg aac atc atg gaa gaa ctg ggt gtt ggc ccg	1075
Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu Leu Gly Val Gly Pro	
310 315 320 325	
cag ttg tct aac tgg ctt gat tcc atg gac cta cct aag tct gtc atg	1123
Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu Pro Lys Ser Val Met	
330 335 340	
gtg atc att gtc tgc atc atg tgc att gtg gtg gca acg cca ctg tcg	1171
Val Ile Ile Val Cys Ile Met Cys Ile Val Val Ala Thr Pro Leu Ser	
345 350 355	
tca aca gca acc gcg gct gcg att ggt gct ccc gct gtc gct gcg ttg	1219
Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro Ala Val Ala Ala Leu	
360 365 370	
gct gcg gta ggt att gat cca act gtg gcg atc gta gtg atc ttg ctg	1267
Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile Val Val Ile Leu Leu	
375 380 385	
tgc act tcc act gaa ggt gca tcc ccg ccg gtg ggc gcg ccg att tac	1315
Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val Gly Ala Pro Ile Tyr	
390 395 400 405	
ctt tct gct gcg atc gcc gat gca aac cca acg aaa atg ttc gta cca	1363
Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr Lys Met Phe Val Pro	
410 415 420	
ctg att acg tac ttt gtt gtc ccc atg att ctg ctt gct tgg cta gtt	1411
Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu Leu Ala Trp Leu Val	
425 430 435	

gga atg gga ttc tta cca gtg att gtt cct acg ggt taaaggggta 1457  
 Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr Gly  
           440                                  445

aaaatgaact caa 1470

<210> 508

<211> 449

<212> PRT

<213> Corynebacterium glutamicum

<400> 508

Met Gly Ile Ile Ala Leu Leu Val Phe Ile Ala Ile Ala Val Ile Leu  
   1                  5                  10                  15

Asn Val Phe Leu Lys Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu  
           20                  25                  30

Val Gly Thr Ala Leu Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile  
           35                  40                  45

Asp Ala Val Val Asp Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met  
           50                  55                  60

Ala Phe Val Phe Met Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp  
           65                  70                  75                  80

Arg Leu Ile Ala Ile Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly  
                   85                  90                  95

Ala Gly Tyr Val Ser Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala  
           100                  105                  110

Gly Ser Thr Ala Gly Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro  
           115                  120                  125

Trp Met Lys Lys Thr Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val  
           130                  135                  140

Ala Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met  
           145                  150                  155                  160

Phe Ile Ile Leu Ala Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln  
                   165                  170                  175

Val Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg  
           180                  185                  190

Leu Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr  
           195                  200                  205

Pro Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp  
           210                  215                  220

Arg Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr  
           225                  230                  235                  240

Ile Gly Pro Leu Ser Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser  
                   245                  250                  255



Gly Val Lys Ser Met Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr  
 260 265 270  
 Ala Ile Ala Leu Ile Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala  
 275 280 285  
 His Phe Arg Val Gln Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val  
 290 295 300  
 Gly Ile Ser Leu Phe Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu  
 305 310 315 320  
 Leu Gly Val Gly Pro Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu  
 325 330 335  
 Pro Lys Ser Val Met Val Ile Ile Val Cys Ile Met Cys Ile Val Val  
 340 345 350  
 Ala Thr Pro Leu Ser Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro  
 355 360 365  
 Ala Val Ala Ala Leu Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile  
 370 375 380  
 Val Val Ile Leu Leu Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val  
 385 390 395 400  
 Gly Ala Pro Ile Tyr Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr  
 405 410 415  
 Lys Met Phe Val Pro Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu  
 420 425 430  
 Leu Ala Trp Leu Val Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr  
 435 440 445

Gly

<210> 509  
 <211> 1203  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1180)  
 <223> RXC00412

<400> 509  
 cttttgacga acaccacgtc gcgtacgctt cctcggggcg ttaaactatt tgtcttccag 60  
 cttttgtccc ccgacttttg tacgaatcga ggacaccgtc gtg tca cac acc gcg 115  
 Val Ser His Thr Ala  
 1 5  
 tcc aca ccg acg cca gag gaa tac tcc gcg cag caa ccc agc acc cag 163  
 Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln Gln Pro Ser Thr Gln  
 10 15 20

ggc act cgc gtt gag ttc cgc ggc ata acc aaa gtc ttt agc aac aat	211
Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys Val Phe Ser Asn Asn	
25 30 35	
aaa tct gct aaa acc acc gcg ctt gat aat gtc act ctc acc gta gaa	259
Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val Thr Leu Thr Val Glu	
40 45 50	
ccc ggt gag gta atc ggc atc atc ggt tac tct ggc gcc ggc aag tcc	307
Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser Gly Ala Gly Lys Ser	
55 60 65	
act ctt gtc cgc ctc atc aat ggc ctt gac tcc ccc acg agc ggt tcg	355
Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser Pro Thr Ser Gly Ser	
70 75 80 85	
ttg ctg ctc aac ggc acc gac atc gtc gga atg ccc gag tct aag ctg	403
Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met Pro Glu Ser Lys Leu	
90 95 100	
cgt aaa ctg cgc agt aat atc ggc atg att ttc cag cag ttc aac ctg	451
Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe Gln Gln Phe Asn Leu	
105 110 115	
ttc cag tcg cgt act gcg gct gga aat gtg gag tac ccg ctg gaa gtt	499
Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu Tyr Pro Leu Glu Val	
120 125 130	
gcc aag atg gac aag gca gct cgt aaa gct cgc gtg caa gaa atg ctc	547
Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg Val Gln Glu Met Leu	
135 140 145	
gag ttc gtc ggc ctg ggc gac aaa ggc aaa aac tac ccc gag cag ctg	595
Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn Tyr Pro Glu Gln Leu	
150 155 160 165	
tcg ggc ggc cag aag cag cgc gtc ggc att gcc cgt gca ctg gcc acc	643
Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg Ala Leu Ala Thr	
170 175 180	
aat cca acg ctt ttg ctt gcc gac gaa gcc acc tcc gct ttg gac cca	691
Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr Ser Ala Leu Asp Pro	
185 190 195	
gaa acc acc cat gaa gtt ctg gag ctg ctg cgc aag gta aac cgc gaa	739
Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg Lys Val Asn Arg Glu	
200 205 210	
ctg ggc atc acc atc gtt gtg atc acc cac gaa atg gaa gtt gtg cgt	787
Leu Gly Ile Thr Ile Val Val Ile Thr His Glu Met Glu Val Val Arg	
215 220 225	
tcc atc gca gac aag gtt gct gtg atg gaa tcc ggc aaa gtt gtg gaa	835
Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser Gly Lys Val Val Glu	
230 235 240 245	
tac ggc agc gtc tac gag gtg ttc tcc aat cca caa aca cag gtt gct	883
Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro Gln Thr Gln Val Ala	
250 255 260	
caa aag ttc gtg gcc acc gcg ctg cgt aac acc cca gac caa gtg gaa	931

Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr Pro Asp Gln Val Glu  
 265 270 275

tcg gaa gat ctg ctt agc cat gag gga cgt ctg ttc acc att gat ctg 979  
 Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu Phe Thr Ile Asp Leu  
 280 285 290

act gaa acg tcc ggc ttc ttt gca gca acc gct cgt gct gcc gaa caa 1027  
 Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala Arg Ala Ala Glu Gln  
 295 300 305

ggt gct ttt gtc aac atc gtt cac ggt ggc gtg acc acc ttg caa cgc 1075  
 Gly Ala Phe Val Asn Ile Val His Gly Gly Val Thr Thr Leu Gln Arg  
 310 315 320 325

caa tca ttt ggc aaa atg act gtt cga ctc acc ggc aac acc gct gcg 1123  
 Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr Gly Asn Thr Ala Ala  
 330 335 340

att gaa gag ttc tat caa acc ttg acc aag acc acg acc atc aag gag 1171  
 Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr Thr Thr Ile Lys Glu  
 345 350 355

atc acc cga tgaacgagat gatcctcgca gct 1203  
 Ile Thr Arg  
 360

&lt;210&gt; 510

&lt;211&gt; 360

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 510

Val Ser His Thr Ala Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln  
 1 5 10 15

Gln Pro Ser Thr Gln Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys  
 20 25 30

Val Phe Ser Asn Asn Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val  
 35 40 45

Thr Leu Thr Val Glu Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser  
 50 55 60

Gly Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser  
 65 70 75 80

Pro Thr Ser Gly Ser Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met  
 85 90 95

Pro Glu Ser Lys Leu Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe  
 100 105 110

Gln Gln Phe Asn Leu Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu  
 115 120 125

Tyr Pro Leu Glu Val Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg  
 130 135 140

Val Gln Glu Met Leu Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn  
 145 150 155 160  
 Tyr Pro Glu Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala  
 165 170 175  
 Arg Ala Leu Ala Thr Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr  
 180 185 190  
 Ser Ala Leu Asp Pro Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg  
 195 200 205  
 Lys Val Asn Arg Glu Leu Gly Ile Thr Ile Val Val Ile Thr His Glu  
 210 215 220  
 Met Glu Val Val Arg Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser  
 225 230 235 240  
 Gly Lys Val Val Glu Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro  
 245 250 255  
 Gln Thr Gln Val Ala Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr  
 260 265 270  
 Pro Asp Gln Val Glu Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu  
 275 280 285  
 Phe Thr Ile Asp Leu Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala  
 290 295 300  
 Arg Ala Ala Glu Gln Gly Ala Phe Val Asn Ile Val His Gly Gly Val  
 305 310 315 320  
 Thr Thr Leu Gln Arg Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr  
 325 330 335  
 Gly Asn Thr Ala Ala Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr  
 340 345 350  
 Thr Thr Ile Lys Glu Ile Thr Arg  
 355 360

<210> 511  
 <211> 813  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(790)  
 <223> RXC00526

<400> 511  
 ggtggagcag gcggcggctc ctttagtcc tgcggccct tttgacctg cagccctgc 60  
 cgtttctgcc aagcaaaccg tgggccaggt gatttagcct atg agc ctc atc gaa 115  
 Met Ser Leu Ile Glu  
 1 5  
 atg cga aat att gtc aag acc tac aac att gga tct gaa ggt gaa ctc 163

Met	Arg	Asn	Ile	Val	Lys	Thr	Tyr	Asn	Ile	Gly	Ser	Glu	Gly	Glu	Leu	
				10					15					20		
acc	gtg	ttg	cac	ggt	gtg	gat	ttc	cat	gtg	gac	cgt	ggc	gaa	ttc	gtg	211
Thr	Val	Leu	His	Gly	Val	Asp	Phe	His	Val	Asp	Arg	Gly	Glu	Phe	Val	
			25					30					35			
tcg	gtt	gtg	ggt	acg	tcc	ggc	tca	ggt	aaa	tca	acg	atg	atg	aac	atc	259
Ser	Val	Val	Gly	Thr	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Met	Met	Asn	Ile	
		40					45					50				
att	ggg	ttg	ttg	gat	aag	cca	act	gat	ggc	acg	tac	acc	ttg	gat	ggc	307
Ile	Gly	Leu	Leu	Asp	Lys	Pro	Thr	Asp	Gly	Thr	Tyr	Thr	Leu	Asp	Gly	
	55					60					65					
gtg	gat	gtg	ttg	gat	atc	agc	gat	gat	gct	ttg	gcg	agc	cac	cgc	gct	355
Val	Asp	Val	Leu	Asp	Ile	Ser	Asp	Asp	Ala	Leu	Ala	Ser	His	Arg	Ala	
	70				75					80					85	
aaa	tcg	att	ggt	ttt	gtg	ttt	cag	aac	ttc	aat	ctg	att	ggc	cgg	atc	403
Lys	Ser	Ile	Gly	Phe	Val	Phe	Gln	Asn	Phe	Asn	Leu	Ile	Gly	Arg	Ile	
				90					95					100		
gat	gcg	ttg	aag	aat	gtg	gaa	atg	ccc	atg	atg	tat	gcg	ggc	att	ccg	451
Asp	Ala	Leu	Lys	Asn	Val	Glu	Met	Pro	Met	Met	Tyr	Ala	Gly	Ile	Pro	
			105					110					115			
gct	aag	cag	cgg	aga	agt	cgt	gcg	gtt	gaa	tta	ttg	gaa	atg	gtc	ggg	499
Ala	Lys	Gln	Arg	Arg	Ser	Arg	Ala	Val	Glu	Leu	Leu	Glu	Met	Val	Gly	
		120				125						130				
atg	ggt	gag	cgt	ctc	aac	cat	gag	ccc	aat	gag	ctt	tcg	ggt	ggt	cag	547
Met	Gly	Glu	Arg	Leu	Asn	His	Glu	Pro	Asn	Glu	Leu	Ser	Gly	Gly	Gln	
	135					140					145					
aag	cag	cgc	gtg	gcc	att	gct	cgc	gcg	ttg	gcg	aac	gat	cct	gag	atc	595
Lys	Gln	Arg	Val	Ala	Ile	Ala	Arg	Ala	Leu	Ala	Asn	Asp	Pro	Glu	Ile	
	150				155				160						165	
att	ctt	gct	gat	gaa	cca	act	ggt	gcg	ttg	gat	tct	gca	acg	ggc	cgg	643
Ile	Leu	Ala	Asp	Glu	Pro	Thr	Gly	Ala	Leu	Asp	Ser	Ala	Thr	Gly	Arg	
				170					175					180		
atg	gtg	atg	gat	att	ttc	cac	cag	ctc	aac	aag	gag	cag	ggc	aaa	acc	691
Met	Val	Met	Asp	Ile	Phe	His	Gln	Leu	Asn	Lys	Glu	Gln	Gly	Lys	Thr	
			185					190					195			
atc	gtg	ttt	att	act	cac	aac	cct	gag	ctt	gct	gat	gaa	tct	gat	cgg	739
Ile	Val	Phe	Ile	Thr	His	Asn	Pro	Glu	Leu	Ala	Asp	Glu	Ser	Asp	Arg	
		200					205					210				
gtg	gtc	acc	atg	gtt	gac	ggg	cgc	atc	att	ggg	tct	gag	gtg	aaa	cac	787
Val	Val	Thr	Met	Val	Asp	Gly	Arg	Ile	Ile	Gly	Ser	Glu	Val	Lys	His	
		215				220					225					
tca	tgagccttgc	agaatcaatt	ctt													813
Ser																
230																

&lt;210&gt; 512

&lt;211&gt; 230

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 512

```

Met Ser Leu Ile Glu Met Arg Asn Ile Val Lys Thr Tyr Asn Ile Gly
 1             5             10             15

Ser Glu Gly Glu Leu Thr Val Leu His Gly Val Asp Phe His Val Asp
      20             25             30

Arg Gly Glu Phe Val Ser Val Val Gly Thr Ser Gly Ser Gly Lys Ser
      35             40             45

Thr Met Met Asn Ile Ile Gly Leu Leu Asp Lys Pro Thr Asp Gly Thr
 50             55             60

Tyr Thr Leu Asp Gly Val Asp Val Leu Asp Ile Ser Asp Asp Ala Leu
 65             70             75             80

Ala Ser His Arg Ala Lys Ser Ile Gly Phe Val Phe Gln Asn Phe Asn
      85             90             95

Leu Ile Gly Arg Ile Asp Ala Leu Lys Asn Val Glu Met Pro Met Met
      100            105            110

Tyr Ala Gly Ile Pro Ala Lys Gln Arg Arg Ser Arg Ala Val Glu Leu
      115            120            125

Leu Glu Met Val Gly Met Gly Glu Arg Leu Asn His Glu Pro Asn Glu
      130            135            140

Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ala
      145            150            155            160

Asn Asp Pro Glu Ile Ile Leu Ala Asp Glu Pro Thr Gly Ala Leu Asp
      165            170            175

Ser Ala Thr Gly Arg Met Val Met Asp Ile Phe His Gln Leu Asn Lys
      180            185            190

Glu Gln Gly Lys Thr Ile Val Phe Ile Thr His Asn Pro Glu Leu Ala
      195            200            205

Asp Glu Ser Asp Arg Val Val Thr Met Val Asp Gly Arg Ile Ile Gly
      210            215            220

Ser Glu Val Lys His Ser
      225            230

```

&lt;210&gt; 513

&lt;211&gt; 1185

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1162)

&lt;223&gt; RXC01004

&lt;400&gt; 513

```

ccggacgctg gatcgacga gtaacggtca tggaagatcg acgcatcgac aaagccgttc 60
tcacccccat caccatgaa gaagcaaagg agtacgaaaa gtg agt att tgg gca 115
                                   Val Ser Ile Trp Ala
                                   1 5
act gtc ctt cta att atc gtc ctt ctt tcc gcc aac gcc ttc ttc gtg 163
Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala Asn Ala Phe Phe Val
                                   10 15 20
gcc gcg gag ttc gca ctg att tcc tcg cgc cgg gac cgc ctg gat tcc 211
Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg Asp Arg Leu Asp Ser
                                   25 30 35
ctg gta tcc cag ggt aaa aag gga gct gaa aag gtt ctc tac gca acc 259
Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys Val Leu Tyr Ala Thr
                                   40 45 50
gag cac ctc tcc atc atg ttg gcg ggc gct cag ttc ggt att acg gtc 307
Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln Phe Gly Ile Thr Val
                                   55 60 65
tgt tct ctg att ctg ggt aaa gtc gca gaa cct gcg atc gcc cac ttc 355
Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro Ala Ile Ala His Phe
                                   70 75 80 85
att gag gtg cct ttc acc tcc tgg ggt gtt cca aat gat ttg atc cac 403
Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro Asn Asp Leu Ile His
                                   90 95 100
cca att tcc ttc gtc atc gca ctg gcg atc atc acc tgg ttg cac att 451
Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile Thr Trp Leu His Ile
                                   105 110 115
ctc ttt ggt gaa atg gtg cca aag aac atc gct att gct ggc cct gaa 499
Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala Ile Ala Gly Pro Glu
                                   120 125 130
acc tta ggc atg tgg ctt gct cca gtg ctc att gcg ttt gtg aag att 547
Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile Ala Phe Val Lys Ile
                                   135 140 145
acc cgc ccg ttg atc gag ttc atg aac tgg atc gcc cgt ctg acc ctt 595
Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile Ala Arg Leu Thr Leu
                                   150 155 160 165
cgc gcc ttt ggt gtg gag caa aaa aac gag ctg gat tcc acc gtg gac 643
Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu Asp Ser Thr Val Asp
                                   170 175 180
cca gag cag ctg gca tca atg att tcc gag tcc cgt tcc gaa ggc ctc 691
Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser Arg Ser Glu Gly Leu
                                   185 190 195
ctt gat gct gaa gag cac gcc cgc ctg tcc aag gcg ctg cgc tct gag 739
Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys Ala Leu Arg Ser Glu
                                   200 205 210
cag cgt tcc atc aag gaa ctg gtg att aag gat gag gac gtg cgc acg 787
Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp Glu Asp Val Arg Thr

```

215	220	225	
ctg gcg ttc ggt aaa tct ggc ccg acc ttg cac cag ttg gag gaa gca			835
Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His Gln Leu Glu Glu Ala			
230	235	240	245
gtc cgc gag acc ggt ttc tcc cgc ttc cct gtc acc ggc cgc gat gga			883
Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val Thr Gly Arg Asp Gly			
250	255		260
tcc tac ttg ggt tat atc cac atc aag gat att ttg cct cgt ctg gct			931
Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile Leu Pro Arg Leu Ala			
265	270		275
gat cct gag atg gat ccc tcc gag acc att ccg cgt tct gca ctg cgc			979
Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro Arg Ser Ala Leu Arg			
280	285		290
cct ttg agc aat gtg gat gcc gac ggc ctc atg gat gac gtc ttg gat			1027
Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met Asp Asp Val Leu Asp			
295	300		305
ttt atg cac tac cgc tcc gcg cac atg gct cag gtt cgc ctc aaa ggt			1075
Phe Met His Tyr Arg Ser Ala His Met Ala Gln Val Arg Leu Lys Gly			
310	315		320
gag ctt ctc ggc gtg att acg ctg gag gat ctc atc gaa gaa tac gtg			1123
Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu Ile Glu Glu Tyr Val			
330	335		340
ggc acc gtc aac gat tgg act cac gaa agc tcc gac gac tagaaatagt			1172
Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser Asp Asp			
345	350		
aactgtgttg gac			1185

&lt;210&gt; 514

&lt;211&gt; 354

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 514

Val Ser Ile Trp Ala Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala
1 5 10 15

Asn Ala Phe Phe Val Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg
20 25 30

Asp Arg Leu Asp Ser Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys
35 40 45

Val Leu Tyr Ala Thr Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln
50 55 60

Phe Gly Ile Thr Val Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro
65 70 75 80

Ala Ile Ala His Phe Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro
85 90 95



```

Asn Asp Leu Ile His Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile
    100                      105                      110

Thr Trp Leu His Ile Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala
    115                      120                      125

Ile Ala Gly Pro Glu Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile
    130                      135                      140

Ala Phe Val Lys Ile Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile
    145                      150                      155                      160

Ala Arg Leu Thr Leu Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu
    165                      170                      175

Asp Ser Thr Val Asp Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser
    180                      185                      190

Arg Ser Glu Gly Leu Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys
    195                      200                      205

Ala Leu Arg Ser Glu Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp
    210                      215                      220

Glu Asp Val Arg Thr Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His
    225                      230                      235                      240

Gln Leu Glu Glu Ala Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val
    245                      250                      255

Thr Gly Arg Asp Gly Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile
    260                      265                      270

Leu Pro Arg Leu Ala Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro
    275                      280                      285

Arg Ser Ala Leu Arg Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met
    290                      295                      300

Asp Asp Val Leu Asp Phe Met His Tyr Arg Ser Ala His Met Ala Gln
    305                      310                      315                      320

Val Arg Leu Lys Gly Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu
    325                      330                      335

Ile Glu Glu Tyr Val Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser
    340                      345                      350

Asp Asp

```

&lt;210&gt; 515

&lt;211&gt; 732

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(709)

&lt;223&gt; RXC01017

&lt;400&gt; 515

```

gaaatttgag ggggcgctac ccttagaagg tgcgcaatga caccacgata gttcgcgcct 60

agtgtggatt gctagaaaac tttaagaaag aggaaataat atg gct caa aaa gta 115
                                         Met Ala Gln Lys Val
                                         1 5

acc ttc tgg ttc gat acc acc tgc cca ttc tgc tgg gtc acc tcc cgc 163
Thr Phe Trp Phe Asp Thr Thr Cys Pro Phe Cys Trp Val Thr Ser Arg
                        10 15 20

tgg att aag gaa gtc gaa caa gtc cgc gat att gaa atc cag tgg gtt 211
Trp Ile Lys Glu Val Glu Gln Val Arg Asp Ile Glu Ile Gln Trp Val
                        25 30 35

cca atg agc ctc gct gtc cta aac gaa ggc cgt gat ctc cca gag gat 259
Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg Asp Leu Pro Glu Asp
                        40 45 50

tac aag gag cgc atg aag gct gca tgg gga cca gca cgc gtt ttc gca 307
Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro Ala Arg Val Phe Ala
                        55 60 65

gct gtc gcc acc gac cat gct gac aag ctc ggc gac ctg tac acc gca 355
Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly Asp Leu Tyr Thr Ala
70 75 80 85

atg ggt acc cgc atc cac aac gac ggt cgc gga cca atc gaa ggt tcc 403
Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly Pro Ile Glu Gly Ser
90 95 100

ttc aat gat gtc atc gca gag gca ctt gaa gag gtc ggc cta gac gct 451
Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu Val Gly Leu Asp Ala
105 110 115

gca ctt ggt gaa gtt gca gac acc acc gaa tgg gac gac gca ctt cgc 499
Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp Asp Asp Ala Leu Arg
120 125 130

gca ttc cac cag acc gca atg gac gag gtc ggc aac gat gtc gga acc 547
Ala Phe His Gln Thr Ala Met Asp Glu Val Gly Asn Asp Val Gly Thr
135 140 145

cca gtg gtc aag ctc ggc gac acc gct ttc ttc ggc cca gtg ctc acc 595
Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe Gly Pro Val Leu Thr
150 155 160 165

cgc atc cca cgc ggc gag gaa gca gga gag atc ttc gac gct tcc ttc 643
Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile Phe Asp Ala Ser Phe
170 175 180

aag ctc gca agc tat ccc cac ttc ttt gaa atc aag cgc agc cgc act 691
Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile Lys Arg Ser Arg Thr
185 190 195

gag aac cca cag ttc gac taattaacgc tgtctctgct tat 732
Glu Asn Pro Gln Phe Asp
200

```

```
<400> 517
cgagaggctt ttttggtctt aagcctttta gtcgtgcgaa cgaaatctta agcagcctcg 60

gtgccaccga gatcgattgg tcgctgtaag gtatctgatt atg tcc agt tcc gaa 115
Met Ser Ser Ser Glu
```

	1	5	
agc tcg cgt tcc gaa ggc tcg cag cca gca ccg tct gta cag cct gaa			163
Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro Ser Val Gln Pro Glu			
	10	15	20
cgc cgt gct gat tca acg ggg gct cct gcg gca gct tcc aag gaa gct			211
Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala Ala Ser Lys Glu Ala			
	25	30	35
tcc caa caa atg gac gct gcc gga gtt ctt gag tgg gcc agg acc gct			259
Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu Trp Ala Arg Thr Ala			
	40	45	50
gtc gag cag ctt tct gaa cgt cgt gca gag atc aat gca ctg aat gtc			307
Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile Asn Ala Leu Asn Val			
	55	60	65
ttt cct gtt cca gat gca gac act gga tca aac atg acc tac acc atg			355
Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn Met Thr Tyr Thr Met			
	70	75	80
aca gct gcg ttg gat gaa gcg ctg aaa ctg ggg gag ttg ggt gat gtc			403
Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly Glu Leu Gly Asp Val			
	90	95	100
gca agg att act gag gct ttg gct gtt ggt tct gtg cgt gga gcc cga			451
Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser Val Arg Gly Ala Arg			
	105	110	115
gga aat tct gga gta gtc ctt agt cag gtc ctt cgc gct att gct cag			499
Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu Arg Ala Ile Ala Gln			
	120	125	130
gca gct gct gac ggg gtt att gat ggc cac aca atc caa gaa gcg cta			547
Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr Ile Gln Glu Ala Leu			
	135	140	145
tcc att gct cgc tcc cta gtt gat cgc gca att aca gat cct gtg gag			595
Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile Thr Asp Pro Val Glu			
	150	155	160
ggc act gtt gtc act gtg ttg cgt tct			622
Gly Thr Val Val Thr Val Leu Arg Ser			
	170		

&lt;210&gt; 518

&lt;211&gt; 174

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 518

Met Ser Ser Ser Glu Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro  
 1 5 10 15

Ser Val Gln Pro Glu Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala  
 20 25 30

Ala Ser Lys Glu Ala Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu  
 35 40 45

Trp Ala Arg Thr Ala Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile  
 50 55 60  
 Asn Ala Leu Asn Val Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn  
 65 70 75 80  
 Met Thr Tyr Thr Met Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly  
 85 90 95  
 Glu Leu Gly Asp Val Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser  
 100 105 110  
 Val Arg Gly Ala Arg Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu  
 115 120 125  
 Arg Ala Ile Ala Gln Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr  
 130 135 140  
 Ile Gln Glu Ala Leu Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile  
 145 150 155 160  
 Thr Asp Pro Val Glu Gly Thr Val Val Thr Val Leu Arg Ser  
 165 170

<210> 519  
 <211> 1047  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1024)  
 <223> RXC01212

<400> 519  
 tttagaagcc acatgacata tgtcatgaaa attatgtgca aagtgcagta atactcctga 60  
 catatggctc taccagcgcc aatgcgaagt aggaagaatt atg cct atg aca acg 115  
 Met Pro Met Thr Thr  
 1 5  
 aca cca gca atc gac gta aca gac ctc gtg aga acc tac ggc gac tac 163  
 Thr Pro Ala Ile Asp Val Thr Asp Leu Val Arg Thr Tyr Gly Asp Tyr  
 10 15 20  
 acc gca gtc aag ggc ctg aat ttc cat gta cag cgc ggt gaa gta ttt 211  
 Thr Ala Val Lys Gly Leu Asn Phe His Val Gln Arg Gly Glu Val Phe  
 25 30 35  
 ggt ctg ctc ggc acc aac ggg gcc ggc aaa acc tcc acc ttg gaa gtc 259  
 Gly Leu Leu Gly Thr Asn Gly Ala Gly Lys Thr Ser Thr Leu Glu Val  
 40 45 50  
 atc gaa gga ctt tcc gca ccc agc tcc ggc acc gtg cgc atc tcc ggg 307  
 Ile Glu Gly Leu Ser Ala Pro Ser Ser Gly Thr Val Arg Ile Ser Gly  
 55 60 65  
 ctt gac ccc gtt gcc gac cgc gcg atc ctg cgc ccc gag ctc ggc atc 355  
 Leu Asp Pro Val Ala Asp Arg Ala Ile Leu Arg Pro Glu Leu Gly Ile

70	75	80	85	
atg ctg caa tca ggc ggc ctg cca tca cag ctc acc gtc gcc gaa acc				403
Met Leu Gln Ser Gly Gly Leu Pro Ser Gln Leu Thr Val Ala Glu Thr	90	95	100	
atg gac atg tgg cac ggc acc tgc acg tat ccg cgc gcc att aaa gat				451
Met Asp Met Trp His Gly Thr Cys Thr Tyr Pro Arg Ala Ile Lys Asp	105	110	115	
gtg ctt gcc gac gtc gac ctc cta cac cgc gaa aac gtc aag gtc ggc				499
Val Leu Ala Asp Val Asp Leu Leu His Arg Glu Asn Val Lys Val Gly	120	125	130	
gcg ctt tcc gga ggc gaa caa cga cgc ctt gat ttg gcc tgc gca ctg				547
Ala Leu Ser Gly Gly Glu Gln Arg Arg Leu Asp Leu Ala Cys Ala Leu	135	140	145	
ctt ggc gac ccc tca att ttg ttc ctc gac gaa ccc acc acc ggc ctc				595
Leu Gly Asp Pro Ser Ile Leu Phe Leu Asp Glu Pro Thr Thr Gly Leu	150	155	160	165
gac cca gaa tct agg cgc cac acc tgg caa ctc ctg ctg gac ctg aaa				643
Asp Pro Glu Ser Arg Arg His Thr Trp Gln Leu Leu Leu Asp Leu Lys	170	175	180	
cag cgc ggc gtc acc atg atg ctg acc acc cac tac ctg gag gaa gcc				691
Gln Arg Gly Val Thr Met Met Leu Thr Thr His Tyr Leu Glu Glu Ala	185	190	195	
gaa ttc ctc tgc gac cgg att gcc atc atg aac gcc ggt gag atc gca				739
Glu Phe Leu Cys Asp Arg Ile Ala Ile Met Asn Ala Gly Glu Ile Ala	200	205	210	
gtg gaa ggc acc ttg gat gaa ctg gtg gcc cgc gag aag tcg atc atc				787
Val Glu Gly Thr Leu Asp Glu Leu Val Ala Arg Glu Lys Ser Ile Ile	215	220	225	
agt ttc gtg ctg cgt ggc ggg cag gtg gag ttg ccg gtc ttg agt ggg				835
Ser Phe Val Leu Arg Gly Gly Gln Val Glu Pro Val Leu Ser Gly	230	235	240	245
gct gaa atc atc cgc gac aac aac cac gtc cgc atc gcc acc acc acc				883
Ala Glu Ile Ile Arg Asp Asn Asn His Val Arg Ile Ala Thr Thr Thr	250	255	260	
ctg cag cag cac acc tta gaa ata ctt acc tgg gct gca gag acc ggg				931
Leu Gln Gln His Thr Leu Glu Ile Leu Thr Trp Ala Ala Glu Thr Gly	265	270	275	
atc gcg ctg gaa ggc ttc gct gca aaa ccc gcc acc ttg gaa tcc gta				979
Ile Ala Leu Glu Gly Phe Ala Ala Lys Pro Ala Thr Leu Glu Ser Val	280	285	290	
ttc atg gac atc gcc tca ctc gag aac acc tcg ctg caa acc gcc				1024
Phe Met Asp Ile Ala Ser Leu Glu Asn Thr Ser Leu Gln Thr Ala	295	300	305	
tagaatcttt aaggagacca caa				1047

<210> 520  
 <211> 308  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 520

```

Met Pro Met Thr Thr Thr Pro Ala Ile Asp Val Thr Asp Leu Val Arg
 1              5              10              15

Thr Tyr Gly Asp Tyr Thr Ala Val Lys Gly Leu Asn Phe His Val Gln
      20              25              30

Arg Gly Glu Val Phe Gly Leu Leu Gly Thr Asn Gly Ala Gly Lys Thr
      35              40              45

Ser Thr Leu Glu Val Ile Glu Gly Leu Ser Ala Pro Ser Ser Gly Thr
 50              55              60

Val Arg Ile Ser Gly Leu Asp Pro Val Ala Asp Arg Ala Ile Leu Arg
 65              70              75              80

Pro Glu Leu Gly Ile Met Leu Gln Ser Gly Gly Leu Pro Ser Gln Leu
      85              90              95

Thr Val Ala Glu Thr Met Asp Met Trp His Gly Thr Cys Thr Tyr Pro
      100             105             110

Arg Ala Ile Lys Asp Val Leu Ala Asp Val Asp Leu Leu His Arg Glu
      115             120             125

Asn Val Lys Val Gly Ala Leu Ser Gly Gly Glu Gln Arg Arg Leu Asp
      130             135             140

Leu Ala Cys Ala Leu Leu Gly Asp Pro Ser Ile Leu Phe Leu Asp Glu
      145             150             155             160

Pro Thr Thr Gly Leu Asp Pro Glu Ser Arg Arg His Thr Trp Gln Leu
      165             170             175

Leu Leu Asp Leu Lys Gln Arg Gly Val Thr Met Met Leu Thr Thr His
      180             185             190

Tyr Leu Glu Glu Ala Glu Phe Leu Cys Asp Arg Ile Ala Ile Met Asn
      195             200             205

Ala Gly Glu Ile Ala Val Glu Gly Thr Leu Asp Glu Leu Val Ala Arg
      210             215             220

Glu Lys Ser Ile Ile Ser Phe Val Leu Arg Gly Gly Gln Val Glu Leu
      225             230             235             240

Pro Val Leu Ser Gly Ala Glu Ile Ile Arg Asp Asn Asn His Val Arg
      245             250             255

Ile Ala Thr Thr Thr Leu Gln Gln His Thr Leu Glu Ile Leu Thr Trp
      260             265             270

Ala Ala Glu Thr Gly Ile Ala Leu Glu Gly Phe Ala Ala Lys Pro Ala
      275             280             285

Thr Leu Glu Ser Val Phe Met Asp Ile Ala Ser Leu Glu Asn Thr Ser

```

290 295 300

Leu Gln Thr Ala  
305

<210> 521  
<211> 1131  
<212> DNA  
<213> *Corynebacterium glutamicum*

<220>  
<221> CDS  
<222> (101)..(1108)  
<223> RXC01306

<400> 521  
tgtttttagag gtagagcgaa acgtgcctgt aaaactggcg ctcgctgtgc tcgaagacca 60  
cccagacaat caccocgctc cgaaggagaa tcgctaagcc atg act gaa tgg tat 115  
Met Thr Glu Trp Tyr  
1 5  
gtc gtt tta ccc gcc act att cta ctc atc gcg ctg tct gcg ttt ttc 163  
Val Val Leu Pro Ala Thr Ile Leu Leu Ile Ala Leu Ser Ala Phe Phe  
10 15 20  
gtc atc att gag ttc gct ttg ctt gca gct agg cgg aac cgg tta gag 211  
Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg Arg Asn Arg Leu Glu  
25 30 35  
gag act gtg gaa acc tcg cgg tct tcc cgc gct gcg ttg cga agc ctc 259  
Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala Ala Leu Arg Ser Leu  
40 45 50  
aat gaa ctt act ctc atg ctc gcg ggc gcg cag ttg gga atc acc atg 307  
Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln Leu Gly Ile Thr Met  
55 60 65  
gtg act ttc gcg ttg ggt gct atc acg aag ccg tgg gtt cat tat gct 355  
Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro Trp Val His Tyr Ala  
70 75 80 85  
ttg atg ccg ctc ttc gaa tgg gcg cgt ata ccg ctg gtt atg gca gat 403  
Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro Leu Val Met Ala Asp  
90 95 100  
gtc att gcg ttt att ttg tcg ctg ttt atc gta acg ttt ctg cac ttg 451  
Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val Thr Phe Leu His Leu  
105 110 115  
gtc atc ggc gaa atg gct ccg aaa tcc tgg gca atc gcg cat ccg gag 499  
Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala Ile Ala His Pro Glu  
120 125 130  
acg gca ctt cga act atc gcg att ccc gca cgg ggc ttc att aac ctg 547  
Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg Gly Phe Ile Asn Leu  
135 140 145  
ttt cgt cca ttg ctg cag tgg atc aac aaa atg gcg aac gat ttg gtc 595  
Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met Ala Asn Asp Leu Val



150	155	160	165	
cgc aaa gtt ggt gaa act ccc gtt gat cga gct gca gct ggt ggc tat				643
Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala Ala Ala Gly Gly Tyr				
170		175	180	
gac acc gat acc ctc cat gcc ctc att gag cat tcc cga gaa act ggc				691
Asp Thr Asp Thr Leu His Ala Leu Ile Glu His Ser Arg Glu Thr Gly				
185		190	195	
gct ctg gat cag caa tcc gcc gcc caa atc agc gga att atc aag ctg				739
Ala Leu Asp Gln Ser Ala Ala Gln Ile Ser Gly Ile Ile Lys Leu				
200		205	210	
gat aaa atc acg gtc ggt caa acc ctg acc gca tct cca ttt acg cac				787
Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala Ser Pro Phe Thr His				
215		220	225	
agc gcc agc gcc acg gtt gct gag gtg caa gcc gca gct cag cgc agt				835
Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala Ala Ala Gln Arg Ser				
230		235	240	245
ggc agc ttg cgt gtg ctt atc gac gcc ccc tcc cac ctt ttc cca cac				883
Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser His Leu Phe Pro His				
250		255	260	
gtc att cat gtg cga gac acc ctt ggt gcc tcg cca gac gag aag gct				931
Val Ile His Val Arg Asp Thr Leu Gly Ala Ser Pro Asp Glu Lys Ala				
265		270	275	
tcg aag tgg tct cgc cca atc ctc acc gtt gct gag acc gac acg tta				979
Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala Glu Thr Asp Thr Leu				
280		285	290	
cac caa gcg ctg gaa tac atg cgg gag cat aac gag cag atc agt gcg				1027
His Gln Ala Leu Glu Tyr Met Arg Glu His Asn Glu Gln Ile Ser Ala				
295		300	305	
gtg ctt tcc gct gat ggg aaa acg gtg ctt ggt gta ata act tgg gat				1075
Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly Val Ile Thr Trp Asp				
310		315	320	325
cac atc ttg aaa tac ctg tgg cct gca tcg gtg tagctaattt gaggtgcgct				1128
His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val				
330		335		
gaa				1131
<210> 522				
<211> 336				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 522				
Met Thr Glu Trp Tyr Val Val Leu Pro Ala Thr Ile Leu Leu Ile Ala				
1	5	10	15	
Leu Ser Ala Phe Phe Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg				
20	25	30		

Arg Asn Arg Leu Glu Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala  
 35 40 45  
 Ala Leu Arg Ser Leu Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln  
 50 55 60  
 Leu Gly Ile Thr Met Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro  
 65 70 75 80  
 Trp Val His Tyr Ala Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro  
 85 90 95  
 Leu Val Met Ala Asp Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val  
 100 105 110  
 Thr Phe Leu His Leu Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala  
 115 120 125  
 Ile Ala His Pro Glu Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg  
 130 135 140  
 Gly Phe Ile Asn Leu Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met  
 145 150 155 160  
 Ala Asn Asp Leu Val Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala  
 165 170 175  
 Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala Leu Ile Glu His  
 180 185 190  
 Ser Arg Glu Thr Gly Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser  
 195 200 205  
 Gly Ile Ile Lys Leu Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala  
 210 215 220  
 Ser Pro Phe Thr His Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala  
 225 230 235 240  
 Ala Ala Gln Arg Ser Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser  
 245 250 255  
 His Leu Phe Pro His Val Ile His Val Arg Asp Thr Leu Gly Ala Ser  
 260 265 270  
 Pro Asp Glu Lys Ala Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala  
 275 280 285  
 Glu Thr Asp Thr Leu His Gln Ala Leu Glu Tyr Met Arg Glu His Asn  
 290 295 300  
 Glu Gln Ile Ser Ala Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly  
 305 310 315 320  
 Val Ile Thr Trp Asp His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val  
 325 330 335

<400> 524  
Val Ser Gln Phe Arg Arg Cys Ser Arg Pro Gly Cys Gly Lys Pro Ala  
1 5 10 15

Val Ala Thr Leu Thr Tyr Ala Tyr Ser Asp Ser Thr Ala Val Val Gly  
                   20                  25                  30

Pro Leu Ala Pro Ala Ala Glu Pro His Ser Trp Asp Leu Cys Glu His  
                   35                  40                  45

His Ala Glu Arg Ile Thr Ala Pro Leu Gly Trp Glu Met Leu Arg Val  
                   50                  55                  60

Asn Asp Ile Lys Val Asp Asp Asp Glu Asp Leu Thr Ala Leu Ala Gln  
                   65                  70                  75                  80

Ala Val Arg Glu Ala Gly Arg Thr Val Ser Gly Leu Val Pro Glu Asp  
                   85                  90                  95

Glu Val Gly Gly Asn His Pro Val Asn Arg Ser Ala Arg Ile Ala Glu  
                   100                  105                  110

Gln Lys Val His Arg Arg Gly His Leu Tyr Val Val Pro Asp Gln Asp  
                   115                  120                  125

Glu Ser  
                   130

<210> 525  
 <211> 614  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(591)  
 <223> RXC01372

<400> 525  
 cag gac acc ttc gtc ctt ccc acc ttg ccc acg gcc gca ggc ttg tcg 48  
 Gln Asp Thr Phe Val Leu Pro Thr Leu Pro Thr Ala Ala Gly Leu Ser  
   1                  5                  10                  15

cct gcc cgc atc gtg gcg tcg ata agc act ctt tta gat ctt tta gaa 96  
 Pro Ala Arg Ile Val Ala Ser Ile Ser Thr Leu Leu Asp Leu Leu Glu  
                   20                  25                  30

gca gac ccc agc att att tcc gac cgc ttg gaa cac ctc gcc gac tgc 144  
 Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys  
                   35                  40                  45

att gat gag gaa gtg gaa tcg cta tcg ccg gaa cgt gac gaa cta gtc 192  
 Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val  
                   50                  55                  60

aat ccc ggc cga aaa ctg cgc gca tac gta gat cac gca cgg atc gtg 240  
 Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val  
                   65                  70                  75                  80

cat acc ggc cga act gat gtg gga ctc gcg att gcc aac gtt atc gcc 288  
 His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala  
                   85                  90                  95

cca atc tgg acc cga cga ggc ctg gta tca gcc gtg ctg gat ttt ccc 336

Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro  
 100 105 110

gag ctc atg gaa tca ttg ccg gaa ctc cgc gga ccc gag cca att acc 384  
 Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr  
 115 120 125

gac gat ata ttc cat gac cca ttc ata gat gac gaa ccc ggg gtg gta 432  
 Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val  
 130 135 140

ccg ttt agg gct gtt gtc tgg gcc gaa gag gaa ccc gga atc ccc gat 480  
 Pro Phe Arg Ala Val Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp  
 145 150 155 160

gcc atg gcg caa agc tgc gac gga cct agc aaa ggg gcg ctg aca caa 528  
 Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln  
 165 170 175

gca ctg cgt ttg ctg gtg cgc gga cag tca gcc acg acc tat tcc att 576  
 Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile  
 180 185 190

gaa gaa aag gac ttg taaatggagc tattggaagg ctc 614  
 Glu Glu Lys Asp Leu  
 195

---

<210> 526  
 <211> 197  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 526  
 Gln Asp Thr Phe Val Leu Pro Thr Leu Pro Thr Ala Ala Gly Leu Ser  
 1 5 10 15

Pro Ala Arg Ile Val Ala Ser Ile Ser Thr Leu Leu Asp Leu Leu Glu  
 20 25 30

Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys  
 35 40 45

Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val  
 50 55 60

Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val  
 65 70 75 80

His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala  
 85 90 95

Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro  
 100 105 110

Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr  
 115 120 125

Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val  
 130 135 140

Pro Phe Arg Ala Val Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp  
 145 150 155 160

Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln  
 165 170 175

Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile  
 180 185 190

Glu Glu Lys Asp Leu  
 195

<210> 527  
 <211> 669  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(646)  
 <223> RXC01659

<400> 527

ttgatgcgcg ccgcggtgag cagcctgccg atccagagcg tgaagaatct gatgatttag 60

tcgagattga taccgtctct ggattccgcc tgctcagtag gtg gcg ggg gtt gcg 115  
 Val Ala Gly Val Ala  
 1 5

cag cgt ttt gtc gac gag cgc att cac gtc ggt ttg gat tcc atg cca 163  
 Gln Arg Phe Val Asp Glu Arg Ile His Val Gly Leu Asp Ser Met Pro  
 10 15 20

gaa gct gtg act gct gtg tgg atg gaa tct gat tgg gtg ttg gcg gaa 211  
 Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp Trp Val Leu Ala Glu  
 25 30 35

acc atc aag ggt tcc acg cct tcc gat tgg gaa gag att ttg cgg ccg 259  
 Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu Glu Ile Leu Arg Pro  
 40 45 50

ttg gcg ctg ctc acg gac gcg tct ttc acg ttg cca cct cgt tcc acg 307  
 Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu Pro Pro Arg Ser Thr  
 55 60 65

cgt gcg caa acc ttg gat ttg aag cat ttg gaa cca agc cgt ctg aag 355  
 Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu Pro Ser Arg Leu Lys  
 70 75 80 85

ccg gag cag cca gaa aag cca gcg ttt act ccc aat gct tcg gaa gaa 403  
 Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro Asn Ala Ser Glu Glu  
 90 95 100

gat ttg tct cag ccg ttg gtg atc cgc ccc gag gag ccg ttg cag atg 451  
 Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu Glu Pro Leu Gln Met  
 105 110 115

ccg gtt cgc ggt gtg cag gaa agc cgc gga gtg gtc gag cca cgg tca 499  
 Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val Val Glu Pro Arg Ser  
 120 125 130

ttg ggt gcg gat gat gtg gag tcg att gcg gag ggc gat cca gag cgt 547  
 Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu Gly Asp Pro Glu Arg  
 135 140 145  
 ccg agc gat ctt tat ggc acg cgt gtg ctg cgt gat ctc aat ggt cag 595  
 Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg Asp Leu Asn Gly Gln  
 150 155 160 165  
 tcc agt att ttc caa gat tcc acc gac gcg gat gag cca cca aaa aag 643  
 Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp Glu Pro Pro Lys Lys  
 170 175 180  
 tgg tagaaaactg gtgtttttcg gcc 669  
 Trp

<210> 528  
 <211> 182  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 528  
 Val Ala Gly Val Ala Gln Arg Phe Val Asp Glu Arg Ile His Val Gly  
 1 5 10 15  
 Leu Asp Ser Met Pro Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp  
 20 25 30  
 Trp Val Leu Ala Glu Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu  
 35 40 45  
 Glu Ile Leu Arg Pro Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu  
 50 55 60  
 Pro Pro Arg Ser Thr Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu  
 65 70 75 80  
 Pro Ser Arg Leu Lys Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro  
 85 90 95  
 Asn Ala Ser Glu Glu Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu  
 100 105 110  
 Glu Pro Leu Gln Met Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val  
 115 120 125  
 Val Glu Pro Arg Ser Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu  
 130 135 140  
 Gly Asp Pro Glu Arg Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg  
 145 150 155 160  
 Asp Leu Asn Gly Gln Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp  
 165 170 175  
 Glu Pro Pro Lys Lys Trp  
 180